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(54) Title: GENES FOR MODIFYING PLANT TRAITS IV

(57) Abstract: The invention relates to plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and methods of using the polynucleotides and polypeptides to produce transgenic plants having advantageous properties compared to a reference plant. Sequence information related to these polynucleotides and polypeptides can also be used in bioinformatic search methods and is also disclosed.

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GENES FOR MODIFYING PLANT TRAITS IV

This application claims priority benefit of: prior U.S application entitled "Plant Trait Modification III," serial no. 60/227,439, filed August 22, 2000; prior U.S. application entitled
5 "Genes for Modifying Plant Traits," attorney docket number MBI-0022, serial no. _____, filed November 16, 2000; and prior U.S. application entitled "Genes for Modifying Plant Traits II," serial no. 09/837,944, filed April 18, 2001. The entire content of each of these applications is hereby incorporated by reference.

10 Field of the Invention and Introduction

This invention relates to the field of plant biology. More particularly, the present invention pertains to compositions and methods for phenotypically modifying a plant.

A plant's traits, such as its biochemical, developmental, or phenotypic characteristics, can be
15 controlled through a number of cellular processes. One important way to manipulate that control is through transcription factors - proteins that influence the expression of a particular gene or sets of genes. Transgenic plants that comprise cells having altered levels of at least one selected transcription factor, for example, possess advantageous or desirable traits. Strategies for manipulating traits by altering a plant cell's transcription factor content can therefore result in
20 plants and crops with commercially valuable properties. Applicants have identified polynucleotides encoding transcription factors, developed numerous transgenic plants using these polynucleotides, and have analyzed the plants for a variety of important traits. In so doing, applicants have identified important polynucleotide and polypeptide sequences for producing commercially valuable plants and crops as well as the methods for making them and using them.
25 Other aspects and embodiments of the invention are described below and can be derived from the teachings of this disclosure as a whole.

Background of the Invention

Transcription factors can modulate gene expression, either increasing or decreasing (inducing or
30 repressing) the rate of transcription. This modulation results in differential levels of gene expression at various developmental stages, in different tissues and cell types, and in response to different exogenous (e.g., environmental) and endogenous stimuli throughout the life cycle of the organism.

35 Because transcription factors are key controlling elements of biological pathways, altering the expression levels of one or more transcription factors can change entire biological pathways in an

organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits.

The present invention provides novel transcription factors useful for modifying a plant's phenotype in desirable ways.

Summary of the Invention

In a first aspect, the invention relates to a recombinant polynucleotide comprising a nucleotide sequence selected from: (a) a nucleotide sequence of the Sequence Listing, or SEQ ID Nos.: 2N-1 where N=1-232, preferably where N=1-232, or a nucleotide sequence encoding a polypeptide comprising an amino acid sequence selected from those of the Sequence Listing, or SEQ ID Nos.: 2N where N=1-232, or a complementary nucleotide sequence of any of these; (b) a nucleotide sequence encoding a polypeptide comprising a variant of a polypeptide of (a) or a variant having one or more, or between 1 and about 5, or between 1 and about 10, or between 1 and about 30, conservative amino acid substitutions; (c) a nucleotide sequence comprising a sequence selected from SEQ ID Nos.: 2N-1 where N=1-232, or a complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising one or more silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence that hybridizes under stringent conditions, high stringent conditions, ultra-high stringent conditions, or ultra-ultra-high stringent conditions over substantially the entire length of a nucleotide sequence of one or more of (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides of a sequence of any of (a)-(e), or at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides outside of a region encoding a conserved domain of any of (a)-(e); (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's characteristic, functions as a transcription factor, results in ectopic expression or altered expression in a transgenic plant, or alters the level of transcription of a gene or transgene in a cell; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60%, or at least 70 %, or at least 80 %, or at least 90 %, or at least 95 % sequence identity to a nucleotide sequence of any of (a)-(g) or a 10 or 15 nucleotide, or at least about 20, or at least about 30 nucleotide region of a sequence of (a)-

(g) that is outside of a region encoding a conserved domain; (j) a nucleotide sequence that encodes a polypeptide having at least 31% sequence identity to a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232; (k) a nucleotide sequence that encodes a polypeptide having at least 60%, or at least 70 %, or at least 80%, or at least 90 %, or at least 95 % sequence identity to a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232; and (l) a nucleotide sequence that encodes a conserved domain of a polypeptide having at least 85%, or at least 90%, or at least 95%, or at least 98% sequence identity to a conserved domain of a polypeptide listed in the Sequence Listing, or SEQ ID No.: 2N-1 where N=1-232. A recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-specific promoter operably linked to a nucleotide sequence listed above. The invention also relates to compositions comprising at least two of the above-described polynucleotides.

In a second aspect, the invention comprises an isolated or recombinant polypeptide having an amino acid sequence of the Sequence Listing, or SEQ ID Nos.: 2N-1 where N=1-232, or a polypeptide comprising a subsequence of at least about 10, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above, or comprising a subsequence of at least about 8, or at least about 12, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids outside of a conserved domain.

In another aspect, the invention is a transgenic plant comprising one or more of the above-described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above-described polypeptide. Further, the invention is a plant lacking a nucleotide sequence encoding a polypeptide described above or substantially lacking a polypeptide described above. The plant may be any appropriate plant, including, but not limited to, *Arabidopsis*, mustard, soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, sugarbeet, canola, peanut, rosaceous fruits, vegetable brassicas, and mint or other labiates.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase, a polymerase and a primer, a cloning vector, or with a cell.

5 Furthermore, the invention relates to a method for producing a plant having a modified trait. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for a modified trait.

10 In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the
15 polypeptide to a promoter sequence, or by detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity
20 or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in a cell of the plant, the expression level of the polypeptide in a cell of the plant, and the modulation of an activity of the polypeptide in a cell of the plant.

25 In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a sequence of the Sequence Listing, SEQ ID Nos.: 1-464, to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium
30 may comprise a link between one or more sequence strings to a modified plant trait.

In yet another aspect, the invention is a method for identifying a sequence similar to or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database, and
35 querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides, such as those of SEQ ID Nos.: 1-464,

to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences. Such a method may also be a method of identifying a homolog sequence from a database, where the database comprises a plurality of known plant sequences. These sequences can be ESTs, cDNA, or genomic fragments. The database may contain sequences that are not "known" in addition to the known sequences, in that sequences may not be assigned or linked to a function or particular characteristic, yet the sequence itself is known. The method of identifying a homolog comprises inputting sequence information selected from one or more of SEQ ID Nos. 1-464; and querying the database to identify a homolog sequence. In this way, homolog sequences from any number of plant species, cultivars, or strains can be identified from the information of an inputted sequence or a fragment of the sequence. For these methods and for the sequence information, a computer readable medium having stored sequence information of one or more of SEQ ID Nos.: 1-464, or 1-37, or any one particular SEQ ID No., or any group of SEQ ID Nos. in between 1 and 464, can be used. The computer readable medium may include, for example, a floppy disc, a hard drive, random access memory (RAM), read only memory (ROM), and/or CD-ROM.

A method of the invention may comprise linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant phenotype.

20 Brief Description of the Sequence Listing and the Appendices

The Sequence Listing provides exemplary polynucleotide (SEQ ID Nos.: 2N-1 where N=1-232) and polypeptide (SEQ ID Nos.: 2N where N=1-232) sequences of the invention. The traits associated with the use of the sequences are included in the Examples or the Appendices.

The Tables of the Appendices include homologous sequences and homologs of specific polynucleotides and polypeptides, specific information about those sequences, and data concerning exemplary transgenic plants of the invention. The data and sequence information can be prepared according to the methods of the Examples or those known in the art. The Appendices include the Tables of this Appendix and those in the files of the Appendices of the priority documents.

Table 3 in the Appendix is a list of: the first 332 sequences from the Sequence Listing; the corresponding GID number (i.e. G28) used throughout to refer to both the cDNA and protein sequence of a particular transcription factor, and referred to or used in the Appendices of the U.S.

priority documents; and the identification of conserved amino acid domain start and stop sites (conserved domain) within the protein sequence.

5 Table 4 in the Appendix is a list of: selected sequences from the Sequence Listing; their corresponding GID number; the type of transgenic plant produced to determine ectopic expression, altered expression, or trait (either Knockout or overexpressor as in the Examples); and general descriptions and specific characteristics of the transgenic plant's traits as compared to a wild type, reference, or control plant.

10 Table 5 of the Appendix is a list of: selected sequences from the Sequence Listing; their corresponding GID number; the identification of the one or more homolog sequences and the corresponding GID numbers; the type of sequence of the particular SEQ ID No.; and the identification of conserved amino acid domain start and stop sites (conserved domain) within the protein sequence.

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Table 6 of the Appendix is a list of selected homologs identified from genomic, EST, or other database, as referred to in the Examples. Table 6 includes: the particular SEQ ID No. in the Sequence Listing used to identify exemplary homologs; the corresponding GID number of the SEQ ID No. sequence; the Genbank NID reference number associated with the exemplary
20 homolog identified (from which one of skill in the art can produce a genomic, cDNA, and/or EST sequence and corresponding polynucleotide); the P-value related to the particular, exemplary homolog comparison to the GID sequence; the percent identity between the GID sequence and the homolog; and the species the exemplary homolog sequence is derived from. All of the sequences referred to in the Table, as well as fragments or parts of these sequences,
25 can be used in accordance with this invention, for example to produce transgenic plants with ectopic expression or altered expression.

Detailed Description of Exemplary Embodiments

In an important aspect, the present invention relates to polynucleotides and polypeptides, e.g. for
30 modifying phenotypes of plants. Throughout this disclosure, various information sources are referred to and/or are specifically incorporated. The information sources include scientific journal articles, patent documents, textbooks, and web pages, for example. While the reference to these information sources clearly indicates that they can be used by one of skill in the art, applicants specifically incorporate each and every one of the information sources cited herein, in
35 their entirety, whether or not a specific mention of "incorporation by reference" is noted. The

contents and teachings of each and every one of the information sources can be relied on and used to make and use embodiments of the invention.

The polynucleotides of the invention encode plant transcription factors or fragments of them.

- 5 As one of ordinary skill in the art recognizes, transcription factors can be identified by the presence of a region or domain of structural similarity or identity to a specific consensus sequence or the presence of a specific consensus DNA-binding site (*see, for example*, Riechmann *et al.*, *Science* 290: 2105-2110 (2000)). The plant transcription factors may belong to one of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family
- 10 (Riechmann and Meyerowitz (1998) *Biol. Chem.* 379:633-646); the MYB transcription factor family (Martin and Paz-Ares, (1997) *Trends Genet.* 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *Biol. Chem.* 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the ankyrin-repeat protein family (Zhang *et al.* (1992) *Plant Cell* 4:1575-1588); the zinc finger protein (Z)
- 15 family (Klug and Schwabe (1995) *FASEB J.* 9: 597-604); the homeobox (HB) protein family (Duboule (1994) *Guidebook to the Homeobox Genes*, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein *et al.* (1996) *Mol. Gen. Genet.* 250:7-16); the NAM protein family (Souer *et al.* (1996) *Cell* 85:159-170); the IAA/AUX proteins (Rouse *et al.*
- 20 (1998) *Science* 279:1371-1373); the HLH/MYC protein family (Littlewood *et al.* (1994) *Prot. Profile* 1:639-709); the DNA-binding protein (DBP) family (Tucker *et al.* (1994) *EMBO J.* 13:2994-3002); the bZIP family of transcription factors (Foster *et al.* (1994) *FASEB J.* 8:192-200); the Box P-binding protein (the BPF-1) family (da Costa e Silva *et al.* (1993) *Plant J.* 4:125-135); the high mobility group (HMG) family (Bustin and Reeves (1996) *Prog. Nucl.*
- 25 *Acids Res. Mol. Biol.* 54:35-100); the scarecrow (SCR) family (Di Laurenzio *et al.* (1996) *Cell* 86:423-433); the GF14 family (Wu *et al.* (1997) *Plant Physiol.* 114:1421-1431); the polycomb (PCOMB) family (Kennison (1995) *Annu. Rev. Genet.* 29:289-303); the teosinte branched (TEO) family (Luo *et al.* (1996) *Nature* 383:794-799); the ABI3 family (Giraudat *et al.* (1992) *Plant Cell* 4:1251-1261); the triple helix (TH) family (Dehesh *et al.* (1990) *Science* 250:1397-1399); the
- 30 EIL family (Chao *et al.* (1997) *Cell* 89:1133-44); the AT-HOOK family (Reeves and Nissen (1990) *Journal of Biological Chemistry* 265:8573-8582); the S1FA family (Zhou *et al.* (1995) *Nucleic Acids Res.* 23:1165-1169); the bZIPT2 family (Lu and Ferl (1995) *Plant Physiol.* 109:723); the YABBY family (Bowman *et al.* (1999) *Development* 126:2387-96); the PAZ family (Bohmert *et al.* (1998) *EMBO J.* 17:170-80); a family of miscellaneous (MISC)
- 35 transcription factors including the DPBF family (Kim *et al.* (1997) *Plant J.* 11:1237-1251) and the SPF1 family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the golden

(GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936), the TUBBY family (Boggin et al, (1999) *Science* 286:2119-2125), the heat shock family (Wu C (1995) *Annu Rev Cell Dev Biol* 11:441-469), the ENBP family (Christiansen et al (1996) *Plant Mol Biol* 32:809-821), the RING-zinc family (Jensen et al. (1998) *FEBS letters* 436:283-287), the PDBP family (Janik et al
5 *Virology*. (1989) 168:320-329), the PCF family (Cubas P, et al. *Plant J.* (1999) 18:215-22), the SRS (SHI-related) family (Fridborg et al *Plant Cell* (1999) 11:1019-1032), the CPP (cysteine-rich polycomb-like) family (Cvitanich et al *Proc. Natl. Acad. Sci. U S A.* (2000) 97:8163-8168), the ARF (auxin response factor) family (Ulmasov, et al. (1999) *Proc. Natl. Acad. Sci. USA* 96: 5844-5849), the SWI/SNF family (Collingwood et al *J. Mol. End.* 23:255-275), the ACBF
10 family (Seguin et al *Plant Mol Biol.* (1997) 35:281-291), PCGL (CG-1 like) family (*Plant Mol Biol.* (1994) 25:921-924) the ARID family (Vazquez et al *Development.* (1999) 126: 733-42), the Jumonji family, Balciunas et al (*Trends Biochem Sci.* (2000) 25: 274-276), the bZIP-NIN family (Schauser et al *Nature.* (1999) 402: 191-195), the E2F family Kaelin et al (1992) *Cell* 70: 351-364) and the GRF-like family (Knaap et al (2000) *Plant Physiol.* 122: 695-704. As indicated by
15 any part of the list above and as known in the art, transcription factors have been sometimes categorized by class, family, and sub-family according to their structural content and consensus DNA-binding site, for example. All of the classes and many of the families and sub-families are listed here. However, the inclusion of one sub-family and not another, or the inclusion of one family and not another, does not mean that the invention does not encompass polynucleotides or
20 polypeptides of a certain family or sub-family. The list provided here is merely an example of the types of transcription factors and the knowledge available concerning the consensus sequences and DNA-binding site motifs that help define them (each of the references noted above are specifically incorporated herein by reference).

25 In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e, expression) of proteins; as regulators of plant gene expression; as diagnostic probes for the presence of complementary or partially complementary nucleic acids
30 (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like; as substrates for cloning e.g., including digestion or ligation reactions; and/or for identifying exogenous or endogenous modulators of the transcription factors.

35 A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least

about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

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A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid. A recombinant polynucleotide of the invention can be a cDNA or cDNA-derived polynucleotide that contains the entire coding region of a protein but does not contain the introns of genomic DNA. A recombinant polynucleotide of the invention can also be, or be derived from, a fragment of an isolated genomic DNA that is a full length coding region in that it contains the start of translation of a particular protein through the termination of translation of that same protein, where the start and termination sites are known.

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An "isolated polynucleotide" is a polynucleotide or nucleic acid molecule, whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

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A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the

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isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

5 The term "transgenic plant" refers to a plant that contains genetic material not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation, but any method can be used as one of skill in the art
10 recognizes.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the
15 expression of the polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cell or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

20 The phrase "ectopic expression or altered expression," or the terms "ectopic expression" or "altered expression" in reference to a polynucleotide or polypeptide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or
25 polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression
30 patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the phrase "ectopic expression or altered expression," or the terms "ectopic expression" or altered expression" may further relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous
35 modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain is a subsequence of the polypeptide that performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding site or domain that binds to a DNA promoter region, an activation domain, or a domain for protein-protein interaction. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically of at least about 15 consecutive nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein. A fragment or domain can be referred to as outside a consensus sequence or outside a consensus DNA-binding site that is known to exist or that exists for a particular transcription factor class, family, or sub-family. In this case, the fragment or domain will not include the exact amino acids of a consensus sequence or consensus DNA-binding site of a transcription factor class, family or sub-family, or the exact amino acids of a particular transcription factor consensus sequence or consensus DNA-binding site. Furthermore, a particular fragment, region, or domain of a polypeptide, or a polynucleotide encoding a polypeptide, can be "outside a conserved domain" if all the amino acids of the fragment, region, or domain fall outside of a defined conserved domain(s) for a polypeptide or protein. The conserved domains for polypeptides of the Sequence Listing are listed in the Tables of the Appendices. Also, many of the polypeptides of the Appendices have conserved domains specifically indicated by start and stop sites. A comparison of the regions of the polypeptides in the Sequence Listing, or of those in the Appendices, allows one of skill in the art to identify conserved domain(s) for any of the polypeptides listed or referred to in this disclosure, including those in the Appendices and homologs from other species, strains, or cultivars.

The term "trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by biochemical techniques, such as detecting the protein, starch or oil content of seed or leaves, or by the observation of the expression level of a gene or genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance. Any technique can be used to measure the

amount of, comparative level of, or difference in any selected chemical compound or macromolecule in the transgenic plants, however.

- “Trait modification” refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.
- Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like; decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

Polynucleotides and Polypeptides of the Invention

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides and homologue polypeptide-encoding polynucleotides (homologs), and isolated or recombinant polynucleotides encoding the polypeptides, or novel variant polypeptides or polynucleotides encoding novel variants of transcription factors derived from the specific sequences provided here. These polypeptides and polynucleotides may be employed to modify one or more of a plant's characteristics or traits.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor or knockout plants and the changes in the characteristic(s) or trait(s) of the plants observed. Therefore, the polynucleotides and polypeptides can be employed to improve the characteristics of plants.

Producing Polypeptides

The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides

can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous, or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed., and 3rd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, ("Sambrook"); Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2001) ("Ausubel"); and Current Protocols in Cell Biology, Bonifacino, J.S. et al. (eds.) 2001 John Wiley & Sons, Inc.

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, *all supra*.

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically
 5 ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable
 10 vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

Homologous Sequences

Sequences homologous, i.e., that share significant sequence identity or similarity, to those
 15 provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as
 20 banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype
 25 can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such
 30 pine, poplar and eucalyptus, or mint or other labiates.

Transcription factors that are homologous to the listed sequences will typically share at least about 30% amino acid sequence identity, or at least about 30% amino acid sequence identity outside of a known consensus sequence or consensus DNA-binding site. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75%
 35 or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences, or with the listed sequences but excluding or outside a known consensus sequence or

consensus DNA-binding site, or with the listed sequences excluding or outside one or all conserved domain. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences, or to the listed sequences but excluding or outside a known consensus sequence or consensus DNA-binding site or outside one or all conserved domain. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences, or to a listed sequence but excluding or outside a known consensus sequence or consensus DNA-binding site, or outside one or all conserved domain. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity, and more preferably at least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity. Transcription factors that are homologous to the listed sequences should share at least 30%, or at least about 60%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95% amino acid sequence identity over the entire length of the polypeptide or the homolog.

20

Identifying Polynucleotides or Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more detail in the references cited above.

30

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH)

35

at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C. For example, high stringency is about 0.2 x SSC, 0.1% SDS at 65° C. Ultra-high stringency will be the same conditions except the wash temperature is raised about 3 or about 5° C, and ultra-ultra-high stringency will be the same conditions except the wash temperature is raised about 6 or about 9°C. For identification of less closely related homologs, washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC, as known in the art.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radioactive label, or the like.

Alternatively, transcription factor homolog polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homolog nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it

is desired to clone additional transcription factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

Sequence Variations

- 5 It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences is capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

10

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid - serine. Accordingly, at each position in the sequence where there is a codon for serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

15

Table 1

Amino acid			Possible Codons							
Alanine	Ala	A	GCA	GCC	GCG	GCU				
Cysteine	Cys	C	TGC	TGT						
Aspartic acid	Asp	D	GAC	GAT						
Glutamic acid	Glu	E	GAA	GAG						
Phenylalanine	Phe	F	TTC	TTT						
Glycine	Gly	G	GGA	GGC	GGG	GGT				
Histidine	His	H	CAC	CAT						
Isoleucine	Ile	I	ATA	ATC	ATT					
Lysine	Lys	K	AAA	AAG						
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT		
Methionine	Met	M	ATG							
Asparagine	Asn	N	AAC	AAT						
Proline	Pro	P	CCA	CCC	CCG	CCT				
Glutamine	Gln	Q	CAA	CAG						
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT		

Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	Thr	T	ACA	ACC	ACG	ACT		
Valine	Val	V	GTA	GTC	GTG	GTT		
Tryptophan	Trp	W	TGG					
Tyrosine	Tyr	Y	TAC	TAT				

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

10 In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide. These conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

5

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The

10 substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side

chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

5 Further Modifying Sequences of the Invention – Mutation/Forced Evolution

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to
10 change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution
15 methods are described, e.g., by Stemmer (1994) Nature 370:389-391, and Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751, and U.S. Patents 5,811,238; 5,811,654; 6,251,604; and 6,177,263. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

20 Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These
25 modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the
30 products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant
35 RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be

modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

- 5 The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to
10 change codon preference, to introduce splice sites, etc.

- Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived
15 from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from
20 bacterial sequences (Ma and Ptashne (1987) Cell 51: 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

Expression and Modification of Polypeptides

- Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or
25 RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

- 30 The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been
35 inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably

linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

- General texts that describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.
- Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).
- Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

- Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see*, e.g., Odel et al. (1985) Nature 313:810); the nopaline

synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al. (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlmeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wun1*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acid, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

The host cell can be an eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York)

pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA
5 plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

10 The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants, which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

15 For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the
20 vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

25 Modified Amino Acids

Polypeptides of the invention may contain one or more modified amino acids. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during
30 recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated
35 amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature.

Identification of Additional Factors

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phenotype or trait of interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homolog of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins:

one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be performed.

15 Identification of Modulators

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northern, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998, and supplements through 2001). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator

composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

5 In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

10

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

25 Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.

30 In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of

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modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

5 Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

10

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of
15 relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

20

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional
25 activators or inhibitors to find modulators that inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

30

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In
35 some cases, an alteration in a plant phenotype can be detected following contact of a plant (or

plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

Subsequences

5 Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like,
10 according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18
15 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologs of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended
20 along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a
25 subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

30

Production of Transgenic Plants

Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve
35 the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or

transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved characteristics, by altering expression levels of a particular transcription factor is described further in the Examples.

5

Antisense and Cosuppression Approaches

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer

5 RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue

10 cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with

15 antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences

20 comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene

25 silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor

30 homologue gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a

35 transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the
5 intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the
10 endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery
15 in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (See, e.g., PCT Publications WO 96/06166 and WO 98/53057, which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

20 The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the
25 polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue
30 of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover,
35 etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.),

Solanaceae (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture—Crop Species. Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

5

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence into a plant in a manner to cause stable or transient expression of the sequence.

15

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

20

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

25

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

30

35 Integrated Systems – Sequence Identity

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link
5 certain functional benefits, such improved characteristics, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public
10 sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of
15 Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence
20 similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods for determining sequence relationships can be used, including manual
25 alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill:

30 One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length
35 W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the

neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters

5 M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring

10 residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62

15 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915). Unless otherwise indicated, "sequence identity" here refers to the % sequence identity generated from a tblastx using the NCBI version of the algorithm at the default settings using gapped alignments with the filter "off" (<http://www.ncbi.nlm.nih.gov/>).

20 In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see*, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For

25 example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using

30 progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character

35 strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity.

The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element, which displays an alignment produced by the alignment instruction set.

- 5 The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may be implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in
10 certain preferred embodiments, the computers may be components of an intranet or an internet.

- Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant
15 phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

- Any sequence herein can be entered into the database, before or after querying the database.
20 This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a
25 remote terminal or computer across an internet or intranet.

Examples

The following examples are intended to illustrate, but not limit, the scope of the present invention.

30

Example I: Full Length Gene Identification and Cloning

- Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower,
35 depending on the length of the query sequence. Putative transcription factor sequence hits were

then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ³²P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO₄ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60°C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSSC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

Example II: Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were

ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

5

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

Example III: Transformation of *Agrobacterium* with the Expression Vector

- 10 After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached.
- 15 Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl
- 20 aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

- Agrobacterium* cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of
- 25 *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100
- 30 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

- Example IV: Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with**
- 35 **Expression Vector**

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μ M benzylamino purine (Sigma), 200 μ L/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

- 10 Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 μ E/m²/sec) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After
15 flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat
20 surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

25 **Example V: Identification of *Arabidopsis* Primary Transformants**

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H₂O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second
30 wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H₂O. The
35 seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH),

1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 $\mu\text{E}/\text{m}^2/\text{sec}$) at 22-23°C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1 generation) were visible and obtained. These seedlings were transferred first to fresh selection
 5 plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T_2) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant
 10 polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

Example VI: Identification of *Arabidopsis* Plants with Transcription Factor Gene

15 Knockouts

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 base pairs to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to
 20 each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the
 25 genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

Example VII: Identification of Modified Phenotypes in Overexpression or Gene Knockout

30 Plants

Experiments were performed to identify those transformants or knockouts that exhibited modified biochemical characteristics. Among the biochemicals that were assayed were insoluble sugars, such as arabinose, fucose, galactose, mannose, rhamnose or xylose or the like; prenol lipids, such as lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or
 35 alpha-, delta- or gamma-tocopherol or the like; fatty acids, such as 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1 (oleic acid), 18:2 (linoleic acid), 20:0, 18:3 (linolenic

acid), 20:1 (eicosenoic acid), 20:2, 22:1 (erucic acid) or the like; waxes, such as by altering the levels of C29, C31, or C33 alkanes; sterols, such as brassicasterol, campesterol, stigmasterol, sitosterol or stigmasterol or the like, glucosinolates, protein or oil levels.

- 5 Fatty acids were measured using two methods depending on whether the tissue was from leaves or seeds. For leaves, lipids were extracted and esterified with hot methanolic H₂SO₄ and partitioned into hexane from methanolic brine. For seed fatty acids, seeds were pulverized and extracted in methanol:heptane:toluene:2,2-dimethoxypropane:H₂SO₄ (39:34:20:5:2) for 90 minutes at 80°C. After cooling to room temperature the upper phase, containing the seed fatty acid esters, was subjected to GC analysis. Fatty acid esters from both seed and leaf tissues were
10 analyzed with a Supelco SP-2330 column.

- Glucosinolates were purified from seeds or leaves by first heating the tissue at 95°C for 10 minutes. Preheated ethanol:water (50:50) is and after heating at 95°C for a further 10 minutes,
15 the extraction solvent is applied to a DEAE Sephadex column which had been previously equilibrated with 0.5 M pyridine acetate. Desulfoglucosinolates were eluted with 300 ul water and analyzed by reverse phase HPLC monitoring at 226 nm.

- For wax alkanes, samples were extracted using an identical method as fatty acids and extracts
20 were analyzed on a HP 5890 GC coupled with a 5973 MSD. Samples were chromatographed on a J&W DB35 mass spectrometer (J&W Scientific).

- To measure prenyl lipids levels, seeds or leaves were pulverized with 1 to 2% pyrogallol as an antioxidant. For seeds, extracted samples were filtered and a portion removed for tocopherol and carotenoid/chlorophyll analysis by HPLC. The remaining material was saponified for sterol
25 determination. For leaves, an aliquot was removed and diluted with methanol and chlorophyll A, chlorophyll B, and total carotenoids measured by spectrophotometry by determining absorbance at 665.2 nm, 652.5 nm, and 470 nm. An aliquot was removed for tocopherol and carotenoid/chlorophyll composition by HPLC using a Waters uBondapak C18 column (4.6 mm x
30 150 mm). The remaining methanolic solution was saponified with 10% KOH at 80°C for one hour. The samples were cooled and diluted with a mixture of methanol and water. A solution of 2% methylene chloride in hexane was mixed in and the samples were centrifuged. The aqueous methanol phase was again re-extracted 2% methylene chloride in hexane and, after centrifugation, the two upper phases were combined and evaporated. 2% methylene chloride in
35 hexane was added to the tubes and the samples were then extracted with one ml of water. The upper phase was removed, dried, and resuspended in 400 ul of 2% methylene chloride in hexane

and analyzed by gas chromatography using a 50 m DB-5ms (0.25 mm ID, 0.25 μ m phase, J&W Scientific).

Insoluble sugar levels were measured by the method essentially described by Reiter et al., Plant Journal 12:335-345. This method analyzes the neutral sugar composition of cell wall polymers found in *Arabidopsis* leaves. Soluble sugars were separated from sugar polymers by extracting leaves with hot 70% ethanol. The remaining residue containing the insoluble polysaccharides was then acid hydrolyzed with allose added as an internal standard. Sugar monomers generated by the hydrolysis were then reduced to the corresponding alditols by treatment with NaBH₄, then
10 were acetylated to generate the volatile alditol acetates which were then analyzed by GC-FID. Identity of the peaks was determined by comparing the retention times of known sugars converted to the corresponding alditol acetates with the retention times of peaks from wild-type plant extracts. Alditol acetates were analyzed on a Supelco SP-2330 capillary column (30 m x 250 μ m x 0.2 μ m) using a temperature program beginning at 180° C for 2 minutes followed by an
15 increase to 220° C in 4 minutes. After holding at 220° C for 10 minutes, the oven temperature is increased to 240° C in 2 minutes and held at this temperature for 10 minutes and brought back to room temperature.

To identify plants with alterations in total seed oil or protein content, 150mg of seeds from T2
20 progeny plants were subjected to analysis by Near Infrared Reflectance (NIR) using a Foss NirSystems Model 6500 with a spinning cup transport system.

Experiments were performed to identify those transformants or knockouts that exhibited an improved pathogen tolerance. For such studies, the transformants were exposed to biotrophic
25 fungal pathogens, such as *Erysiphe orontii*, and necrotrophic fungal pathogens, such as *Fusarium oxysporum*. *Fusarium oxysporum* isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was
30 prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the plate, swirled, and pipetted into 50 ml Armstrong *Fusarium* medium. Spores were grown overnight in *Fusarium* medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection.

35

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20 C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20 C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

Botrytis cinerea is a necrotrophic pathogen. *Botrytis cinerea* was grown on potato dextrose agar in the light. A spore culture was made by spreading 10 ml of sterile water on the fungus plate, swirling and transferring spores to 10 ml of sterile water. The spore inoculum (approx. 105 spores/ml) was used to spray 10 day-old seedlings grown under sterile conditions on MS (-sucrose) media. Symptoms were evaluated every day up to approximately 1 week.

Infection with bacterial pathogens *Pseudomonas syringae* pv *maculicola* strain 4326 and pv *maculicola* strain 4326 was performed by hand inoculation at two doses. Two inoculation doses allows the differentiation between plants with enhanced susceptibility and plants with enhanced resistance to the pathogen. Plants were grown for 3 weeks in the greenhouse, then transferred to the growth chamber for the remainder of their growth. Psm ES4326 was hand inoculated with 1 ml syringe on 3 fully-expanded leaves per plant (4 1/2 wk old), using at least 9 plants per overexpressing line at two inoculation doses, OD=0.005 and OD=0.0005. Disease scoring occurred at day 3 post-inoculation with pictures of the plants and leaves taken in parallel.

In some instances, expression patterns of the pathogen-induced genes (such as defense genes) was monitored by microarray experiments. cDNAs were generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999) *Meth. in Enzymol.* 303:179-205). The cDNAs were spotted on microscope glass slides coated with polylysine. The prepared cDNAs were aliquoted into 384 well plates and spotted on the slides using an x-y-z gantry (OmniGrid) purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays were cured for a minimum of one week at room temperature, rehydrated and blocked following the protocol recommended by Eisen and Brown (1999).

Sample total RNA (10 ug) samples were labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples were resuspended in 4X SSC/0.03% SDS/4 ug salmon sperm DNA/2 ug tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The array was then covered with a glass coverslip and placed in a sealed chamber. The chamber was then kept in a water bath at 62°C overnight. The arrays were washed as described in Eisen and

Brown (1999) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using Imagene software purchased from BioDiscovery (Los Angeles, CA).

5 Experiments were performed to identify those transformants or knockouts that exhibited an improved environmental stress tolerance. For such studies, the transformants were exposed to a variety of environmental stresses. Plants were exposed to chilling stress (6 hour exposure to 4-8° C), heat stress (6 hour exposure to 32-37° C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour
10 exposure to 3 M mannitol), or nutrient limitation (nitrogen, phosphate, and potassium) (Nitrogen: all components of MS medium remained constant except N was reduced to 20mg/L of NH_4NO_3 , or Phosphate: All components of MS medium except KH_2PO_4 , which was replaced by K_2SO_4 , Potassium: All components of MS medium except removal of KNO_3 and KH_2PO_4 , which were replaced by NaH_2PO_4).

15 Experiments were performed to identify those transformants or knockouts that exhibited a modified structure and development characteristics. For such studies, the transformants were observed by eye to identify novel structural or developmental characteristics associated with the ectopic expression of the polynucleotides or polypeptides of the invention.

20 Experiments were performed to identify those transformants or knockouts that exhibited modified sugar-sensing. For such studies, seeds from transformants were germinated on media containing 5% glucose or 9.4% sucrose which normally partially restrict hypocotyl elongation. Plants with altered sugar sensing may have either longer or shorter hypocotyls than normal plants
25 when grown on this media. Additionally, other plant traits may be varied such as root mass.

Flowering time was measured by the number of rosette leaves present when a visible inflorescence of approximately 3 cm is apparent. Rosette and total leaf number on the progeny stem are tightly correlated with the timing of flowering (Koornneef et al (1991) *Mol. Gen. Genet*
30 229:57-66). The vernalization response was measured. For vernalization treatments, seeds were sown to MS agar plates, sealed with micropore tape, and placed in a 4°C cold room with low light levels for 6-8 weeks. The plates were then transferred to the growth rooms alongside plates containing freshly sown non-vernalized controls. Rosette leaves were counted when a visible inflorescence of approximately 3 cm was apparent.

35

Modified phenotypes observed for particular overexpressor or knockout plants are provided in Table 4 of the Appendix and the Appendices of the priority documents. For a particular overexpressor that shows a less beneficial characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a less beneficial characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

The sequences of the Sequence Listing SEQ ID Nos. 1-464 or those disclosed here can be used to prepare transgenic plants and plants with altered traits. The specific transgenic plants listed below are produced from the sequences of the Sequence Listing, as noted. The Tables of the Appendix and the Appendices of the priority documents provide exemplary polynucleotide (cDNA) and polypeptide (protein) sequences of the invention. The Tables include SEQ ID Nos., the corresponding reference number (GID), and/or the identification of the start and stop residues of any conserved domain in the polypeptide sequence.

The transgenic plants of the invention display an ectopic expression or altered expression of one or more polypeptides encoded by the full length coding regions in the Sequence Listing, the homologs and/or fragments of the Tables of the Appendices, and/or another polypeptide described in this document, when the transgenic plant is compared to a wild type, control, or reference plant. As a result, the transgenic plants possess advantageous traits, as detailed by the limited and exemplary discussion of comparison data below.

Some of the polypeptides encoded by the full length coding regions in the Sequence Listing and the homologs and fragments of them noted in the Tables of the Appendices modulate a plant's defense response and even confer multipathogen resistance. These traits are extremely useful in many commercial crops and plants. For example, plants overexpressing G28 (SEQ ID NO.: 1 and 2) are more tolerant to infection by fungal pathogens, such as *Erysiphe orontii*, *Sclerotinia sclerotiorum*, or *Botrytis cinerea*. Similarly, plants overexpressing G1792 (SEQ ID NO.: 5 and 6) are more tolerant to infection by necrotrophic fungal pathogens, such as *Fusarium oxysporum* or *Botrytis cinerea*, and display increased resistance to fungal pathogens and to *Erysiphe orontii*. Increased tolerance to infection by *Fusarium oxysporum* is observed in G1047 (SEQ ID NO.: 23 and 24) and G1363 (SEQ ID NO.: 29 and 30) overexpressing plants. Knockout mutants also demonstrate the particular polypeptide's involvement in a defense response. A G1880 (SEQ ID NO.: 435 and 436) knockout mutant is more tolerant to *Botrytis cinerea*. G1196 (SEQ ID NO.: 27 and 28) knockout mutant plants show increased susceptibility to *Botrytis cinerea*. Manipulating the content or expression of any of these polypeptides, or fragments or homologs

of them, can therefore improve a plant's defense response, tolerance, or susceptibility to pathogens and infection.

5 A number of the polypeptides encoded by the full length coding regions in the Sequence Listing, and homologs and fragments of them noted in the Tables of the Appendices, regulate the transition from vegetative to reproductive growth. These traits can be useful in crops and plants where fruit or seed is commercially valuable, for example. Overexpression of G180 (SEQ ID NO.: 53 and 54), G227 (SEQ ID NO.: 313 and 314), G1841 (SEQ ID NO.: 455 and 456), and G2347 (SEQ ID NO.: 477 and 478) results in an early flowering phenotype, whereas
10 overexpression of G748 (SEQ ID NO.: 125 and 126) or G2007 (SEQ ID NO.: 457 and 458) results in late flowering. Other polypeptides and polynucleotides for modulating flowering time include G590 (SEQ ID NO.: 107 and 108), G1760 (SEQ ID NO.: 31 and 32), G1820 (SEQ ID NO.: 33 and 34), and G2010 (SEQ ID NO.: 37 and 38).

15 The response to a variety of abiotic or environmental stresses is modified by an additional set of polypeptides encoded by the full length coding regions of the Sequence Listing and the homologs and fragments listed in the Tables of the Appendices. These traits can be useful in manipulating the growth medium or environment for plants, for example. G226 overexpressing plants are more tolerant to low nitrogen and high salt stress. G2130 (SEQ ID NO.: 417 and 418)
20 overexpressors show improved heat stress tolerance in a germination assay. G867 (SEQ ID NO.: 15 and 16) and G1930 (SEQ ID NO.: 35 and 36) overexpressing plants show increased seedling vigor in germination assays on both high salt and high sucrose containing media. G912 (SEQ ID NO.: 19 and 20) is a member of the AP2 family related to the CBF1, CBF2 and CBF3 genes. Plants overexpressing G912 (SEQ ID NO.: 19 and 20) exhibit increased freezing and drought
25 tolerance. Additional polypeptides and polynucleotides modifying stress responses include G175 (SEQ ID NO.: 9 and 10), G926 (SEQ ID NO.: 459 and 460), and G1820 (SEQ ID NO.: 33 and 34).

Several transcription factors have been identified that can affect metabolic processes. These
30 plants can be used to optimize or improve production of various plants extracts used for commercial products including, for example, foodstuffs, paper and paper-related products, edible plants, fruits and vegetables with improved properties, organic compounds, oils and alcohols, additives and binders for pharmaceutical or cosmetic products, and industrial products. For instance, plants overexpressing G1750 (SEQ ID NO.: 395 and 396) produce seed with increased
35 seed oil content. Overexpression of G280 (SEQ ID NO.: 461 and 462) results in an increase in gamma and delta tocopherol in leaves. G663 (SEQ ID NO.: 13 and 14) overexpressors exhibit

constitutive anthocyanin production in seeds, leaves and roots. In contrast, seeds of G156 (SEQ ID NO.: 7 and 8) knockout mutant plants exhibit a colorless phenotype indicative of the involvement of the gene in the regulation of the anthocyanin pathway.

- 5 Also of particular interest are polypeptides involved in plant growth and development. The following polypeptides encoded by the full length coding regions of the Sequence Listing and the homologs and fragments listed in the Tables of the Appendices are some examples. Transgenic plants overexpressing G1073 exhibit a substantial increase in size. An increase in size is also observed in G189 (SEQ ID NO.: 11 and 12) overexpressing plants. Transgenic plants
- 10 overexpressing G634 (SEQ ID NO.: 3 and 4) exhibit a substantial increase in trichome number. Null mutations in G374 (SEQ ID NO.: 463 and 464) and in G877 (SEQ ID NO.: 17 and 18) result in embryo lethality. A G979 (SEQ ID NO.: 153 and 154) knockout mutation results in delayed seed ripening.
- 15 G987 (SEQ ID NO.: 21 and 22) knockout mutant plants can only be grown on sucrose-containing medium. In addition, G987 appears to control an aspect of thylakoid membrane development and the tocopherol, carotenoid, and/or chlorophyll content of the plant is altered. Since the compounds represented by these groups are commercially important in a number of industries, including use as dietary supplements, a transgenic plant's altered tocopherol,
- 20 carotenoid, and/or chlorophyll content is an advantageous and valuable trait.

G634 (SEQ ID. Nos 3 and 4), G1841 (SEQ ID. Nos 455 and 456), G979 (SEQ ID. Nos 153 and 154): modified plant development

- 25 **G634:** Overexpression of G634 produced an increase in trichome density on later arising rosette leaves, cauline leaves, inflorescence stems and sepals. Trichomes of 35S::G634 plants also appeared slightly larger than those of wild type, and stem trichomes were more highly branched. These effects were not apparent in young seedlings and became most prominent at the later vegetative and early reproductive phase. The trichome phenotype was apparent in approximately
- 30 50% of primary transformants and two out of the three T2 lines.

- G1841:** Overexpression of G1841 markedly reduced the time to flowering. This early flowering phenotype was consistently observed over multiple plantings for each of the three T2 lines, and in a majority of primary transformants. Additionally, 35S::G1841 plants appeared slightly pale
- 35 and had rather flat leaves compared to wild-type controls.

In continuous light conditions, 35S::G1841 plants produced flower buds up to five days earlier than wild-type controls. In repeat sowings the plants appeared to grow slightly faster than controls; although they switched to making flower buds several days early, they had a similar number of primary rosette leaves to wild type.

5

In addition to showing accelerated flowering under 24 hours light, plants from all three T2 populations produced flowers up to 2 weeks earlier than controls under a 12 hour photoperiod.

G979: Seeds homozygous for a T-DNA insertion within G979 showed delayed ripening, slow germination, and developed into small, poorly fertile plants, indicating that G979 might be involved in seed development processes.

10

Silques of heterozygous plants were examined for seed abnormalities. Approximately 25% of the seeds contained in young green siliques were pale in coloration. In older, brown siliques, approximately 25% of the seeds were green and appeared slow ripening, whereas the remaining seeds were brown. Thus, it seemed likely that the seeds with altered development were homozygous for the T-DNA insertion, whereas the normal seeds were wild type and heterozygous segregants.

15

Furthermore, it was observed that approximately 25% of the seed from G979 KO heterozygous plants showed impaired (delayed) germination. Upon germination, these seeds produced extremely tiny seedlings that often did not survive transplantation. A few homozygous plants, small and sickly looking, could be grown, and produced siliques that contained seeds that were small and wrinkled compared to wild type.

20

On the basis of these results obtained with G979 knockout mutant lines, G979 can be used to alter or modify seed germination properties and performance.

G1792 (SEQ ID. Nos 5 and 6), G2130 (SEQ ID. Nos 417 and 418), G926 (SEQ ID. Nos. 459 and 460): modified stress response

25

G1792: 35S::G1792 plants were more tolerant to the fungal pathogens *Fusarium oxysporum* and *Botrytis cinerea*; they showed fewer symptoms after inoculation with a low dose of each pathogen. This result was confirmed using individual T2 lines.

30

35S::G1792 plants also showed more tolerance to growth under nitrogen-limiting conditions. In a root growth assay under conditions of limiting N, 35S::G1792 lines were slightly less stunted. In a germination assay that monitors the effect of C on N signaling through anthocyanin production on high sucrose plus and minus, the 35S::G1792 lines make less anthocyanin on high sucrose plus glutamine, suggesting that the gene could be involved in the plants ability to monitor their carbon and nitrogen status.

G1792 overexpressing plants also showed several mild morphological alterations such as abnormal phyllotaxy, alterations in leaf and flower development, and flowering time.

G2130: G2130 overexpressing lines show more seedling vigor in a heat stress tolerance germination assay compared to wild-type controls. No difference from wild-type was detected in the heat stress response assay performed on older seedlings suggesting the phenotype could be specific for germination in the G2130 overexpressors. Lines G2130-3 and G2130-4 show the heat tolerant phenotype, line G2130-2 show the weakest phenotype. G2130 overexpressing lines are also somewhat more sensitive to chilling, the plants are more chlorotic and stunted when grown at 8°C compared to the wild-type controls. They also show more disease symptoms following inoculation with a low dose of the fungal pathogen *Botrytis cinerea* in two separate experiments.

G926: G926 knockout mutant plants show more tolerance to osmotic stress in a germination assay in three separate experiments. They show more seedling vigor than wild-type controls when germinated on plates containing high salt and high sucrose. They also show insensitivity to ABA in repeated germination assays.

These analyses revealed that in the absence of G926 function, plants are more tolerant to osmotic stress. This osmotic stress tolerance could be related to the plant's apparent insensitivity to the growth hormone ABA because ABA plays an important regulatory role in the initiation and maintenance of seed dormancy. G926 may function as part of a checkpoint for germinating seeds and loss of G926 function promotes germination regardless of the osmotic status of the environment. G926 has utility in modifying plant stress responses.

G280 (SEQ ID. Nos. 461 and 462), G1323 (SEQ ID. Nos 203 and 204): modified biochemistry

G280: Overexpression of G280 in *Arabidopsis* resulted in an increase in leaf gamma and delta tocopherol in all three lines tested. Overexpression of G280 produced a reduction in overall plant size and accelerated the rate of leaf senescence in the rosette.

- 5 **G1323:** In two G1323 overexpressing lines, line 5 and 7, seeds had more protein and less oil than controls. Otherwise, overexpression of G1323 in *Arabidopsis* did not result in any biochemical phenotype. These experiments were repeated and a similar biochemical phenotype was observed.

10 **G2557 (SEQ ID Nos. 289 and 290), G2143 (SEQ ID Nos. 285 and 286), G1063 (SEQ ID Nos 167 and 168) (HLH/MYC)**

Overexpression of each of these genes affected plant growth, inflorescence architecture, and resulted in the development of carpelloid tissues in ectopic positions.

- 15 **G2557:** Twenty independent 35S::G2557 *Arabidopsis* primary transformants were obtained. Of these plants, 19/20 exhibited carpelloid tissue in the outer whorl organs of flowers. In some instances ovules developed from these ectopic carpels. The central carpel of 35S::G2557 flowers was also sometimes borne on a long pedicel-like structure, indicating that overexpression of this gene could influence determinacy of the floral meristem. Additionally, 35S::G2557 plants were
20 often smaller, darker green and possessed narrow leaves and elongated cotyledons compared to wild type.

- G2143:** Twenty independent 35S::G2143 *Arabidopsis* primary transformants were obtained. All 20 plants developed ectopic carpelloid tissue. In some cases entire flowers were replaced by
25 a disorganized mass of this tissue. Additionally, 35S::G2143 plants were often smaller, darker green and possessed narrow leaves and elongated cotyledons compared to wild type. In some cases the shoot tips of G2143 plants aborted in a 'pin-like' structure.

- G1063:** Seventeen independent 35S::G1063 *Arabidopsis* primary transformants were obtained.
30 5/17 of these lines exhibited flowers in which outer whorl organs displayed carpelloid features. In some cases flowers were completely replaced by a carpelloid mass of tissue and defined individual organs could not be distinguished. The shoots of these plants also occasionally terminated in a 'pin-like' structure. The majority of 35S::G1063 plants were smaller than wild
type and often had altered leaf shape.

35

Based on the above phenotypes, these genes might be applied to manipulate flower structure and development, fertility, seed-pod development, leaf coloration and overall plant architecture. Specifically, the genes might be used to manipulate floral organ identity or instigate the formation of carpel-derived structures including ovules, embryos and seeds.

5

G2509 (SEQ ID Nos 287 and 288) (AP2)

Twenty independent 35S::G2509 *Arabidopsis* primary transformants were obtained. All plants exhibited increased secondary shoot development and loss of apical dominance, leading to a shorter bushier stature than wild type. G2509 could be used to modify plant architecture. This could produce plants more resistant to wind and rain and influence yield. Additionally, changing plant architecture could generate novel interesting forms for the ornamental plant market.

10

G353 (SEQ ID Nos 79 and 80) and G354 (SEQ ID Nos. 81 and 82) (Z(C2H2))

G353 and G354 constitute a pair of closely related Z(C2H2) genes that influence shoot architecture. Both genes produced comparable effects when overexpressed.

15

G353: A consistent phenotype was noted on inflorescences of 35S::G353 plants. Flowers were oriented downwards and pedicels of flowers and siliques were reduced in length or absent. Floral internodes were also very short. Furthermore, secondary shoots were often observed to grow in a downward direction. These phenotypes were observed in both primary transformants and T2 generation plants. Overexpression of G353 produced additional effects; 35S::G353 were sometimes smaller than wild-type, had abnormal branching patterns and flat leaves.

20

G354: 35S::G354 plants displayed abnormal inflorescences in which flowers were oriented downwards and pedicels were absent or reduced in length. Floral internodes were also short. Additionally, many of the 35S::G354 plants were reduced in size compared to wild type.

25

These genes could be used to modify plant architecture. Specifically, altering the length of flower and fruit stalks could permit more efficient harvesting. In species such as strawberry, changing the length of the fruit stalk could allow fruits to develop above the leaf canopy and reduce the likelihood of fungal infection. The genes might also have applications in producing novel forms of ornamental species in which branches, flowers and fruits develop with unusual orientations.

30

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G1494 (SEQ ID Nos. 223 and 224) (HLH/MYC)

The phenotype of transgenic *Arabidopsis*, over-expressing G1494, indicates that this gene is a core component of the plant light perception/response machinery. 35S::G1494 seedlings displayed very long hypocotyls, bolted early, and exhibited elongation of rosette internodes.

- 5 This latter characteristic resulted in the absence of a defined rosette. The plants also possessed very spindly stems, and narrow pale leaves with elongated petioles. Such features were consistently observed in both primary transformants and T2 generation plants. These phenotypes are comparable to those of mutants defective in the *PHYTOCHROME* genes, which encode proteins involved in the perception of light conditions. In particular, the 35S::G1494 phenotype
10 is almost identical to that described for the *phyA;phyB;phyD* triple mutant (Devlin et al., Plant Physiology 119, 909-915). Based upon the 35S::G1494 phenotype, this gene might be applied to manipulate many of the traits which are influenced by the perception and response to light, including seed germination, flowering time, shade response, leaf orientation, architecture and growth habit.

- 15 Additional phenotypes that were observed included G634 (SEQ ID Nos. 3 and 4) (overexpressors had substantially more trichomes on its leaf surfaces), G971 (SEQ ID Nos. 17 and 18) (overexpressors enhanced terpenoid biosynthesis levels) and G1792 (SEQ ID Nos. 5 and 6) (overexpressors showed a broad-based disease resistance).

20

Example VIII: Identification of Homologous Sequences

- Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool
25 (BLAST) (Altschul et al. (1990) *J. Mol. Biol.* 215:403-410; and Altschul et al. (1997) *Nucl. Acid Res.* 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) *Proc. Natl. Acad. Sci. USA* 89: 10915-10919).

- 30 Identified *Arabidopsis* homologous sequences are provided in the Tables of the Appendices. The percent sequence identity among these sequences can be as low as 47%, or even 31% or lower sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and
35 excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences are compared to sequences representing genes of SEQ IDs Nos. 1-16 using the Washington

University TBLASTX algorithm (version 2.0a19MP) at the default settings using gapped alignments with the filter "off," as performed on July 16, 2001 or previously. For each gene of the Sequence Listing, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of 3.6×10^{-40} is 3.6×10^{-40} . In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length.

In addition to computer-based methods for identifying homologs, or indeed in conjunction with them, a fragment of a sequence from the sequence listing, from the Tables of the Appendices, or derived from a homolog sequence identified from a database, is radiolabeled with ^{32}P by random priming (Sambrook et al., *Molecular Cloning. A Laboratory Manual*, 2nd Ed., or 3rd Ed., Cold Spring Harbor Laboratory Press, New York) and used to screen a plant cDNA or genomic library. As merely one example, total plant DNA from *Arabidopsis thaliana*, *Nicotiana tabacum*, *Lycopersicon pimpinellifolium*, *Prunus avium*, *Prunus cerasus*, *Cucumis sativus*, or *Oryza sativa* is isolated (Stockinger, E.J., et al., (1996), *J. Heredity*, 87:214-218). Alternatively, cDNA clones of a selected cDNA library are used. Approximately 2 to 10 μg of each DNA sample is restriction digested, transferred to nylon membrane (Micron Separations, Westboro, MA) and hybridized. Alternatively, a library is plated out on growth medium and partially transferred *in situ* to the nylon membrane for hybridization. Exemplary hybridization conditions are: 42°C in 50% formamide, 5X SSC, 20 mM phosphate buffer, 1X Denhardt's, 10% dextran sulfate, and 100 $\mu\text{g}/\text{ml}$ herring sperm DNA. Four low stringency washes at RT in 2X SSC, 0.05% sodium sarcosyl and 0.02% sodium pyrophosphate are performed prior to high stringency washes at 55°C in 0.2X SSC, 0.05% sodium sarcosyl and 0.01% sodium pyrophosphate. High stringency washes are performed until no counts are detected in the washout (Walling, L.L., et al., *Nucl. Acids Res.* 16:10477-10492(1988)). The areas of radioactivity on the membrane correspond to homologous sequences from the library or genomic DNA sample and the associated DNA can be identified, isolated, and cloned into an appropriate vector so that any homologous sequence(s) can be used. Alterations in the stringency of washes, such as employing ultra-high stringency, and ultra-ultra-high stringency, can also be made.

Example IX

As noted previously, the introduction of polynucleotides of the invention and full length coding sequences of the invention into the target plant or cell can be accomplished by a variety of techniques known in the art, such as calcium phosphate-DNA precipitation, electroporation,

microinjection, *Agrobacterium* infection, liposomes, or microprojectile bombardment, for example. Those of ordinary skill in the art can refer to the literature for details and select suitable techniques without undue experimentation. For some plants, using *Agrobacterium* is a preferred and easy method for transforming plants and cells. This type of transformation has been used for genetic manipulation of more than 120 species of at least 35 different families of plants, including major economic crops such as vegetables, ornamentals, medicinals, fruit, trees and pasture plants (see, for example, Birch, R.G., *Annual Rev. Plant Physiology and Plant Molec. Biology* 48:297-326 (1997); Gould J.H., *Transformation of the Cereals using Agrobacterium*, In: R.S. Tuan (Ed.), *Methods in Molecular Biology*, Humana Press Inc., Totowa, NJ, vol. 62:489-499 (1997)). In fact, this method has become so routine and commonplace that the idea that some species cannot accept the integration of foreign DNA into its genome or that a species lacks the capacity to be transformed has become unacceptable in the art (see de la Riva et al., *Electr. J. Biotechnol. Agrobacterium tumefaciens: a natural tool for plant transformation*, vol. 1, no. 13, issue of Dec. 15, 1998).

A number of vectors can be used to produce transgenic plants. Some of these vectors can replicate in bacterial hosts, plant host cells, and *Agrobacterium*, as known through many techniques of the art. Expression vectors typically comprise a cassette or region for inserting a coding sequence or transgene that is flanked by a promoter/enhancer and a poly A site. Many variations are possible, including the use of sequences incorporating preferred codons, 5' UTR, 3' UTR, splice donor and acceptor or other intron sequences, internal ribosome entry sites, repressor or suppressor binding sequences, tissue-specific promoters and enhancers, developmentally regulated promoters and enhancers, and inducible promoters and enhancers, for example. Examples of inducible promoters useful in plants include those induced by chemical means, such as the yeast metallothionein promoter, which is activated by concentrations of copper or heavy metal ions. Any appropriate inducible promoter, enhancer, or promoter/enhancer can be selected. One skilled in the art can devise many variations and permutations in selecting and using expression vectors. The vectors may also contain selectable markers for more easily identifying transformed plants. Many types of selectable marker genes are known in the art.

If using *Agrobacterium*, one can select armed or disarmed Ti genes for transforming cells and plants. Either Ti plasmids of *Agrobacterium tumefaciens* (*A. tumefaciens*) or root-inducing (Ri) plasmids of *Agrobacterium rhizogenes* (*A. rhizogenes*) can be selected. (For reviews of exemplary techniques see, for example, Weissbach & Weissbach, (1988) *Methods for Plant Molecular Biology*, Academic Press, NY, Section VIII, pp. 421-463; and Grierson & Corey

(1988) Plant Molecular Biology, 2d Ed., Blackie, London, Ch. 7-9, and Horsch et al., Science 227:1229 (1985), incorporated herein by reference). The selection of either *A. tumefaciens* or *A. rhizogenes* will depend on the plant being transformed. In general *A. tumefaciens* is the preferred organism for transformation. Most dicotyledons, some gymnosperms, and a few
5 monocotyledons (e.g. certain members of the Liliales and Arales) are easily susceptible to infection with *A. tumefaciens*. *A. rhizogenes* also has a wide host range, including most dicots and gymnosperms, which includes members of the Leguminosae, Compositae and Chenopodiaceae. Selecting a type of vector and the components of the vector is well within the ordinary skill of the art.

10

A general and exemplary method for plant transformation with *Agrobacterium* follows. The polynucleotide or the full length coding region (transgene) is inserted into an intermediate or shuttle vector capable of replicating in *E. coli* and suitable for the type of plant used and typically containing a selectable marker. The vector is introduced into an acceptor *A. tumefaciens* strain
15 through triparental mating (reciprocal recombination between the intermediate vector and the T-DNA region of the acceptor plasmid occurs during triparental mating and the transgene is now part of the T-DNA region that will be transferred). The engineered *A. tumefaciens* strain containing the transgene is cocultivated with a plant explant, from which regenerated plants can be obtained. The explants are cultured in the presence of a selection agent and selecting resistant
20 cells grow shoots and rooted-shoots. These are regenerated into plants and the regenerated plants screened for the expression of the transgene and selectable marker. The progeny of the transgenic plant is grown and the inheritance of the introduced transgene is determined.

A transgenic plant transformed using *Agrobacterium* typically contains a single copy of the
25 introduced transgene on one chromosome – it is heterozygous for the transgene. Homozygous plants can also be prepared and can be preferred or more stable in certain plants. One skilled in the art is familiar with breeding and crossing techniques to produce homozygous plants regardless of the type of transformation used. For example, homozygous transgenic plants can be produced through sexually mating an independent segregant that contains a single transgene,
30 germinating the seed of the plant, and selecting the plants produced for the transgene. In addition, two transformed or transgenic plants can be mated to produce plants having two independently segregating transgenes. Sexually mating progeny produces homozygous plants for both transgenes. Those of skill in the art are also familiar with techniques, such as back-crossing to parental plants, out-crossing with a wild type or non-transgenic plant, and vegetative
35 propagation, for example, to manipulate plants having one or more transgenes. Any of these

techniques can be employed to produce transgenic plants, seeds, plant cells, or plant tissue or extracts having a polynucleotide or polypeptide of the invention.

- Another common transformation protocol employs plant protoplasts using methods based on
- 5 calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of these. The selection of a protoplast method depends upon the ability to regenerate that particular plant strain from protoplasts. Many methods for regenerating plants from protoplasts exist and any can be selected for use (see, for example Shillito, R.D. and Saul, M.W., Protoplast Isolation and Transformation, In: Plant molecular biology, A Practical
- 10 Approach, IRL Press, UK (1988), particularly pp. 161-186; Methods in Enzymology, vol. 118, (Plant Molecular Biology), eds. Weissbach, A. and Weissbach, H., Academic Press, Orlando, Florida (1985); Methods in Enzymology, vol. 153 (Recombinant DNA), eds. Wu, R. and Grossman, L., Academic Press, Orlando, Florida, (1987).
- 15 To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, plants can be regenerated from immature embryos or explants following introduction of vector or expression cassette DNA containing the transgene. The methods used to regenerate transformed cells into whole plants are not critical to this invention and any method suitable for the target plant can be employed. The
- 20 literature describes numerous techniques for regenerating specific plant types (for example, somatic embryogenesis, Umbeck, P., et al., Genetically transformed cotton (*Gossypium hirsutum* L.) plants, *Bio/Technology* 5:263-266 (1987)), and other techniques are continually becoming known. One of ordinary skill in the art can refer to the literature for details and select suitable techniques without undue experimentation. In practice, a large number of transformed plants can
- 25 be routinely regenerated from a transformed plant cell or tissue to increase and maintain a sterile line. Many methods for culturing plant cells and regenerating transformed plants from cells are known in the art and any appropriate method can be selected (see, for example, *Plant Tissue and Cell Culture*, C. E. Green, D. A. et al., (Eds.), Alan R. Liss, Inc., New York; *Experiments in Plant Tissue Culture*, Dodds, J. H. et al. (Eds.), 1985, Cambridge University Press; *Cell Structure and Somatic Cell Genetics of Plants*, Vasil, I. K. (Ed.), 1984, Academic Press; *Handbook of Plant Cell Culture*, Volume 4, Techniques and Applications, Evans, D.A. et al. (Eds.), 1986, Macmillan Publishing Company).
- 30

- In addition, microprojectile bombardment techniques can be used and many have been described
- 35 in the art. Here, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles (see, for example McCabe et al., *Bio/Technology* 6:923 (1988)). The metal

particles penetrate through several layers of cells and allow the transformation of cells within tissue explants. These explants or cells of them can then be regenerated into plants.

5 For example, if soybean is selected, the following method can be used. Somatic embryos, cotyledons, 3-5 mm in length, are dissected from surface of sterilized, immature seeds of the soybean cultivar chosen, and the embryos cultured in light or darkness at 26°C on an appropriate agar medium for 6-10 weeks. Somatic embryos that produce secondary embryos are then excised and placed into a suitable liquid medium. After repeated selection for clusters of somatic embryos that multiply, the suspensions are maintained in suspension culture.

10

The soybean embryogenic suspension cultures can be maintained in 35 ml liquid media on a rotary shaker, 150 rpm, at 26°C with fluorescent lighting on a 16:8 hour day/night schedule. Sub-culturing every two weeks by inoculating approximately 35 mg of tissue into 35 ml of liquid medium maintains the cells.

15

A DuPont Biolistic PDS1000/HE instrument, a BIO RAD PDS-1000/He or other microprojectile device can be used for these transformations. DNA-coated microcarriers, typically tungsten or gold microparticles, are used according to the instruction manual. To 50 µl of a 60 mg/ml 1 µm gold particle suspension is added 5 µl DNA (1 µg/µl), 20 µl spermidine (0.1 M), and 50 µl CaCl₂ (2.5 M). The particle preparation is agitated for three minutes, spun in a microfuge for 10 seconds, and the supernatant is removed. The DNA-coated particles are then washed once in 400 µl 70% ethanol and resuspended in 40 µl of anhydrous ethanol. The DNA/particle suspension can be sonicated three times for one second each. Five µl of the DNA-coated gold particles is loaded on the disk or appropriate carrier for the particle gun.

25

Approximately 300-400 mg of a two-week-old suspension culture is placed in an empty petri dish and the residual liquid removed from the tissue with a pipette. For each transformation, approximately 5-10 plates of tissue are normally used. Membrane rupture pressure is set at approximately 1100 psi. The tissue is placed approximately 3.5 inches away from the retaining screen and bombarded three times. Following treatment, the tissue can be divided in half and placed back into liquid and cultured as above.

30

Five to seven days post bombardment, the liquid media is exchanged with fresh media, and eleven to twelve days post bombardment with fresh media containing selection media (if the vector or DNA used also encodes a selectable marker, as it preferably will). The selection media is replaced approximately every week. Seven to eight weeks post bombardment, green,

35

transformed tissue may be observed growing from un-transformed, necrotic embryogenic clusters. Isolated green tissue is removed and inoculated into individual flasks to generate new, clonally propagated, transformed embryogenic suspension cultures. Each new line may be treated independently. These suspensions can then be sub-cultured and maintained as clusters of
5 immature embryos or regenerated into whole plants by maturation and germination of individual somatic embryos.

If maize is selected, immature embryos are excised from cleaned and sterilized ears and placed embryo axis side down (scutellum side up) in a petri plate. These are cultured in 560L medium
10 for 4 days in the dark. To prepare for bombardment, the embryos are transferred to 560Y medium for 4 hours and arranged within the device target zone.

The DNA is prepared with Tungsten microparticles, for example, using 1 ug DNA in Tris EDTA buffer, 2.5 M CaCl₂, and 0.1 M spermidine while vortexing. The mixture is sonicated briefly
15 and incubated under constant vortexing for ten minutes. After a precipitation period, the tubes are centrifuged briefly, and the liquid is removed. The particles are washed with 100% ethanol, centrifuged, and resuspended in 100% ethanol. For particle gun bombardment, the tungsten/DNA particles are briefly sonicated and 10 ul spotted onto the center of each carrier and allowed to dry about 2 minutes before bombardment.

20 All samples receive a single shot at approximately 650 psi. Following bombardment, the embryos are cultured in 560Y medium for 2 days then transferred to 560R selection medium and sub-cultured every 2 weeks. After approximately 10 weeks of selection, selection-resistant callus clones are sampled by PCR for transgene content and/or activity analysis. Positive lines are
25 transferred to 288J medium to initiate plant regeneration. Following somatic embryo maturation period of 2-4 weeks, well-developed somatic embryos are transferred to 272V medium for germination and then transferred to a lighted culture room. Approximately 7-10 days later, developing plantlets are transferred to 272V medium in tubes for 7-10 days until plantlets are well established. Plants are then transferred to potting soil and grown for 1 week in a growth
30 chamber, and subsequently grown 1-2 weeks in the greenhouse, then grown to maturity.

Example X. Transformation of Cereal Plants with Expression Vector

A cereal plant, such as corn, wheat, rice, sorghum or barley, can also be transformed with a plasmid vector containing a sequence or polynucleotide of the invention, together with an
35 operably linked constitutive or inducible promoter, to modify a trait or produce ectopic or altered expression. In these cases, a cloning vector, pMEN020 for example, is modified to replace the

NptII coding region with the BAR gene of *Streptomyces hygroscopicus* to confer resistance to phosphinothricin. The KpnI and BglII sites of the Bar (bialaphos resistance) gene are removed by site-directed mutagenesis with silent codon changes. Preferably, a maize or other plant ubiquitin promoter is inserted in place of the 35S promoter of pMEN020 (see, for example, 5 Christensen et al., *Plant Mol. Biol.* 12:619-632 (1992); and Christensen, et al., *Plant Mol. Biol.* 18:675-689 (1992); Christensen et al., *Transgenic Res.* 5:213-8(1996)). The polypeptide-encoding sequence or cDNA is then inserted downstream of the promoter. Additional expression vector elements can also be inserted, as discussed elsewhere in this document, to optimize expression.

10

Plasmids according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile bombardment, with the A188XB73 genotype as the preferred genotype (Fromm et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). After microprojectile bombardment 15 the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)).

20 Various homologs, derivative polypeptides, or polypeptide-encoding polynucleotides can be identified and produced from the information in this document. Any technique available can be used and the examples below are merely exemplary.

To identify exemplary variant or derivative polypeptides, polynucleotides, and homologs of the 25 sequences listed here, many techniques, such as using the BLAST program to screen a public (NCBI for example) or commercial (Incyte for example) sequence databases, screening a cDNA or genomic library by hybridization at low or high stringency, and using PCR techniques using degenerate or non-degenerate primers designed to hybridise against the gene you wish to clone, are known in the art. Any GID polynucleotide or cDNA clone can be selected as well as any 30 sequence of the sequence listing. For example, G1073 can be selected. Transgenic plants overexpressing G1073 have the advantageous properties of being large, late flowering, and/or have serrated leaves. The large size and/or late flowering traits would be extremely useful in crops where the vegetative portion of the plant can be commercially harvested (often, vegetative growth stops when plants make the transition to flowering). In this case, it would be 35 advantageous to prevent or delay flowering in order to increase yield or biomass. The plants would also be extremely useful in preparing recombinant therapeutic proteins, such as antibodies

or single chain antibodies. Prevention of flowering would also be useful in plants and crops in order to prevent the spread of transgenic pollen and/or to prevent seed set. G1073 can also be used to manipulate leaf shape.

- 5 In this example, a homolog of G1073 from Glycine max is identified and a construct expressing this Glycine max cDNA is provided. As noted in the Appendices, the NCBI database is screened using the BLAST algorithm and sequences similar to G1073 are identified, including Glycine max cDNA clones or genomic sequences (BF067277, AW349284 and AI736668).
- 10 Using standard techniques, a Glycine max cDNA library is screened using probes derived from the sequence BF067277, AW349284 or AI736668 and a full-length clone is isolated. This full length Glycine max clone can be subcloned into an appropriate expression vector using restriction sites or full-length sequences can be amplified from cDNA or genomic DNA by PCR and subcloned into an appropriate expression vector. Also using standard techniques, a fragment
- 15 incorporating all or part of the Glycine max sequence, or a fragment of another homolog, is produced with substitution or site-specific mutations. This fragment can be used in PCR amplification to replace all or any of the nucleotides to result in amino acid changes or codon changes. Alternatively, oligos incorporating the substitution change(s) can be used in homologous recombination techniques to replace nucleotides in a sequence. Other available
- 20 techniques, known in the art, can also be used. Once the sequence differences between any sequence listed or described here to that of a known sequence is displayed, one of skill in the art can use any available method to make one or more substitution changes in the nucleotides or the polypeptides. These changes will preferably result in changes in the amino acid sequence of the encoded polypeptide, creating a derivative or variant polypeptide.
- 25 The changes or substitutions can also incorporate preferred codons for a particular species or group of plants. Preferred codons for a number of different plants are known in the art. The changes can also delete or add amino acid residues. One skilled in the art is familiar with a variety of techniques for manipulating a polypeptide-encoding sequence to make one or more
- 30 changes, substitutions, deletions, or additions, as desired.

As shown here, the sequences listed have homologs in other plant species. Any of the manipulations, procedures for producing transgenic plants, or analysis of the transgenic plants, can be performed using the homolog sequence in place of the specifically listed sequence. Thus,

35 for example, transgenic plants employing the homolog of G1073 from, for example, *Lycopersicon esculentum*, *Medicago truncatula*, *Oryza sativa*, *Hordeum vulgare*, *Glycine max*,

- Lotus japonicus, Solanum tuberosum, Sorghum propinquum, Pinus taeda, Triticum aestivum, Pisum sativu, Antirrhinum majus, Daucus carota, Nicotiana tabacum, Brassica napus, Zea mays, Volvox carteri f. nagariensis, or Chlamydomonas reinhardtii can be used to create plants having ectopic expression or altered expression of the G1073 homolog. Chimeric sequences, employing
- 5 parts of more than one homolog or parts of a specific sequence, such as G1073, and its homolog(s), can also be created and used. More than one homolog or recombinant polynucleotide can be introduced into a plant to produce a transgenic plant, as known in the art.
- 10 All references, publications, patent documents, web pages, links, sequences of Genbank identifiers, sequences of genomic or EST database identifiers, and other documents cited or mentioned herein are hereby incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to specific embodiments and examples,
- 15 departing from the spirit of the invention. The scope of the invention is not limited to the specific embodiments and examples provided.

What is claimed is:

1. A transgenic plant comprising a recombinant polynucleotide having a nucleotide sequence selected from the group:
 - 5 (a) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence selected from those of SEQ ID NOs.: 2N where N= 1-232, or a complementary nucleotide sequence thereof;
 - (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
 - 10 (c) one of SEQ ID NOs.: 2N-1 where N=1-232, or a complementary nucleotide sequence thereof;
 - (d) a nucleotide sequence comprising one or more silent substitutions in a nucleotide sequence of (c);
 - (e) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
 - 15 (f) a nucleotide sequence comprising at least 15 consecutive nucleotides outside of a conserved domain of any of (a)-(e);
 - (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies one or more of a plant's traits;
 - (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any
 - 20 of (a)-(g);
 - (i) a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence of any of (a)-(g);
 - (j) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of any of (a)-(g);
 - 25 (k) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
 - (l) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.:
 - 30 2N where N=1-232; or
 - (m) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
 - (n) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity outside
 - 35 of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;

- (o) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least 86% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;
- 5 (p) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 90% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;
- (q) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 95% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;
- 10 (r) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 98% sequence identity to a conserved domain of a polypeptide of one of SEQ ID Nos: 2N where N=1-232;
- (s) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos.: 2N where N=1-232;
- 15 (t) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos.: 2N where N=1-232;
- (u) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity over the entire length of a polypeptide of one of SEQ ID Nos. 2N where N=1-232;
- (v) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity over the
20 entire length of a polypeptide of one of SEQ ID Nos. 2N where N=1-232,

wherein the plant possesses an altered trait as compared to a wild type or reference plant, or the plant exhibits an altered phenotype as compared to a wild type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a
25 plant trait as compared to a wild type plant.

2. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said recombinant nucleotide.
- 30 3. The transgenic plant of claim 1, wherein the plant is selected from the following group: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, *Arabidopsis*, spinach, squash, sweet corn, tobacco, tomato, watermelon, mint and
35 other labiates, rosaceous fruits, and vegetable brassicas.

4. An isolated or recombinant polynucleotide having a nucleotide sequence selected from the following group:
- (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from those of SEQ ID Nos: 2N where N=1-232, or a complementary nucleotide sequence thereof;
 - 5 (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
 - (c) one of SEQ ID NOs. 2N-1 where N=1-232, or a complementary nucleotide sequence thereof;
 - (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
 - (e) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
 - 10 (f) a nucleotide sequence comprising at least 15 consecutive nucleotides outside of a conserved domain of any of (a)-(e);
 - (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies one or more of a plant's traits;
 - 15 (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
 - (i) a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence of any of (a)-(g);
 - (j) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of any of (a)-(g);
 - 20 (k) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
 - (l) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232; or
 - 25 (m) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
 - 30 (n) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
 - (o) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least 86% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
 - 35

- (p) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 90% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (q) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 95% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232; and
- (r) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 98% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (s) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (t) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (u) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232;
- (v) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232.

5. The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to the polynucleotide nucleotide.

25

6. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.

7. A method of using the isolated or recombinant polynucleotide of claim 4 for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide, inserting the polynucleotide into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide, thereby producing a modified plant, and selecting for a modified trait.

8. The transgenic plant of claim 1, wherein the trait is selected from the group: enhanced tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced

tolerance to drought; enhanced tolerance to water saturation; enhanced tolerance to radiation;
enhanced tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to
fungal disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation;
decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up
5 heavy metals; and enhanced growth under poor photoconditions.

9. The transgenic plant of claim 1, wherein the trait is an alteration in the level of one or
more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols,
phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins,
10 prenyllipids, glucosinolates, and terpenoids.

10. The transgenic plant of claim 1, wherein the trait is an alteration in one or more physical
characteristics selected from the group: number of trichomes; fruit and seed size and number;
yield of stems; yield of leaves; yield of roots; stability of seeds during storage; susceptibility of
15 the seed to shattering; root hair length; root hair quantity; internode distances; and the quality of
seed coat.

11. The transgenic plant of claim 1, wherein the trait is an alteration in a plant growth
characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants;
20 vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time;
flower abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical
dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.

12. The transgenic plant of claim 1, wherein the trait is an alteration in one or more
25 characteristics selected from the group: protein production; oil production; seed protein
production; seed oil production; insoluble sugar level; soluble sugar level; and starch
composition.

13. The method of claim 7, wherein the trait is selected from the group: enhanced tolerance
30 to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to
drought; enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced
tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to fungal
disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation; decreased
herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy
35 metals; and enhanced growth under poor photoconditions.

14. The method of claim 7, wherein the trait is an alteration in the level of one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyl lipids, glucosinolates, and terpenoids.
- 5
15. The method of claim 7, wherein the trait is an alteration in one or more physical characteristics selected from the group: number of trichomes; fruit and seed size and number; yield of stems; yield of leaves; yield of roots; stability of seeds during storage; susceptibility of the seed to shattering; root hair length; root hair quantity; internode distances; and the quality of seed coat.
- 10
16. The method of claim 7, wherein the trait is an alteration in a plant growth characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.
- 15
17. The method of claim 7, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.
- 20
18. A plant produced by the method of claim 13.
19. A plant produced by the method of claim 14.
- 25
20. A plant produced by the method of claim 15.
21. A plant produced by the method of claim 16.
22. A plant produced by the method of claim 17.
- 30
23. A method of using the isolated or recombinant polynucleotide of claim 4 for producing a plant having a modified trait, the method comprising selecting a polynucleotide that when expressed produces an antisense nucleic acid, inserting the polynucleotide into an expression vector, introducing the vector into a plant or a cell of a plant to express the antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait.
- 35

24. The method of claim 23, wherein the trait is selected from the group: enhanced tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to drought; enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced tolerance to ozone; enhanced tolerance to microbial disease; enhanced tolerance to fungal disease; enhanced tolerance to viral disease; enhanced tolerance to pest infestation; decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy metals; and enhanced growth under poor photoconditions.
25. The method of claim 23, wherein the trait is an alteration in the level of one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids, glucosinolates, and terpenoids.
26. The method of claim 23, wherein the trait is an alteration in one or more physical characteristics selected from the group consisting of: the number of trichomes, fruit and seed size and number, yield of stems, leaves, or roots, stability of seeds during storage, susceptibility of the seed to shattering, root hair length and quantity, internode distances, or the quality of seed coat.
27. The method of claim 23, wherein the trait is an alteration in a plant growth characteristic selected from the group: growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.
28. The method of claim 23, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.
29. A plant produced by the method of claim 24.
30. A plant produced by the method of claim 25.
31. A plant produced by the method of claim 26.
32. A plant produced by the method of claim 27.

33. A plant produced by the method of claim 28.
34. An isolated or recombinant polypeptide comprising a subsequence of at least about 10
5 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim
4, wherein the contiguous amino acids are outside of a conserved domain.
35. An isolated or recombinant polypeptide comprising a subsequence of at least about 20
10 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim
4, wherein the contiguous amino acids are outside of a conserved domain.
36. An isolated or recombinant polypeptide comprising a subsequence of at least about 30
contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim
4, wherein the contiguous amino acids are outside of a conserved domain.
15
37. An isolated or recombinant polypeptide comprising a subsequence of at least about 10
contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim
4, wherein the contiguous amino acids are within a conserved domain.
- 20 38. An isolated or recombinant polypeptide comprising a subsequence of at least about 20
contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim
4, wherein the contiguous amino acids are within a conserved domain.
39. An isolated or recombinant polypeptide comprising a subsequence of at least about 30
25 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim
4, wherein the contiguous amino acids are within a conserved domain.
40. An isolated or recombinant polypeptide having at least 31% sequence identity over the
entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N
30 where N=1-232, or the length of the polypeptide itself.
41. An isolated or recombinant polypeptide having at least 60% sequence identity over the
entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N
35 where N=1-232, or the length of the polypeptide itself.

42. An isolated or recombinant polypeptide having at least 75% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232, or the length of the polypeptide itself.
- 5 43. An isolated or recombinant polypeptide having at least 95% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-232, or the length of the polypeptide itself.
44. An isolated or recombinant polynucleotide having the sequence one of SEQ ID Nos.: 2N-1 where N=1-232, or a complementary nucleotide sequence thereof..
- 10
45. The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 37.
46. The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 53, 79, 81, 107, 125, 153, 167, 203, 223, 289, 285, or 287.
- 15
47. The polynucleotide of claim 44, which has the sequence of one of SEQ ID Nos.: 313, 345, 365, 395, 417, 425, 435, 455, 457, 459, 461, or 463.
- 20
48. A computer readable medium having stored sequence information comprising the polynucleotide sequence of claim 44.
49. The computer readable medium of claim 48, having stored sequence information comprising the sequence of one of SEQ ID Nos.: 1-37.
- 25
50. The computer readable medium of claim 48, having stored sequence information comprising the sequence of one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.
- 30
51. The computer readable medium of claim 48, having stored sequence information comprising the polynucleotide sequence of one of SEQ ID Nos.: 313, 314, 345, 346, 365, 366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461, 462, 463, or 464.
- 35

52. A method of identifying a homolog sequence from a database comprising a plurality of known plant sequences, the method comprising: inputting sequence information selected from one or more of SEQ ID Nos. 1-464; and querying the database to identify a homolog sequence.
53. The method of claim 52, wherein the database being queried comprises a database of known genomic, cDNA, EST, or protein sequences.
54. The method of claim 52, wherein inputting sequence information comprises copying the sequence information from a CD.
55. The method of claim 52, wherein the sequence data comprises one of SEQ ID Nos.: 1-37.
56. The method of claim 52, wherein the sequence data comprises one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.
57. The method of claim 52, wherein the sequence data comprises of SEQ ID Nos.: 313, 314, 345, 346, 365, 366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461, 462, 463, or 464.
58. The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acid region of one of SEQ ID Nos.: 1-37.
59. The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acids region one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.
60. The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acid region of one of SEQ ID Nos.: 313, 314, 345, 346, 365, 366, 395, 396, 461, 462, 417, 418, 425, 426, 435, 436, 455, 456, 457, 458, 459, 460, 461, 462, 463, or 464.
61. A homolog identified by the method of claim 52.
62. The homolog of claim 61, identified by the method of claim 53.

63. The homolog of claim 61, identified by the method of claim 54.
64. The homolog of claim 61, identified by the method of claim 55.
- 5 65. The homolog of claim 61, identified by the method of claim 55.
66. The homolog of claim 61, identified by the method of claim 56.
- 10 67. The homolog of claim 61, identified by the method of claim 57.
68. The homolog of claim 61, identified by the method of claim 58.
69. The homolog of claim 61, identified by the method of claim 59.
- 15 70. The homolog of claim 61, identified by the method of claim 60.

SEQUENCE LISTING

<110> Pilgrim, Marsha
 Creelman, Robert
 Dubell, Arnold
 Heard, Jacqueline
 Jiang, Cai-Zhong
 Keddie, James
 Adam, Luc
 Ratcliffe, Oliver
 Reuber, T. Lynne
 Riechmann, Jose Luis
 Yu, Guo-Liang
 Pineda, Omaira

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 203

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Thr Glu Ser Trp Gly Asp Leu Pro Leu Lys Glu Asn Asp Ser Glu Asp
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Met Leu Val Tyr Gly Ile Leu Asn Asp Ala Phe His Gly Gly Trp Glu
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Lys Ile Glu Thr Pro Glu Ser Phe Ala Ala Val Asp Ser Val Pro Val
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Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Lys Ser Lys Arg Ser Ser
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Phe Ser Ser Ser Asn Glu Asn Gly Ala Pro Lys Lys Arg Arg Thr Val
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 Ser Pro Ile Ser Ser Arg Pro Pro Ala Asn Asn Leu Glu Glu Leu Met
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 Arg Phe Ser Ala Ala Ala Asp Asp Gly Gly Leu Gly Gly Gly Gly Gly
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gga gga gga gga gga agt gct tct tct tca tcg gga aat cga tgg ccg
 192
 Gly Gly Gly Gly Gly Ser Ala Ser Ser Ser Ser Gly Asn Arg Trp Pro
 50 55 60

aga gaa gaa act tta gct ctt ctt cgg atc cga tcc gat atg gat tct
 240
 Arg Glu Glu Thr Leu Ala Leu Leu Arg Ile Arg Ser Asp Met Asp Ser
 65 70 75 80

act ttt cgt gat gct act ctc aaa gct cct ctt tgg gaa cat gtt tcc
 288
 Thr Phe Arg Asp Ala Thr Leu Lys Ala Pro Leu Trp Glu His Val Ser
 85 90 95

agg aag cta ttg gag tta ggt tac aaa cga agt tca aag aaa tgc aaa
 336
 Arg Lys Leu Leu Glu Leu Gly Tyr Lys Arg Ser Ser Lys Lys Cys Lys
 100 105 110

gag aaa ttc gaa aac gtt cag aaa tat tac aaa cgt act aaa gaa act
 384
 Glu Lys Phe Glu Asn Val Gln Lys Tyr Tyr Lys Arg Thr Lys Glu Thr
 115 120 125

cgc ggt ggt cgt cat gat ggt aaa gct tac aag ttc ttc tct cag ctt
432

Arg Gly Gly Arg His Asp Gly Lys Ala Tyr Lys Phe Phe Ser Gln Leu
130 135 140

gaa gct ctc aac act act cct cct cct cct cct tct cat cct cac gct
480

Glu Ala Leu Asn Thr Thr Pro Pro Pro Pro Pro Ser His Pro His Ala
145 150 155 160

cat caa cca gaa cag aaa caa caa caa cca caa caa gag atg gtc
528

His Gln Pro Glu Gln Lys Gln Gln Gln Gln Pro Gln Gln Glu Met Val
165 170 175

atg agc tcg gaa caa tca tca tta cca tca tca tca aga tgg cca aag
576

Met Ser Ser Glu Gln Ser Ser Leu Pro Ser Ser Ser Arg Trp Pro Lys
180 185 190

gca gag att cta gcg ctt ata aac ctg aga agt gga atg gaa cca agg
624

Ala Glu Ile Leu Ala Leu Ile Asn Leu Arg Ser Gly Met Glu Pro Arg
195 200 205

tac caa gat aat gta cct aaa gga ctt cta tgg gaa gag atc tca act
672

Tyr Gln Asp Asn Val Pro Lys Gly Leu Leu Trp Glu Glu Ile Ser Thr
210 215 220

tca atg aag aga atg gga tac aac aga aac gct aag aga tgt aaa gag
720

Ser Met Lys Arg Met Gly Tyr Asn Arg Asn Ala Lys Arg Cys Lys Glu
225 230 235 240

aaa tgg gaa aac ata aac aaa tac tac aag aaa gtt aaa gaa agc aac
768

Lys Trp Glu Asn Ile Asn Lys Tyr Tyr Lys Lys Val Lys Glu Ser Asn
245 250 255

aac agc aac tac aac aac aag aat caa tga

798

Asn Ser Asn Tyr Asn Asn Lys Asn Gln
260 265

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Ser Pro Ile Ser Ser Arg Pro Pro Ala Asn Asn Leu Glu Glu Leu Met
20 25 30

Arg Phe Ser Ala Ala Ala Asp Asp Gly Gly Leu Gly Gly Gly Gly Gly
35 40 45

Gly Gly Gly Gly Gly Ser Ala Ser Ser Ser Ser Gly Asn Arg Trp Pro

50 55 60
 Arg Glu Glu Thr Leu Ala Leu Leu Arg Ile Arg Ser Asp Met Asp Ser
 65 70 75 80
 Thr Phe Arg Asp Ala Thr Leu Lys Ala Pro Leu Trp Glu His Val Ser
 85 90 95
 Arg Lys Leu Leu Glu Leu Gly Tyr Lys Arg Ser Ser Lys Lys Cys Lys
 100 105 110
 Glu Lys Phe Glu Asn Val Gln Lys Tyr Tyr Lys Arg Thr Lys Glu Thr
 115 120 125
 Arg Gly Gly Arg His Asp Gly Lys Ala Tyr Lys Phe Phe Ser Gln Leu
 130 135 140
 Glu Ala Leu Asn Thr Thr Pro Pro Pro Pro Pro Ser His Pro His Ala
 145 150 155 160
 His Gln Pro Glu Gln Lys Gln Gln Gln Gln Pro Gln Gln Glu Met Val
 165 170 175
 Met Ser Ser Glu Gln Ser Ser Leu Pro Ser Ser Ser Arg Trp Pro Lys
 180 185 190
 Ala Glu Ile Leu Ala Leu Ile Asn Leu Arg Ser Gly Met Glu Pro Arg
 195 200 205
 Tyr Gln Asp Asn Val Pro Lys Gly Leu Leu Trp Glu Glu Ile Ser Thr
 210 215 220
 Ser Met Lys Arg Met Gly Tyr Asn Arg Asn Ala Lys Arg Cys Lys Glu
 225 230 235 240
 Lys Trp Glu Asn Ile Asn Lys Tyr Tyr Lys Lys Val Lys Glu Ser Asn
 245 250 255
 Asn Ser Asn Tyr Asn Asn Lys Asn Gln
 260 265

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tagaacacca aagtta atg gag agc tca aac agg agc agc aac aac caa tca
112

Met Glu Ser Ser Asn Arg Ser Ser Asn Asn Gln Ser
1 5 10

caa gat gac aag caa gct cgt ttc cgg gga gtt cga aga agg cct tgg
160

Gln Asp Asp Lys Gln Ala Arg Phe Arg Gly Val Arg Arg Arg Pro Trp
15 20 25

gga aag ttt gca gca gag att cga gac ccg tcg aga aac ggt gcc cgt
208

Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg
30 35 40

ctt tgg ctc ggg aca ttt gag acc gct gag gag gca gca agg gct tat
256

Leu Trp Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr
45 50 55 60

gac cga gca gcc ttt aac ctt agg ggt cat ctc gct ata ctc aac ttc
304

Asp Arg Ala Ala Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe
65 70 75

cct aat gag tat tat cca cgt atg gac gac tac tcg ctt cgc cct cct
352

Pro Asn Glu Tyr Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro
80 85 90

tat gct tct tct tct tcg tcg tcg tca tcg ggt tca act tct act aat
400

Tyr Ala Ser Ser Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn
95 100 105

gtg agt cga caa aac caa aga gaa gtt ttc gag ttt gag tat ttg gac
448

Val Ser Arg Gln Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp
110 115 120

gat aag gtt ctt gaa gaa ctt ctt gat tca gaa gaa agg aag aga taa
496

Asp Lys Val Leu Glu Glu Leu Leu Asp Ser Glu Glu Arg Lys Arg
125 130 135

tcacgattag ttttgtttg atattttatg tggcactggt gtggctacct acgtgcatta
556

tgtgcatgta taggtcgctt gattagtact ttataacatg catgccacga ccataaattg
616

taagagaaga cgtactttgc gttttcatga aatatgaatg ttagatgggt tgagtacaaa
676

aaaaaaaaa aaaaaaaaaa
696

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1 5 10 15

Gln Ala Arg Phe Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
20 25 30

Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg Leu Trp Leu Gly
35 40 45

Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala
50 55 60

Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe Pro Asn Glu Tyr
65 70 75 80

Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro Tyr Ala Ser Ser
85 90 95

Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn Val Ser Arg Gln
100 105 110

Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp Asp Lys Val Leu
115 120 125

Glu Glu Leu Leu Asp Ser Glu Glu Arg Lys Arg
130 135

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56

Met Gly Arg Gly Lys Ile
1 5

gag ata aag aag ata gag aat cag acg gcg agg caa gtg acc ttc tcc
104

Glu Ile Lys Lys Ile Glu Asn Gln Thr Ala Arg Gln Val Thr Phe Ser
10 15 20

aag aga aga act ggt ctt ata aag aag act cgt gag ctc tct att ctc
152

Lys Arg Arg Thr Gly Leu Ile Lys Lys Thr Arg Glu Leu Ser Ile Leu
25 30 35

tgt gac gct cac ato ggt ctc atc gtc ttc tca gcc acc gga aag ctt
200

Cys Asp Ala His Ile Gly Leu Ile Val Phe Ser Ala Thr Gly Lys Leu
40 45 50

tcc gag ttc tgc tcc gaa cag aac agg atg cct caa ctc att gac cga
 248
 Ser Glu Phe Cys Ser Glu Gln Asn Arg Met Pro Gln Leu Ile Asp Arg
 55 60 65 70
 tac ttg cat acc aac gga ttg cga ctt cct gat cat cat gac gac cag
 296
 Tyr Leu His Thr Asn Gly Leu Arg Leu Pro Asp His His Asp Asp Gln
 75 80 85
 gag caa ttg cac cat gag atg gaa cta cta aga aga gag aca tgt aac
 344
 Glu Gln Leu His His Glu Met Glu Leu Leu Arg Arg Glu Thr Cys Asn
 90 95 100
 ctt gag ctt cgt ctg cgt cca ttc cat gga cat gac tta gcc tcc att
 392
 Leu Glu Leu Arg Leu Arg Pro Phe His Gly His Asp Leu Ala Ser Ile
 105 110 115
 cct cct aat gag ctt gac gga ctc gag aga cag cta gaa cat tct gtc
 440
 Pro Pro Asn Glu Leu Asp Gly Leu Glu Arg Gln Leu Glu His Ser Val
 120 125 130
 ctc aaa gtc cgt gag cgt aag agg agg atg cta gaa gaa gat aac aac
 488
 Leu Lys Val Arg Glu Arg Lys Arg Arg Met Leu Glu Glu Asp Asn Asn
 135 140 145 150
 aac atg tac cgt tgg ctt cat gag cat cgt gca gcg atg gag ttt caa
 536
 Asn Met Tyr Arg Trp Leu His Glu His Arg Ala Ala Met Glu Phe Gln
 155 160 165
 caa gct ggg ata gat acc aaa cca ggg gag tat caa cag ttt ata gag
 584
 Gln Ala Gly Ile Asp Thr Lys Pro Gly Glu Tyr Gln Gln Phe Ile Glu
 170 175 180
 cag ctt cag tgc tat aaa cca ggg gag tat cag cag ttt cta gag cag
 632
 Gln Leu Gln Cys Tyr Lys Pro Gly Glu Tyr Gln Gln Phe Leu Glu Gln
 185 190 195
 cag caa caa caa cca aac agc gtt ctt cag ctt gct aca ctt cct tct
 680
 Gln Gln Gln Gln Pro Asn Ser Val Leu Gln Leu Ala Thr Leu Pro Ser
 200 205 210
 gag att gat cct act tac aat ctc cag ctt gct cag cct aat ctt caa
 728
 Glu Ile Asp Pro Thr Tyr Asn Leu Gln Leu Ala Gln Pro Asn Leu Gln
 215 220 225 230
 aac gat cca acg gcc cag aat gat taa tacaattctc aatagatc
 775
 Asn Asp Pro Thr Ala Gln Asn Asp
 235

tactctttct ttatggagac agattcatga acttttatta cctatatattt gataagccag
835

tgtctttctt tgtgtggcta tggaacctt gtttaaagca caatgcactt gagttcttgg
895

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944

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1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Thr Gly Leu Ile Lys Lys Thr
20 25 30

Arg Glu Leu Ser Ile Leu Cys Asp Ala His Ile Gly Leu Ile Val Phe
35 40 45

Ser Ala Thr Gly Lys Leu Ser Glu Phe Cys Ser Glu Gln Asn Arg Met
50 55 60

Pro Gln Leu Ile Asp Arg Tyr Leu His Thr Asn Gly Leu Arg Leu Pro
65 70 75 80

Asp His His Asp Asp Gln Glu Gln Leu His His Glu Met Glu Leu Leu
85 90 95

Arg Arg Glu Thr Cys Asn Leu Glu Leu Arg Leu Arg Pro Phe His Gly
100 105 110

His Asp Leu Ala Ser Ile Pro Pro Asn Glu Leu Asp Gly Leu Glu Arg
115 120 125

Gln Leu Glu His Ser Val Leu Lys Val Arg Glu Arg Lys Arg Arg Met
130 135 140

Leu Glu Glu Asp Asn Asn Asn Met Tyr Arg Trp Leu His Glu His Arg
145 150 155 160

Ala Ala Met Glu Phe Gln Gln Ala Gly Ile Asp Thr Lys Pro Gly Glu
165 170 175

Tyr Gln Gln Phe Ile Glu Gln Leu Gln Cys Tyr Lys Pro Gly Glu Tyr
180 185 190

Gln Gln Phe Leu Glu Gln Gln Gln Gln Gln Pro Asn Ser Val Leu Gln

195 200 205

Leu Ala Thr Leu Pro Ser Glu Ile Asp Pro Thr Tyr Asn Leu Gln Leu
210 215 220

Ala Gln Pro Asn Leu Gln Asn Asp Pro Thr Ala Gln Asn Asp
225 230 235

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120

aagctgtgta aatctcttgt agtttttctg ccgatataca ttttcattgt gttgagggtg
180

aacgataatc aagaacgaga gagagagaga gcaagagcaa gagatttcta ctacagaaga
240

tttattatat tgatcatttt gtgtgatcaa cccataaaaa cagagagaca tagacaagtc
300

catgtttcga tgtttcgatc tctcttactg tctaaacggc gaaataaaaa gtctgatggg
360

tgtaacttat tgcattgtata ttagtaaadc agcttgagcc caagttaaag ctgaaacttg
420

ggtttgca atg gct ggt att gat aat aaa gct gct gta atg gga gaa tgg
470

Met Ala Gly Ile Asp Asn Lys Ala Ala Val Met Gly Glu Trp
1 5 10

ttc gac tgt agt act act aac cac agg aag aga tcg aaa gcg gaa ctt
518

Phe Asp Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu
15 20 25 30

ggt aga gag ttt tct tta aat tac atc aag aat gag gat tct ttg caa
566

Gly Arg Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln
35 40 45

acc acc ttt caa gaa agt tca cga gga gct ctt cgt gaa agg att gct
614

Thr Thr Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala
50 55 60

gcg aga tcc ggg ttt aat gca ccg tgg tta aac act gag gat att ctt
662

Ala Arg Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu
65 70 75

cag tcg aaa tct tta acc atc tct tct cct ggt ctt agt cct gca act
 710
 Gln Ser Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr
 80 85 90

ctg tta gag tet cct gtt ttc ctc tca aac cct ttg cta tct cca aca
 758
 Leu Leu Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr
 95 100 105 110

acc ggg aag ctc tca tca gta cct tct gat aag gct aaa gct gag tta
 806
 Thr Gly Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu
 115 120 125

ttt gac gac att acc aca tcc tta gcc ttc caa acc att tca gga agt
 854
 Phe Asp Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser
 130 135 140

ggc ctt gat cct act aac atc gct tta gaa ccc gat gat tcc caa gac
 902
 Gly Leu Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp
 145 150 155

tat gaa gaa aga cag ctc ggc ggt tta gga gac tcg atg gct tgt tgt
 950
 Tyr Glu Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys
 160 165 170

gca cct gca gat gat gga tac aac tgg aga aaa tat gga caa aag cta
 998
 Ala Pro Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu
 175 180 185 190

gtt aaa gga agt gag tat ccg cgg agc tat tac aag tgc acg cac ccg
 1046
 Val Lys Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro
 195 200 205

aat tgt gag gcc aag aag aag gtt gaa cgg tct cgg gaa ggt cat att
 1094
 Asn Cys Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile
 210 215 220

ata gag atc ata tac aca gga gat cat ata cac agc aaa cct cca cct
 1142
 Ile Glu Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro
 225 230 235

aac cgc cgg tca ggg att gga tca tcc ggt act ggc caa gac atg caa
 1190
 Asn Arg Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln
 240 245 250

ata gat gca acc gaa tac gaa ggt ttt gct gga acc aat gag aac ata
 1238
 Ile Asp Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile
 255 260 265 270

gaa tgg aca tca cct gta tct gca gag ctc gaa tac gga agc cat tca
 1286
 Glu Trp Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser
 275 280 285

gga tca atg cag gtt caa aac ggg act cat cag ttc ggg tat ggt gat
 1334
 Gly Ser Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp
 290 295 300

gca gca gct gat gcc tta tat aga gat gaa aac gaa gat gat cgc acg
 1382
 Ala Ala Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr
 305 310 315

tcc cac atg agt gtt tcc ctg act tac gat gga gag gta gaa gag tcc
 1430
 Ser His Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser
 320 325 330

gaa tca aag aga agg aaa cta gaa gct tat gca aca gaa acg agt gga
 1478
 Glu Ser Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly
 335 340 345 350

tca acc aga gcc agc cgt gag cca aga gtt gtg gtg cag acc aca agt
 1526
 Ser Thr Arg Ala Ser Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser
 355 360 365

gac att gac atc ctc gat gat ggt tat cgc tgg cgc aag tat ggg caa
 1574
 Asp Ile Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln
 370 375 380

aaa gtc gtt aaa gga aac ccg aat cca agg agc tac tat aaa tgc aca
 1622
 Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr
 385 390 395

gct aat gga tgt acc gta acg aag cat gta gag aga gcc tct gat gac
 1670
 Ala Asn Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp
 400 405 410

ttc aag agc gta cta aca act tat ata ggc aag cac acc cac gtt gta
 1718
 Phe Lys Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val
 415 420 425 430

cca gca gca cgc aac agc agc cac gtc ggt gca ggc agt tca ggg act
 1766
 Pro Ala Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr
 435 440 445

ctc caa ggc agt tta gcg act cag acc cac aac cac aat gtg cac tat
 1814
 Leu Gln Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr
 450 455 460

cca atg cca cac agt aga tct gag gga ctg gcc aca gcc aac tca tct
 1862
 Pro Met Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser
 465 470 475

cta ttt gac ttc cag tca cac ctg agg cat cct aca ggt ttc tcc gtt
 1910
 Leu Phe Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val
 480 485 490

tac ata ggc caa tct gag ctt tct gat ctt tca atg cct ggt cta act
 1958
 Tyr Ile Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr
 495 500 505 510

att ggg caa gag aag ctt acc agc ctg cag gcg cct gac att ggg gat
 2006
 Ile Gly Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp
 515 520 525

cca act ggc cta atg ttg cag tta gca gca cag ccg aag gtg gaa cca
 2054
 Pro Thr Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro
 530 535 540

gtg tca cca caa cag gga ctt gat ttg tca gcg agc tca ttg ata tgc
 2102
 Val Ser Pro Gln Gln Gly Leu Asp Leu Ser Ala Ser Ser Leu Ile Cys
 545 550 555

aga gag atg ttg agt aga tta cga cag ata tga aacaaatctc tttgttcaact
 2155
 Arg Glu Met Leu Ser Arg Leu Arg Gln Ile
 560 565

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 2215

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Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu Gly Arg
 20 25 30

Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln Thr Thr
 35 40 45

Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala Ala Arg
 50 55 60

Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu Gln Ser
 65 70 75 80

Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu
 85 90 95

Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr Thr Gly
 100 105 110

Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu Phe Asp
 115 120 125

Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser Gly Leu
 130 135 140

Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp Tyr Glu
 145 150 155 160

Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys Ala Pro
 165 170 175

Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys
 180 185 190

Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro Asn Cys
 195 200 205

Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile Ile Glu
 210 215 220

Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro Asn Arg
 225 230 235 240

Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln Ile Asp
 245 250 255

Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile Glu Trp
 260 265 270

Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser Gly Ser
 275 280 285

Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp Ala Ala
 290 295 300

Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr Ser His
 305 310 315 320

Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser Glu Ser
 325 330 335

Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly Ser Thr
 340 345 350

Arg Ala Ser Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser Asp Ile
 355 360 365

Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val
 370 375 380

Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ala Asn
 385 390 395 400

Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp Phe Lys
 405 410 415

Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val Pro Ala
 420 425 430

Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr Leu Gln
 435 440 445

Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr Pro Met
 450 455 460

Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser Leu Phe
 465 470 475 480

Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val Tyr Ile
 485 490 495

Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr Ile Gly
 500 505 510

Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp Pro Thr
 515 520 525

Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro Val Ser
 530 535 540

Pro Gln Gln Gly Leu Asp Leu Ser Ala Ser Ser Leu Ile Cys Arg Glu
 545 550 555 560

Met Leu Ser Arg Leu Arg Gln Ile

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Met Ala Val Glu Leu Met Thr
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cgg aat tac atc tcc ggc gtc gga gct gat agc ttc gcc gtt caa gaa
 102

Arg Asn Tyr Ile Ser Gly Val Gly Ala Asp Ser Phe Ala Val Gln Glu
 10 15 20

gca gct gct tca gga ctg aaa agt atc gaa aat ttc atc ggt tta atg
 150

Ala Ala Ala Ser Gly Leu Lys Ser Ile Glu Asn Phe Ile Gly Leu Met
 25 30 35

tct cgt gat agc ttt aac tct gat cag cca tct tct tcc gcc tcc
 198

Ser Arg Asp Ser Phe Asn Ser Asp Gln Pro Ser Ser Ser Ser Ala Ser
 40 45 50 55

gcc tcc gcc tcc gcc gcc gca gat ctt gaa tca gct cgt aac aca acg
 246

Ala Ser Ala Ser Ala Ala Ala Asp Leu Glu Ser Ala Arg Asn Thr Thr
 60 65 70

gcg gac gcg gct gtt tca aag ttt aaa aga gtc ata tct ctg tta gat
 294

Ala Asp Ala Ala Val Ser Lys Phe Lys Arg Val Ile Ser Leu Leu Asp
 75 80 85

cga act cga acc gga cac gcc cgg ttt aga cgt gct ccg gtt cat gtt
 342

Arg Thr Arg Thr Gly His Ala Arg Phe Arg Arg Ala Pro Val His Val
 90 95 100

att tct ccg gtt ctt tta caa gaa gaa cca aaa acg acg ccg ttt cag
 390

Ile Ser Pro Val Leu Leu Gln Glu Glu Pro Lys Thr Thr Pro Phe Gln
 105 110 115

tct cct ctt cct cct ccg ccg caa atg atc cga aaa ggt tcg ttt tct
 438

Ser Pro Leu Pro Pro Pro Pro Gln Met Ile Arg Lys Gly Ser Phe Ser
 120 125 130 135

tca tcg atg aaa acg att gat ttc tca tct ctg tcc tct gta aca acg
 486

Ser Ser Met Lys Thr Ile Asp Phe Ser Ser Leu Ser Ser Val Thr Thr
 140 145 150

gaa tca gac aac cag aag aag att cat cat cat caa cgt ccc tct gaa
 534

Glu Ser Asp Asn Gln Lys Lys Ile His His His Gln Arg Pro Ser Glu
 155 160 165

acg gcg ccg ttt gcg tct caa act caa agc ctc tcc acg acg gtc tcg
582

Thr Ala Pro Phe Ala Ser Gln Thr Gln Ser Leu Ser Thr Thr Val Ser
170 175 180

tct ttc tca aaa tca aca aag aga aaa tgt aac tct gag aat ctt ctc
630

Ser Phe Ser Lys Ser Thr Lys Arg Lys Cys Asn Ser Glu Asn Leu Leu
185 190 195

acc gga aaa tgc gct tcc gct tct tcc tcc ggt cgt tgt cat tgc tcg
678

Thr Gly Lys Cys Ala Ser Ala Ser Ser Ser Gly Arg Cys His Cys Ser
200 205 210 215

aag aaa aga aag ata aaa cag agg aga ata att agg gtt ccg gcg ata
726

Lys Lys Arg Lys Ile Lys Gln Arg Arg Ile Ile Arg Val Pro Ala Ile
220 225 230

agt gca aaa atg tcc gat gta cca ccg gac gat tat tca tgg agg aaa
774

Ser Ala Lys Met Ser Asp Val Pro Pro Asp Asp Tyr Ser Trp Arg Lys
235 240 245

tac gga caa aaa cca att aaa gga tct cca cat cca aga gga tat tat
822

Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr
250 255 260

aag tgt agt agc gta aga ggt tgt cca gca cgt aaa cat gtt gag aga
870

Lys Cys Ser Ser Val Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg
265 270 275

gca gct gat gat tcg tcc atg ttg att gtt act tat gaa gga gat cat
918

Ala Ala Asp Asp Ser Ser Met Leu Ile Val Thr Tyr Glu Gly Asp His
280 285 290 295

aat cat tct ctc tcc gcc gct gat ctc gcc gga gcc gcc gtt gct gat
966

Asn His Ser Leu Ser Ala Ala Asp Leu Ala Gly Ala Ala Val Ala Asp
300 305 310

ctt att ttg gaa tcg tct tga aaagaacaaa tctttattta aggtttttat
1017

Leu Ile Leu Glu Ser Ser
315

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1077

caaaatcaaa aagcttttgc taaaaaaaaa aaaaaaaaa
1115

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 Glu Asn Phe Ile Gly Leu Met Ser Arg Asp Ser Phe Asn Ser Asp Gln
 35 40 45
 Pro Ser Ser Ser Ser Ala Ser Ala Ser Ala Ser Ala Ala Ala Asp Leu
 50 55 60
 Glu Ser Ala Arg Asn Thr Thr Ala Asp Ala Ala Val Ser Lys Phe Lys
 65 70 75 80
 Arg Val Ile Ser Leu Leu Asp Arg Thr Arg Thr Gly His Ala Arg Phe
 85 90 95
 Arg Arg Ala Pro Val His Val Ile Ser Pro Val Leu Leu Gln Glu Glu
 100 105 110
 Pro Lys Thr Thr Pro Phe Gln Ser Pro Leu Pro Pro Pro Pro Gln Met
 115 120 125
 Ile Arg Lys Gly Ser Phe Ser Ser Ser Met Lys Thr Ile Asp Phe Ser
 130 135 140
 Ser Leu Ser Ser Val Thr Thr Glu Ser Asp Asn Gln Lys Lys Ile His
 145 150 155 160
 His His Gln Arg Pro Ser Glu Thr Ala Pro Phe Ala Ser Gln Thr Gln
 165 170 175
 Ser Leu Ser Thr Thr Val Ser Ser Phe Ser Lys Ser Thr Lys Arg Lys
 180 185 190
 Cys Asn Ser Glu Asn Leu Leu Thr Gly Lys Cys Ala Ser Ala Ser Ser
 195 200 205
 Ser Gly Arg Cys His Cys Ser Lys Lys Arg Lys Ile Lys Gln Arg Arg
 210 215 220
 Ile Ile Arg Val Pro Ala Ile Ser Ala Lys Met Ser Asp Val Pro Pro
 225 230 235 240
 Asp Asp Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser

20

gat gtc aaa aat tac tgg aac acc cat ctg agt aaa aaa cat gag tct
454
Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His Glu Ser
100 105 110

tcg tgt tgt aag tct aaa atg aaa aag aaa aac att att tcc cct cct
502
Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser Pro Pro
115 120 125 130

aca aca ccg gtc caa aaa atc ggt gtt ttt aag cct cga cct cga tcc
550
Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro Arg Ser
135 140 145

ttc tct gtt aac aat ggt tgc agc cat ctc aat ggt ctg cca gaa gtt
598
Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro Glu Val
150 155 160

gat tta att cct tca tgc ctt gga ctc aag aaa aat aat gtt tgt gaa
646
Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val Cys Glu
165 170 175

aat agt atc aca tgt aac aaa gat gat gag aaa gat gat ttt gtg aat
694
Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe Val Asn
180 185 190

aat cta atg aat gga gat aat atg tgg ttg gag aat tta ctg ggg gaa
742
Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu Gly Glu
195 200 205 210

aac caa gaa gct gat gcg att gtt cct gaa gcg acg aca gct gaa cat
790
Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala Glu His
215 220 225

ggg gcc act ttg gcg ttt gac gtt gag caa ctt tgg agt ctg ttt gat
838
Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu Phe Asp
230 235 240

gga gag act gtt gaa ctt gat tag tggtttctcac cgtttgttta agattgtggg
892
Gly Glu Thr Val Glu Leu Asp
245

tggtttttct ttcgtatttt agtaatgtat ttttctgtat gaagtaaaga atttcagcat
952

tttaagaaaa atgggttatgt ttctacgtaa taataaaaaa cgttatttat aaaaaaaaaa
1012

aaaaaaaaaa aaaaaaaaaa a
1033

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Glu Asp Ser Leu Leu Arg Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys
20 25 30

Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50 55 60

Arg Leu Ser Asn Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Glu Ser Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser
115 120 125

Pro Pro Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro
130 135 140

Arg Ser Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro
145 150 155 160

Glu Val Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val
165 170 175

Cys Glu Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe
180 185 190

Val Asn Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu
195 200 205

Gly Glu Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala
210 215 220

Glu His Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu
225 230 235 240

Phe Asp Gly Glu Thr Val Glu Leu Asp
245

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taa atg gaa tcg agt agc gtt gat gag agt act aca agt aca ggt tcc
108
Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser
1 5 10 15

atc tgt gaa acc ccg gcg ata act ccg gcg aaa aag tcg tcg gta ggt
156
Ile Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly
20 25 30

aac tta tac agg atg gga agc gga tca agc gtt gtg tta gat tca gag
204
Asn Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu
35 40 45

aac ggc gta gaa gct gaa tct agg aag ctt ccg tcg tca aaa tac aaa
252
Asn Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys
50 55 60

ggt gtg gtg cca caa cca aac gga aga tgg gga gct cag att tac gag
300
Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu
65 70 75

aaa cac cag cgc gtg tgg ctc ggg aca ttc aac gaa gaa gac gaa gcc
348
Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala
80 85 90 95

gct cgt gcc tac gac gtc gcg gtt cac agg ttc cgt cgc cgt gac gcc
396
Ala Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala
100 105 110

gtc aca aat ttc aaa gac gtg aag atg gac gaa gac gag gtc gat ttc
444
Val Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe
115 120 125

ttg aat tct cat tcg aaa tct gag atc gtt gat atg ttg agg aaa cat
492
Leu Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His
130 135 140

act tat aac gaa gag tta gag cag agt aaa cgg cgt cgt aat ggt aac
540
Thr Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn

145	150	155
gga aac atg act agg acg ttg tta acg tcg ggg ttg agt aat gat ggt		
588		
Gly Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly		
160	165	170 175
gtt tct acg acg ggg ttt aga tcg gcg gag gca ctg ttt gag aaa gcg		
636		
Val Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala		
	180	185 190
gta acg cca agc gac gtt ggg aag cta aac cgt ttg gtt ata ccg aaa		
684		
Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys		
	195	200 205
cat cac gca gag aaa cat ttt ccg tta ccg tca agt aac gtt tcc gtg		
732		
His His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val		
	210	215 220
aaa gga gtg ttg ttg aac ttt gag gac gtt aac ggg aaa gtg tgg agg		
780		
Lys Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg		
	225	230 235
ttc cgt tac tcg tat tgg aac agt agt cag agt tat gtt ttg act aaa		
828		
Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys		
240	245	250 255
ggg tgg agc agg ttc gtt aag gag aag aat cta cgt gct ggt gac gtg		
876		
Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val		
	260	265 270
gtt agt ttc agt aga tct aac ggt cag gat caa cag ttg tac att ggg		
924		
Val Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly		
	275	280 285
tgg aag tcg aga tcc ggg tca gat tta gat gcg ggt cgg gtt ttg aga		
972		
Trp Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg		
	290	295 300
ttg ttc gga gtt aac att tca ccg gag agt tca aga aac gac gtc gta		
1020		
Leu Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val		
	305	310 315
gga aac aaa aga gtg aac gat act gag atg tta tcg ttg gtg tgt agc		
1068		
Gly Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser		
320	325	330 335
aag aag caa cgc atc ttt cac gcc tcg taa caactcttct tctttttttt		
1118		
Lys Lys Gln Arg Ile Phe His Ala Ser		
	340	

tcttttggtg ttttaataat ttttaaaaac tccattttcg ttttctttat ttgcatcggt
1178

ttctttcttc ttgtttacca aaggttcatg agttgttttt gttgtattga tgaactgtaa
1238

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1281

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Met Glu Ser Ser Ser Val Asp Glu Ser Thr Thr Ser Thr Gly Ser Ile
1 5 10 15

Cys Glu Thr Pro Ala Ile Thr Pro Ala Lys Lys Ser Ser Val Gly Asn
20 25 30

Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp Ser Glu Asn
35 40 45

Gly Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly
50 55 60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65 70 75 80

His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
85 90 95

Arg Ala Tyr Asp Val Ala Val His Arg Phe Arg Arg Arg Asp Ala Val
100 105 110

Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe Leu
115 120 125

Asn Ser His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr
130 135 140

Tyr Asn Glu Glu Leu Glu Gln Ser Lys Arg Arg Arg Asn Gly Asn Gly
145 150 155 160

Asn Met Thr Arg Thr Leu Leu Thr Ser Gly Leu Ser Asn Asp Gly Val
165 170 175

Ser Thr Thr Gly Phe Arg Ser Ala Glu Ala Leu Phe Glu Lys Ala Val
180 185 190

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His
 195 200 205

His Ala Glu Lys His Phe Pro Leu Pro Ser Ser Asn Val Ser Val Lys
 210 215 220

Gly Val Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe
 225 230 235 240

Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly
 245 250 255

Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val
 260 265 270

Ser Phe Ser Arg Ser Asn Gly Gln Asp Gln Gln Leu Tyr Ile Gly Trp
 275 280 285

Lys Ser Arg Ser Gly Ser Asp Leu Asp Ala Gly Arg Val Leu Arg Leu
 290 295 300

Phe Gly Val Asn Ile Ser Pro Glu Ser Ser Arg Asn Asp Val Val Gly
 305 310 315 320

Asn Lys Arg Val Asn Asp Thr Glu Met Leu Ser Leu Val Cys Ser Lys
 325 330 335

Lys Gln Arg Ile Phe His Ala Ser
 340

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 <221> CDS <222> (397)..(2460) <223> G877

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 120

agagaggaag aaggagaaga aaaaaatatt tctttctctc cggctttcaa caaaatctct
 180

cttttttctt tcatcagtgt taaattcgga tccgggtcgg gtgggttttc gggttttggg
 240

gttcggatca gagcacagtt ggatgtagc gacggaactg aggatttcag tttgcggctg
 300

cgggcggtgt gacgggtgtt gtgtgtcgtc ttcttttatt aatcaggagt ttcatcacag
360

tttgatcaga gattcagcca aattcttgga tactaa atg gct ggt ttt gat gaa
414

Met Ala Gly Phe Asp Glu
1 5

aat gtt gct gtg atg gga gaa tgg gtg cct cgt agt cct agt ccc ggg
462

Asn Val Ala Val Met Gly Glu Trp Val Pro Arg Ser Pro Ser Pro Gly
10 15 20

aca ctt ttc tcc tct gct att gga gaa gag aag agc tcg aaa cgt gtt
510

Thr Leu Phe Ser Ser Ala Ile Gly Glu Glu Lys Ser Ser Lys Arg Val
25 30 35

ctt gaa aga gag tta tct ttg aat cat ggt caa gtt att ggt tta gaa
558

Leu Glu Arg Glu Leu Ser Leu Asn His Gly Gln Val Ile Gly Leu Glu
40 45 50

gaa gac act agt agt aat cat aac aag gat tct tca caa agc aat gtt
606

Glu Asp Thr Ser Ser Asn His Asn Lys Asp Ser Ser Gln Ser Asn Val
55 60 65 70

ttt cga ggt ggt ctc agt gaa aga att gct gca aga gct gga ttt aat
654

Phe Arg Gly Gly Leu Ser Glu Arg Ile Ala Ala Arg Ala Gly Phe Asn
75 80 85

gct cca agg ttg aac act gag aat atc cgc acc aac acc gac ttt tcc
702

Ala Pro Arg Leu Asn Thr Glu Asn Ile Arg Thr Asn Thr Asp Phe Ser
90 95 100

att gac tct aac ctt cga tct cct tgc tta acc atc tct tct cct ggc
750

Ile Asp Ser Asn Leu Arg Ser Pro Cys Leu Thr Ile Ser Ser Pro Gly
105 110 115

ctt agc cct gca aca ctc ttg gaa tct cct gtt ttc ctt tct aac cca
798

Leu Ser Pro Ala Thr Leu Leu Glu Ser Pro Val Phe Leu Ser Asn Pro
120 125 130

ttg gct caa cct tct cca act acc ggg aaa ttt cca ttt ctt cct ggt
846

Leu Ala Gln Pro Ser Pro Thr Thr Gly Lys Phe Pro Phe Leu Pro Gly
135 140 145 150

gtt aat ggt aat gca ttg tct tct gag aaa gcg aaa gac gag ttc ttt
894

Val Asn Gly Asn Ala Leu Ser Ser Glu Lys Ala Lys Asp Glu Phe Phe
155 160 165

gat gat att gga gca tca ttc agc ttc cat cct gtt tca aga tca tct
942

Asp Asp Ile Gly Ala Ser Phe Ser Phe His Pro Val Ser Arg Ser Ser

170	175	180
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Ser Ser Phe Phe Gln Gly Thr Thr Glu Met Met Ser Val Asp Tyr Gly 185 190 195		
aac tac aac aat aga tct tct tct cat caa tcc gca gaa gaa gta aaa 1038		
Asn Tyr Asn Asn Arg Ser Ser Ser His Gln Ser Ala Glu Glu Val Lys 200 205 210		
cct ggc tct gaa aac ata gaa agc tcc aat ctt tat ggg att gaa act 1086		
Pro Gly Ser Glu Asn Ile Glu Ser Ser Asn Leu Tyr Gly Ile Glu Thr 215 220 225 230		
gac aat caa aac ggg cag aac aag aca tct gat gtc act aca aac acc 1134		
Asp Asn Gln Asn Gly Gln Asn Lys Thr Ser Asp Val Thr Thr Asn Thr 235 240 245		
agt ctt gaa acc gtg gat cat caa gag gaa gaa gaa gag caa aga cgc 1182		
Ser Leu Glu Thr Val Asp His Gln Glu Glu Glu Glu Gln Arg Arg 250 255 260		
ggg gat tcg atg gct ggt ggt ggc cct gca gag gat gga tat aac tgg 1230		
Gly Asp Ser Met Ala Gly Gly Ala Pro Ala Glu Asp Gly Tyr Asn Trp 265 270 275		
agg aaa tac gga caa aag ttg gtc aaa gga agt gag tat ccg cga agc 1278		
Arg Lys Tyr Gly Gln Lys Leu Val Lys Gly Ser Glu Tyr Pro Arg Ser 280 285 290		
tat tac aag tgc aca aac ccg aat tgt cag gtg aag aag aaa gtt gag 1326		
Tyr Tyr Lys Cys Thr Asn Pro Asn Cys Gln Val Lys Lys Lys Val Glu 295 300 305 310		
aga tca agg gaa ggt cac atc aca gag att ata tac aaa gga gct cat 1374		
Arg Ser Arg Glu Gly His Ile Thr Glu Ile Ile Tyr Lys Gly Ala His 315 320 325		
aat cat ctt aaa cct cca cct aat cgc cgc tca ggg atg caa gta gat 1422		
Asn His Leu Lys Pro Pro Pro Asn Arg Arg Ser Gly Met Gln Val Asp 330 335 340		
gga act gaa caa gtt gaa caa caa caa caa cag aga gat tct gct gca 1470		
Gly Thr Glu Gln Val Glu Gln Gln Gln Gln Arg Asp Ser Ala Ala 345 350 355		
acg tgg gtt agt tgt aat aac act caa caa caa ggt gga agc aat gag 1518		
Thr Trp Val Ser Cys Asn Asn Thr Gln Gln Gln Gly Gly Ser Asn Glu 360 365 370		

aac aat gtc gaa gag gga fct acg aga ttc gag tat gga aac caa tct
 1566
 Asn Asn Val Glu Glu Gly Ser Thr Arg Phe Glu Tyr Gly Asn Gln Ser
 375 380 385 390

 gga tca att caa gct caa acc gga ggt caa tac gag tca ggt gat cct
 1614
 Gly Ser Ile Gln Ala Gln Thr Gly Gly Gln Tyr Glu Ser Gly Asp Pro
 395 400 405

 gtg gtt gtg gtt gat gct tct tca aca ttc tct aat gat gaa gat gaa
 1662
 Val Val Val Val Asp Ala Ser Ser Thr Phe Ser Asn Asp Glu Asp Glu
 410 415 420

 gat gat cga ggg aca cat gga agt gtt tct ttg ggt tac gat gga gga
 1710
 Asp Asp Arg Gly Thr His Gly Ser Val Ser Leu Gly Tyr Asp Gly Gly
 425 430 435

 gga gga ggt ggg gga gga gaa gga gat gaa tca gag tcg aaa aga agg
 1758
 Gly Gly Gly Gly Gly Gly Glu Gly Asp Glu Ser Glu Ser Lys Arg Arg
 440 445 450

 aaa cta gaa gct ttt gca gca gag atg agt gga tca aca aga gcc ata
 1806
 Lys Leu Glu Ala Phe Ala Ala Glu Met Ser Gly Ser Thr Arg Ala Ile
 455 460 465 470

 cgt gag cca aga gtt gtt gtg cag aca acg agt gat gtt gac att ctt
 1854
 Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser Asp Val Asp Ile Leu
 475 480 485

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 1902
 Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly
 490 495 500

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 1950
 Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ala Pro Gly Cys Thr
 505 510 515

 gtg agg aaa cat gtt gaa aga gct tct cat gat ctc aaa tcc gtt ata
 1998
 Val Arg Lys His Val Glu Arg Ala Ser His Asp Leu Lys Ser Val Ile
 520 525 530

 aca act tac gaa ggc aaa cat aac cat gac gtc ccc gct gca cgc aac
 2046
 Thr Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Ala Ala Arg Asn
 535 540 545 550

 agc agc cac gga ggc ggt ggt gat agt ggt aac ggt aac agc ggc ggt
 2094
 Ser Ser His Gly Gly Gly Gly Asp Ser Gly Asn Gly Asn Ser Gly Gly
 555 560 565

tca gcc gca gtt tct cac cat tac cac aac ggt cat cac tca gag ccg
2142

Ser Ala Ala Val Ser His His Tyr His Asn Gly His His Ser Glu Pro
570 575 580

cca cgt ggg aga ttc gac aga caa gtc aca act aac aat cag tct cct
2190

Pro Arg Gly Arg Phe Asp Arg Gln Val Thr Thr Asn Asn Gln Ser Pro
585 590 595

ttt agc cgt ccc ttt agc ttt cag cca cat ttg ggt cct cct tct ggt
2238

Phe Ser Arg Pro Phe Ser Phe Gln Pro His Leu Gly Pro Pro Ser Gly
600 605 610

ttc tcc ttc ggt tta gga caa acc ggt ttg gtt aat ctt tca atg cct
2286

Phe Ser Phe Gly Leu Gly Gln Thr Gly Leu Val Asn Leu Ser Met Pro
615 620 625 630

ggt tta gcg tat ggt caa ggg aaa atg ccg ggt ttg cct cac ccg tat
2334

Gly Leu Ala Tyr Gly Gln Gly Lys Met Pro Gly Leu Pro His Pro Tyr
635 640 645

atg aca caa ccg gtt ggg atg agt gaa gca atg atg cag aga ggg atg
2382

Met Thr Gln Pro Val Gly Met Ser Glu Ala Met Met Gln Arg Gly Met
650 655 660

gaa cca aag gtt gaa ccg gtt tca gat tca gga caa tcg gta tat aac
2430

Glu Pro Lys Val Glu Pro Val Ser Asp Ser Gly Gln Ser Val Tyr Asn
665 670 675

cag atc atg agt aga tta cct cag att tga aatttactct tcttcttctt
2480

Gln Ile Met Ser Arg Leu Pro Gln Ile
680 685

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2540

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2600

aaa
2603

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20 25 30

Lys Ser Ser Lys Arg Val Leu Glu Arg Glu Leu Ser Leu Asn His Gly
 35 40 45
 Gln Val Ile Gly Leu Glu Glu Asp Thr Ser Ser Asn His Asn Lys Asp
 50 55 60
 Ser Ser Gln Ser Asn Val Phe Arg Gly Gly Leu Ser Glu Arg Ile Ala
 65 70 75 80
 Ala Arg Ala Gly Phe Asn Ala Pro Arg Leu Asn Thr Glu Asn Ile Arg
 85 90 95
 Thr Asn Thr Asp Phe Ser Ile Asp Ser Asn Leu Arg Ser Pro Cys Leu
 100 105 110
 Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu Glu Ser Pro
 115 120 125
 Val Phe Leu Ser Asn Pro Leu Ala Gln Pro Ser Pro Thr Thr Gly Lys
 130 135 140
 Phe Pro Phe Leu Pro Gly Val Asn Gly Asn Ala Leu Ser Ser Glu Lys
 145 150 155 160
 Ala Lys Asp Glu Phe Phe Asp Asp Ile Gly Ala Ser Phe Ser Phe His
 165 170 175
 Pro Val Ser Arg Ser Ser Ser Ser Phe Phe Gln Gly Thr Thr Glu Met
 180 185 190
 Met Ser Val Asp Tyr Gly Asn Tyr Asn Asn Arg Ser Ser Ser His Gln
 195 200 205
 Ser Ala Glu Glu Val Lys Pro Gly Ser Glu Asn Ile Glu Ser Ser Asn
 210 215 220
 Leu Tyr Gly Ile Glu Thr Asp Asn Gln Asn Gly Gln Asn Lys Thr Ser
 225 230 235 240
 Asp Val Thr Thr Asn Thr Ser Leu Glu Thr Val Asp His Gln Glu Glu
 245 250 255
 Glu Glu Glu Gln Arg Arg Gly Asp Ser Met Ala Gly Gly Ala Pro Ala
 260 265 270
 Glu Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys Gly

275		280		285
Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr Asn Pro Asn Cys Gln				
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 Lys Thr Ser Thr Ser Asp Met Leu Lys Ala Tyr Gln Thr Tyr Ile Ser
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 Val Cys Pro Phe Lys Lys Ile Ala Ile Ile Phe Ala Asn His Ser Ile
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 Met Arg Leu Ala Ser Ser Ala Asn Ala Lys Thr Ile His Ile Ile Asp
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 Phe Gly Ile Ser Asp Gly Phe Gln Trp Pro Ser Leu Ile His Arg Leu
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 Ala Trp Arg Arg Gly Ser Ser Cys Lys Leu Arg Ile Thr Gly Ile Glu

450 455 460
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 530 535 540
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 545 550 555 560
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 Val Leu Phe His Tyr Ser Ser Leu Phe Asp Met Cys Asp Thr Asn Leu
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 Thr Arg Glu Asp Pro Met Arg Val Met Phe Glu Lys Glu Phe Tyr Gly
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 Arg Glu Ile Met Asn Val Val Ala Cys Glu Gly Thr Glu Arg Val Glu
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 Cys His Trp Leu Leu Gln Gly Trp Lys Gly Arg Ile Val Tyr Gly Ser
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Phe Asp Gly Asn Pro Asn Leu Leu Thr Asp Pro Met Glu Asp Gln Tyr
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Pro Pro Pro Ser Asp Thr Leu Leu Lys Tyr Val Ser Glu Ile Leu Met
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Glu Glu Ser Asn Gly Asp Tyr Lys Gln Ser Met Phe Tyr Asp Ser Leu
755 760 765

Ala Leu Arg Lys Thr Glu Glu Met Leu Gln Gln Val Ile Thr Asp Ser
770 775 780

Gln Asn Gln Ser Phe Ser Pro Ala Asp Ser Leu Ile Thr Asn Ser Trp
785 790 795 800

Asp Ala Ser Gly Ser Ile Asp Glu Ser Ala Tyr Ser Ala Asp Pro Gln
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Pro Val Asn Glu Ile Met Val Lys Ser Met Phe Ser Asp Ala Glu Ser
820 825 830

Ala Leu Gln Phe Lys Lys Gly Val Glu Glu Ala Ser Lys Phe Leu Pro
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850 855 860

Arg Asp Ser Val Lys Glu Glu Met Gly Leu Asp Gln Leu Arg Val Lys
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Lys Asn His Glu Arg Asp Phe Glu Glu Val Arg Ser Ser Lys Gln Phe
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 Pro Trp Glu Leu Asn Cys Ser Asp Leu Phe Ser Thr Ile His Leu Glu

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Lys Ile Asn Thr Asp Phe Asn Gly Phe Asp Glu Ser Cys Ile Gly Ser
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Ile Lys Thr Asn Ser Gly Ser Asp Asp Ser Asn Leu Phe His Gly Val
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Pro Ser Pro Gln Ser Asp Glu Leu Asp Ser Lys Asn Thr Lys Ile Arg
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436
Gln Val Thr Asp Asp Arg Lys Arg Lys Arg Met Glu Ser Asn Arg Glu
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Ser Ala Lys Arg Ser Arg Met Arg Lys Gln Arg His Ile Asp Asn Leu
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Lys Asp Glu Ala Asn Arg Leu Gly Leu Glu Asn Arg Glu Leu Ala Asn
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Arg Leu Arg Ile Val Leu Tyr Asn Ile Ala Leu Met Cys Thr Asp Asn
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Met Arg Gln Ile Leu Ile Phe Arg Gln Leu Gln Leu Asn Pro Ser Leu
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Phe Asn Gly Phe Asp Glu Ser Cys Ile Gly Ser Ile Lys Thr Asn Ser
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Gly Ser Asp Asp Ser Asn Leu Phe His Gly Val Pro Ser Pro Gln Ser
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Asp Glu Leu Asp Ser Lys Asn Thr Lys Ile Arg Ser Asn Ala Thr Asn
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His Asn Arg Asn Lys Leu Asn Arg Ser Val Leu Gln Val Thr Asp Asp
115 120 125

Arg Lys Arg Lys Arg Met Glu Ser Asn Arg Glu Ser Ala Lys Arg Ser
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Arg Met Arg Lys Gln Arg His Ile Asp Asn Leu Lys Asp Glu Ala Asn
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Arg Leu Gly Leu Glu Asn Arg Glu Leu Ala Asn Arg Leu Arg Ile Val
165 170 175

Leu Tyr Asn Ile Ala Leu Met Cys Thr Asp Asn Asn Gln Leu Leu Ser
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His Met Ile
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240

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299

Met
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347

Gly Leu Asp Gly Asn Asn Gly Gly Gly Val Trp Leu Asn Gly Gly Gly
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395

Gly Glu Arg Glu Glu Asn Glu Glu Gly Ser Trp Gly Arg Asn Gln Glu
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Asp Gly Ser Ser Gln Phe Lys Pro Met Leu Glu Gly Asp Trp Phe Ser
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Ser Asn Gln Pro His Pro Gln Asp Leu Gln Met Leu Gln Asn Gln Pro
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Asp Phe Arg Tyr Phe Gly Gly Phe Pro Phe Asn Pro Asn Asp Asn Leu
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587

Leu Leu Gln His Ser Ile Asp Ser Ser Ser Ser Cys Ser Pro Ser Gln
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 Arg Leu Tyr Met Leu Arg Ser Val Val Pro Lys Ile Ser Lys Met Asp
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 Ser Leu Pro Pro Thr Ser Ser Ser Phe His Pro Leu Thr Pro Thr Pro
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 470 475 480

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 1781
 Ala Val Leu Phe Asp Thr Ala Gly Tyr Ala Gly Met Ile
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2026

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Pro Asp Phe Arg Tyr Phe Gly Gly Phe Pro Phe Asn Pro Asn Asp Asn
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Leu Leu Leu Gln His Ser Ile Asp Ser Ser Ser Ser Cys Ser Pro Ser
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Gln Ala Phe Ser Leu Asp Pro Ser Gln Gln Asn Gln Phe Leu Ser Thr
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Asn Asn Asn Lys Gly Cys Leu Leu Asn Val Pro Ser Ser Ala Asn Pro
115 120 125

Phe Asp Asn Ala Phe Glu Phe Gly Ser Glu Ser Gly Phe Leu Asn Gln
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Ile His Ala Pro Ile Ser Met Gly Phe Gly Ser Leu Thr Gln Leu Gly
145 150 155 160

Asn Arg Asp Leu Ser Ser Val Pro Asp Phe Leu Ser Ala Arg Ser Leu
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Thr Ala Pro Leu Glu Leu Glu Gly Phe Gly Ser Pro Ala Asn Gly Gly
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Gly Leu Asn Tyr Glu Ser Asp Glu Ile Asn Glu Ser Gly Lys Ala Ala
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Pro Ala Lys Asn Leu Met Ala Glu Arg Arg Arg Arg Lys Lys Leu Asn
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Asp Arg Leu Tyr Met Leu Arg Ser Val Val Pro Lys Ile Ser Lys Met
325 330 335

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340 345 350

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Gly Ser Leu Pro Pro Thr Ser Ser Ser Phe His Pro Leu Thr Pro Thr
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Met Ala Ala Thr Ala Ile Glu Pro
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 461

Ser Ser Ser Ile Ser Phe Thr Ser Ser His Leu Ser Asn Pro Ser Pro
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 509

Val Val Thr Thr Tyr His Ser Ala Ala Asn Leu Glu Glu Leu Ser Ser
 25 30 35 40

aac ttg gag cag ctt ctc act aat cca gat tgc gat tac act gac gca
 557

Asn Leu Glu Gln Leu Leu Thr Asn Pro Asp Cys Asp Tyr Thr Asp Ala

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653		
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701		
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797		
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893		
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 265 270 275 280
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 1277
 Ile Arg Arg Asn Pro Leu Val Ser Gly Asp Thr Pro Thr Cys Ser His
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 tcg atg ccc gag gat ctc caa atg agg ttg tta tac tta gaa aag cga
 1325
 Ser Met Pro Glu Asp Leu Gln Met Arg Leu Leu Tyr Leu Glu Lys Arg
 300 305 310
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 1373
 Val Gly Leu Ala Gln Leu Phe Phe Pro Ala Glu Ala Asn Val Ala Met
 315 320 325
 gac gtt gct aat gtt gaa ggg aca agc gag tgc aca ggt ctt cta act
 1421
 Asp Val Ala Asn Val Glu Gly Thr Ser Glu Cys Thr Gly Leu Leu Thr
 330 335 340
 cca cct cca tca aat gat aca act gaa aac ttg ggt aaa gtc gat tta
 1469
 Pro Pro Pro Ser Asn Asp Thr Thr Glu Asn Leu Gly Lys Val Asp Leu
 345 350 355 360
 aat gaa acg cct tat gtg caa acg aaa aga atg ctt aca cgt atg aaa
 1517
 Asn Glu Thr Pro Tyr Val Gln Thr Lys Arg Met Leu Thr Arg Met Lys
 365 370 375
 gcc ctc atg aaa aca gtt gag aca ggt cgg aga tac ttc cca tct tgt
 1565
 Ala Leu Met Lys Thr Val Glu Thr Gly Arg Arg Tyr Phe Pro Ser Cys
 380 385 390
 tat gag gtt ctg gat aag tac atg gat cag tat atg gac gaa gaa atc
 1613
 Tyr Glu Val Leu Asp Lys Tyr Met Asp Gln Tyr Met Asp Glu Glu Ile
 395 400 405
 cct gat atg tcg tat ccc gag aaa ggc act gtg aaa gag aga aga cag
 1661
 Pro Asp Met Ser Tyr Pro Glu Lys Gly Thr Val Lys Glu Arg Arg Gln
 410 415 420
 aag agg atg aga tat aac gag ctg aag aac gac gtt aaa aaa gca tat
 1709
 Lys Arg Met Arg Tyr Asn Glu Leu Lys Asn Asp Val Lys Lys Ala Tyr
 425 430 435 440

agc aaa gac aaa gtc gcg cgg tct tgt ctt tct tct tca tca cca gct
1757

Ser Lys Asp Lys Val Ala Arg Ser Cys Leu Ser Ser Ser Ser Pro Ala
445 450 455

tct tct ctt aga gaa gcc tta gag aat cca aca tga tctgtccca

1803

Ser Ser Leu Arg Glu Ala Leu Glu Asn Pro Thr
460 465

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1863

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1923

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1983

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2043

gcaaaaaaaaa a

2054

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10

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20

25

30

Ala Asn Leu Glu Glu Leu Ser Ser Asn Leu Glu Gln Leu Leu Thr Asn

35

40

45

Pro Asp Cys Asp Tyr Thr Asp Ala Glu Ile Ile Ile Glu Glu Glu Ala

50

55

60

Asn Pro Arg Lys Leu Arg Asn Tyr Val Glu Lys Ser Leu Val Glu Asn

65

70

75

80

Val Leu Pro Ile Leu Leu Val Ala Phe His Cys Asp Leu Thr Gln Leu

85

90

95

Leu Asp Gln Cys Ile Glu Arg Val Ala Arg Ser Asp Leu Asp Arg Phe

100

105

110

Cys Ile Glu Lys Glu Leu Pro Leu Glu Val Leu Glu Lys Ile Lys Gln

115

120

125

Leu Arg Val Lys Ser Val Asn Ile Pro Glu Val Glu Asp Lys Ser Ile
 130 135 140

Glu Arg Thr Gly Lys Val Leu Lys Ala Leu Asp Ser Asp Asp Val Glu
 145 150 155 160

Leu Val Lys Leu Leu Leu Thr Glu Ser Asp Ile Thr Leu Asp Gln Ala
 165 170 175

Asn Gly Leu His Tyr Ala Val Ala Tyr Ser Asp Pro Lys Val Val Thr
 180 185 190

Gln Val Leu Asp Leu Asp Met Ala Asp Val Asn Phe Arg Asn Ser Arg
 195 200 205

Gly Tyr Thr Val Leu His Ile Ala Ala Met Arg Arg Glu Pro Thr Ile
 210 215 220

Ile Ile Pro Leu Ile Gln Lys Gly Ala Asn Ala Ser Asp Phe Thr Phe
 225 230 235 240

Asp Gly Arg Ser Ala Val Asn Ile Cys Arg Arg Leu Thr Arg Pro Lys
 245 250 255

Asp Tyr His Thr Lys Thr Ser Arg Lys Glu Pro Ser Lys Tyr Arg Leu
 260 265 270

Cys Ile Asp Ile Leu Glu Arg Glu Ile Arg Arg Asn Pro Leu Val Ser
 275 280 285

Gly Asp Thr Pro Thr Cys Ser His Ser Met Pro Glu Asp Leu Gln Met
 290 295 300

Arg Leu Leu Tyr Leu Glu Lys Arg Val Gly Leu Ala Gln Leu Phe Phe
 305 310 315 320

Pro Ala Glu Ala Asn Val Ala Met Asp Val Ala Asn Val Glu Gly Thr
 325 330 335

Ser Glu Cys Thr Gly Leu Leu Thr Pro Pro Pro Ser Asn Asp Thr Thr
 340 345 350

Glu Asn Leu Gly Lys Val Asp Leu Asn Glu Thr Pro Tyr Val Gln Thr
 355 360 365

Lys Arg Met Leu Thr Arg Met Lys Ala Leu Met Lys Thr Val Glu Thr

370 375 380
 Gly Arg Arg Tyr Phe Pro Ser Cys Tyr Glu Val Leu Asp Lys Tyr Met
 385 390 395 400
 Asp Gln Tyr Met Asp Glu Glu Ile Pro Asp Met Ser Tyr Pro Glu Lys
 405 410 415
 Gly Thr Val Lys Glu Arg Arg Gln Lys Arg Met Arg Tyr Asn Glu Leu
 420 425 430
 Lys Asn Asp Val Lys Lys Ala Tyr Ser Lys Asp Lys Val Ala Arg Ser
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 Cys Leu Ser Ser Ser Ser Pro Ala Ser Ser Leu Arg Glu Ala Leu Glu
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 Asn Pro Thr
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 107
 Gln Glu Phe His Ser Ser Lys Asp Ser Leu Pro Cys Pro Ala Thr Ser
 5 10 15
 tgg gat aac tct gtc ttc acc aac tca aat gtc caa gga tca tca tcc
 155
 Trp Asp Asn Ser Val Phe Thr Asn Ser Asn Val Gln Gly Ser Ser Ser
 20 25 30
 ttg acc gat aac aac act tta agc ttg aca atg gag atg aaa caa act
 203
 Leu Thr Asp Asn Asn Thr Leu Ser Leu Thr Met Glu Met Lys Gln Thr
 35 40 45
 ggt ttt caa atg cag cac tat gat tcc tcc tct act caa tcc act gga
 251
 Gly Phe Gln Met Gln His Tyr Asp Ser Ser Ser Thr Gln Ser Thr Gly
 50 55 60 65
 gga gaa tca tat agt gaa gtt gct agc tta agt gaa cct act aat cgt
 299
 Gly Glu Ser Tyr Ser Glu Val Ala Ser Leu Ser Glu Pro Thr Asn Arg
 70 75 80

tat ggc cac aac att gtt gtc act cat ctc tca ggt tac aaa gaa aac
 347
 Tyr Gly His Asn Ile Val Val Thr His Leu Ser Gly Tyr Lys Glu Asn
 85 90 95

ccg gaa aat cct att gga agt cat tcg ata tca aag gtg tct caa gat
 395
 Pro Glu Asn Pro Ile Gly Ser His Ser Ile Ser Lys Val Ser Gln Asp
 100 105 110

tca gtg gtt ctt cct att gag gcg gct tct tgg cct tta cac ggc aat
 443
 Ser Val Val Leu Pro Ile Glu Ala Ala Ser Trp Pro Leu His Gly Asn
 115 120 125

gta acg cca cat ttc aat ggt ttc ttg tct ttt cct tat gca tca caa
 491
 Val Thr Pro His Phe Asn Gly Phe Leu Ser Phe Pro Tyr Ala Ser Gln
 130 135 140 145

cac acg gtg cag cat cct caa atc aga ggg ttg gtt ccg tct aga atg
 539
 His Thr Val Gln His Pro Gln Ile Arg Gly Leu Val Pro Ser Arg Met
 150 155 160

cct ttg cct cac aac att cca gag aac gaa cca att ttc gtc aat gca
 587
 Pro Leu Pro His Asn Ile Pro Glu Asn Glu Pro Ile Phe Val Asn Ala
 165 170 175

aaa cag tac caa gcc att ctc cgc cgc aga gag cgc cgt gca aag ctt
 635
 Lys Gln Tyr Gln Ala Ile Leu Arg Arg Arg Glu Arg Arg Ala Lys Leu
 180 185 190

gaa gct cag aac aag ctc atc aaa gtc cgc aaa cca tat ctt cac gag
 683
 Glu Ala Gln Asn Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His Glu
 195 200 205

tcg cgg cac ctc cat gca cta aag aga gtt aga ggc tct ggt gga cgt
 731
 Ser Arg His Leu His Ala Leu Lys Arg Val Arg Gly Ser Gly Gly Arg
 210 215 220 225

ttc ctc aac aca aag aag cat caa gaa tca aat tcc tca cta tct cct
 779
 Phe Leu Asn Thr Lys Lys His Gln Glu Ser Asn Ser Ser Leu Ser Pro
 230 235 240

cca ttc ttg att cca cct cat gtc ttc aag aac tct cca gga aag ttc
 827
 Pro Phe Leu Ile Pro Pro His Val Phe Lys Asn Ser Pro Gly Lys Phe
 245 250 255

cgg caa atg gac att tca agg ggt ggg gtt gtg tct agt gtc tcg aca
 875
 Arg Gln Met Asp Ile Ser Arg Gly Gly Val Val Ser Ser Val Ser Thr
 260 265 270

aca tct tgc tcg gac ata acc ggg aac aac aac gac atg ttc cag caa
923

Thr Ser Cys Ser Asp Ile Thr Gly Asn Asn Asn Asp Met Phe Gln Gln
275 280 285

aac cca caa ttc agg ttc tca ggt tat cca tca aac cac cat gtc tca

971
Asn Pro Gln Phe Arg Phe Ser Gly Tyr Pro Ser Asn His His Val Ser
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1011

Val Leu Met

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Ser Trp Asp Asn Ser Val Phe Thr Asn Ser Asn Val Gln Gly Ser Ser
20 25 30

Ser Leu Thr Asp Asn Asn Thr Leu Ser Leu Thr Met Glu Met Lys Gln
35 40 45

Thr Gly Phe Gln Met Gln His Tyr Asp Ser Ser Ser Thr Gln Ser Thr
50 55 60

Gly Gly Glu Ser Tyr Ser Glu Val Ala Ser Leu Ser Glu Pro Thr Asn
65 70 75 80

Arg Tyr Gly His Asn Ile Val Val Thr His Leu Ser Gly Tyr Lys Glu
85 90 95

Asn Pro Glu Asn Pro Ile Gly Ser His Ser Ile Ser Lys Val Ser Gln
100 105 110

Asp Ser Val Val Leu Pro Ile Glu Ala Ala Ser Trp Pro Leu His Gly
115 120 125

Asn Val Thr Pro His Phe Asn Gly Phe Leu Ser Phe Pro Tyr Ala Ser
130 135 140

Gln His Thr Val Gln His Pro Gln Ile Arg Gly Leu Val Pro Ser Arg
145 150 155 160

Met Pro Leu Pro His Asn Ile Pro Glu Asn Glu Pro Ile Phe Val Asn
165 170 175

Ala Lys Gln Tyr Gln Ala Ile Leu Arg Arg Arg Glu Arg Arg Ala Lys
 180 185 190

Leu Glu Ala Gln Asn Lys Leu Ile Lys Val Arg Lys Pro Tyr Leu His
 195 200 205

Glu Ser Arg His Leu His Ala Leu Lys Arg Val Arg Gly Ser Gly Gly
 210 215 220

Arg Phe Leu Asn Thr Lys Lys His Gln Glu Ser Asn Ser Ser Leu Ser
 225 230 235 240

Pro Pro Phe Leu Ile Pro Pro His Val Phe Lys Asn Ser Pro Gly Lys
 245 250 255

Phe Arg Gln Met Asp Ile Ser Arg Gly Gly Val Val Ser Ser Val Ser
 260 265 270

Thr Thr Ser Cys Ser Asp Ile Thr Gly Asn Asn Asn Asp Met Phe Gln
 275 280 285

Gln Asn Pro Gln Phe Arg Phe Ser Gly Tyr Pro Ser Asn His His Val
 290 295 300

Ser Val Leu Met
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Met Gly Arg
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 106

Gly Lys Ile Val Ile Gln Arg Ile Asp Asp Ser Thr Ser Arg Gln Val
 5 10 15

act ttc tcc aaa cga aga aag ggc ctt atc aag aaa gcc aaa gag cta
 154

Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala Lys Glu Leu
 20 25 30 35

gct att ctc tgt gat gcc gag gtc ggt ctc atc atc ttc tct agc acc
 202

Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Ile Ile Phe Ser Ser Thr
 40 45 50

gga aag ctc tat gac ttt gca agc tcc agc atg aag tcg gtt att gat
 250
 Gly Lys Leu Tyr Asp Phe Ala Ser Ser Ser Met Lys Ser Val Ile Asp
 55 60 65

aga tac aac aag agc aag atc gag caa caa caa cta ttg aac ccc gca
 298
 Arg Tyr Asn Lys Ser Lys Ile Glu Gln Gln Gln Leu Leu Asn Pro Ala
 70 75 80

tca gaa gtc aag ttt tgg cag aga gaa gct gct gtt cta aga caa gaa
 346
 Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Ala Val Leu Arg Gln Glu
 85 90 95

ctg cat gct ttg caa gaa aat cat cgg caa atg atg gga gaa cag cta
 394
 Leu His Ala Leu Gln Glu Asn His Arg Gln Met Met Gly Glu Gln Leu
 100 105 110 115

aat ggt tta agt gtt aac gag cta aac agt ctt gag aat caa att gag
 442
 Asn Gly Leu Ser Val Asn Glu Leu Asn Ser Leu Glu Asn Gln Ile Glu
 120 125 130

ata agt ttg cgt gga att cgt atg aga aag gaa caa ctg ttg act caa
 490
 Ile Ser Leu Arg Gly Ile Arg Met Arg Lys Glu Gln Leu Leu Thr Gln
 135 140 145

gaa atc caa gaa cta agc caa aag agg aat ctt att cat cag gaa aac
 538
 Glu Ile Gln Glu Leu Ser Gln Lys Arg Asn Leu Ile His Gln Glu Asn
 150 155 160

ctc gat tta tct agg aaa gta caa cgg att cat caa gaa aat gtg gag
 586
 Leu Asp Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu Asn Val Glu
 165 170 175

ctc tac aag aag gct tat atg gca aac aca aac ggg ttt aca cac cgt
 634
 Leu Tyr Lys Lys Ala Tyr Met Ala Asn Thr Asn Gly Phe Thr His Arg
 180 185 190 195

gaa gta gct gtt gcg gat gat gaa tca cac act cag att cgg ctg caa
 682
 Glu Val Ala Val Ala Asp Asp Glu Ser His Thr Gln Ile Arg Leu Gln
 200 205 210

cta agc cag cct gaa cat tcc gat tat gac act cca cca aga gca aac
 730
 Leu Ser Gln Pro Glu His Ser Asp Tyr Asp Thr Pro Pro Arg Ala Asn
 215 220 225

gaa taa cagagagatt gaagttggaa gataccatga tggtgaagaa cactccaaag
 786
 Glu

gccttggttt gaataagggtt cttgaactgg aaacctctat acaccaagcc acgtacgata
846

agcagcatgg ttctttctaac atagtcatat tttcaatcct aaatataatt aaagcatata
906

taattaaaat ccggtgttgt tatactcatc ttgagtatta atattgtact tggtttataac
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1026

aaaaaaaaaa aa
1038

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Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala
20 25 30

Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Ile Ile Phe
35 40 45

Ser Ser Thr Gly Lys Leu Tyr Asp Phe Ala Ser Ser Ser Met Lys Ser
50 55 60

Val Ile Asp Arg Tyr Asn Lys Ser Lys Ile Glu Gln Gln Gln Leu Leu
65 70 75 80

Asn Pro Ala Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Ala Val Leu
85 90 95

Arg Gln Glu Leu His Ala Leu Gln Glu Asn His Arg Gln Met Met Gly
100 105 110

Glu Gln Leu Asn Gly Leu Ser Val Asn Glu Leu Asn Ser Leu Glu Asn
115 120 125

Gln Ile Glu Ile Ser Leu Arg Gly Ile Arg Met Arg Lys Glu Gln Leu
130 135 140

Leu Thr Gln Glu Ile Gln Glu Leu Ser Gln Lys Arg Asn Leu Ile His
145 150 155 160

Gln Glu Asn Leu Asp Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu
165 170 175

Asn Val Glu Leu Tyr Lys Lys Ala Tyr Met Ala Asn Thr Asn Gly Phe
 180 185 190

Thr His Arg Glu Val Ala Val Ala Asp Asp Glu Ser His Thr Gln Ile
 195 200 205

Arg Leu Gln Leu Ser Gln Pro Glu His Ser Asp Tyr Asp Thr Pro Pro
 210 215 220

Arg Ala Asn Glu
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 96
 His Gln Gln Pro Pro Ser Tyr Ser Gln Leu Pro Pro Met Ala Ser Ser
 20 25 30

aac cct cag tta cgt aat tac tgg att gag cag atg gaa acc gtc tcg
 144
 Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser
 35 40 45

gat ttc aaa aac cgt cag ctt cca ttg gct cga att aag aag atc atg
 192
 Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
 50 55 60

aag gct gat cca gat gtg cac atg gtc tcc gca gag gct ccg atc atc
 240
 Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile
 65 70 75 80

ttc gca aag gct tgc gaa atg ttc atc gtt gat ctc acg atg cgg tcg
 288
 Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser
 85 90 95

tgg ctc aaa gcc gag gag aac aaa cgc cac acg ctt cag aaa tcg gat
 336
 Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp
 100 105 110

atc tcc aac gca gtg gct agc tct ttc acc tac gat ttc ctt ctt gat
 384
 Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp
 115 120 125

gtt gtc cct aag gac gag tct atc gcc acc gct gat cct ggc ttt gtg
432

Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val
130 135 140

gct atg cca cat cct gac ggt gga gga gta ccg caa tat tat tat cca
480

Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro
145 150 155 160

ccg gga gtg gtg atg gga act cct atg gtt ggt agt gga atg tac gcg
528

Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala
165 170 175

cca tcg cag gcg tgg cca gca gcg gct ggt gac ggg gag gat gat gct
576

Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala
180 185 190

gag gat aat gga gga aac ggc ggc gga aat tga
609

Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn
195 200

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20 25 30

Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser
35 40 45

Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
50 55 60

Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile
65 70 75 80

Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser
85 90 95

Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp
100 105 110

Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp
115 120 125

Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val
 130 135 140

Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro
 145 150 155 160

Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala
 165 170 175

Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala
 180 185 190

Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn
 195 200

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atttcgtttc ataac atg gat gcc atg agt agc gta gac gag agc tct aca
 111

Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr
 1 5 10

act aca gat tcc att ccg gcg aga aag tca tcg tct ccg gcg agt tta
 159

Thr Thr Asp Ser Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu
 15 20 25

cta tat aga atg gga agc gga aca agc gtg gta ctt gat tca gag aac
 207

Leu Tyr Arg Met Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn
 30 35 40

ggg gtc gaa gtc gaa gtc gaa gcc gaa tca aga aag ctt cct tct tca
 255

Gly Val Glu Val Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser
 45 50 55 60

aga ttc aaa ggt gtt gtt cct caa cca aat gga aga tgg gga gct cag
 303

Arg Phe Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln
 65 70 75

att tac gag aaa cat caa cgc gtg tgg ctt ggt act ttc aac gag gaa
 351

Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu
 80 85 90

gac gaa gca gct cgt gct tac gac gtc gcg gct cac cgt ttc cgt ggc
 399

Asp Glu Ala Ala Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly

95	100	105
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Arg Asp Ala Val Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val 110 115 120		
gag ttc tta aac gcg cat tcg aaa tca gag atc gta gat atg ttg aga 495		
Glu Phe Leu Asn Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg 125 130 135 140		
aaa cac act tac aaa gaa gag tta gac caa agg aaa cgt aac cgt gac 543		
Lys His Thr Tyr Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp 145 150 155		
ggt aac gga aaa gag acg acg gcg ttt gct ttg gct tcg atg gtg gtt 591		
Gly Asn Gly Lys Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val 160 165 170		
atg acg ggg ttt aaa acg gcg gag tta ctg ttt gag aaa acg gta acg 639		
Met Thr Gly Phe Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr 175 180 185		
cca agt gac gtc ggg aaa cta aac cgt tta gtt ata cca aaa cac caa 687		
Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln 190 195 200		
gcg gag aaa cat ttt ccg tta ccg tta ggt aat aat aac gtc tcc gtt 735		
Ala Glu Lys His Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val 205 210 215 220		
aaa ggt atg ctg ttg aat ttc gaa gac gtt aac ggg aaa gtg tgg agg 783		
Lys Gly Met Leu Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg 225 230 235		
ttc cgt tac tct tat tgg aat agt agt caa agt tat gtg ttg acc aaa 831		
Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys 240 245 250		
ggt tgg agt aga ttc gtt aaa gag aag aga ctt tgt gct ggt gat ttg 879		
Gly Trp Ser Arg Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu 255 260 265		
atc agt ttt aaa aga tcc aac gat caa gat caa aaa ttc ttt atc ggg 927		
Ile Ser Phe Lys Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly 270 275 280		
tgg aaa tcg aaa tcc ggg ttg gat cta gag acg ggt cgg gtt atg aga 975		
Trp Lys Ser Lys Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg 285 290 295 300		

ttg ttt ggg gtt gat att tct tta aac gcc gtc gtt gta gtg aag gaa
1023

Leu Phe Gly Val Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu
305 310 315

aca acg gag gtg tta atg tcg tcg tta agg tgt aag aag caa cga gtt
1071

Thr Thr Glu Val Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val
320 325 330

ttg taa taacaattta acaacttggg aaagaaaaaa aagctttttg attttaattt
1127

Leu

ctcttcaacg ttaatcttgc tgagatta
1155

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20 25 30

Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val
35 40 45

Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly
50 55 60

Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65 70 75 80

His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
85 90 95

Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val
100 105 110

Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn
115 120 125

Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
130 135 140

Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys
145 150 155 160

Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe
 165 170 175

Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val
 180 185 190

Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His
 195 200 205

Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu
 210 215 220

Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser
 225 230 235 240

Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
 245 250 255

Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys
 260 265 270

Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys
 275 280 285

Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val
 290 295 300

Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu Thr Thr Glu Val
 305 310 315 320

Leu Met Ser Ser Leu Arg Cys Lys Lys Gln Arg Val Leu
 325 330

<210> 37 <211> 525 <212> DNA <213> Arabidopsis thaliana <220>
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 48
 Met Glu Gly Lys Arg Ser Gln Gly Gln Gly Tyr Met Lys Lys Lys Ser
 1 5 10 15

tac ctt gtg gaa gaa gat atg gag act gat acg gat gaa gaa gag gaa
 96
 Tyr Leu Val Glu Glu Asp Met Glu Thr Asp Thr Asp Glu Glu Glu Glu
 20 25 30

gta ggt agg gat aga gtt aga ggg tct aga ggt agc atc aat cgt ggt
144

Val Gly Arg Asp Arg Val Arg Gly Ser Arg Gly Ser Ile Asn Arg Gly
35 40 45

ggc tcg ttg cgg ctt tgc caa gta gat aga tgc aca gct gat atg aaa
192

Gly Ser Leu Arg Leu Cys Gln Val Asp Arg Cys Thr Ala Asp Met Lys
50 55 60

gag gca aaa ctg tat cac cgg aga cac aaa gtg tgt gaa gtt cat gca
240

Glu Ala Lys Leu Tyr His Arg Arg His Lys Val Cys Glu Val His Ala
65 70 75 80

aag gca tct tct gtc ttt ctc tca gga ctt aac caa cgc ttt tgt caa
288

Lys Ala Ser Ser Val Phe Leu Ser Gly Leu Asn Gln Arg Phe Cys Gln
85 90 95

caa tgc agt agg ttt cat gac ctc caa gag ttt gat gaa gct aag aga
336

Gln Cys Ser Arg Phe His Asp Leu Gln Glu Phe Asp Glu Ala Lys Arg
100 105 110

agt tgc agg agg cgc tta gct gga cac aat gag cga aga agg aag agc
384

Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser
115 120 125

tct ggt gag agt act tat gga gaa gga tca ggt cgg aga gga atc aat
432

Ser Gly Glu Ser Thr Tyr Gly Glu Gly Ser Gly Arg Arg Gly Ile Asn
130 135 140

ggt cag gtg gtg atg cag aat caa gaa aga tca agg gta gag atg aca
480

Gly Gln Val Val Met Gln Asn Gln Glu Arg Ser Arg Val Glu Met Thr
145 150 155 160

ctt cct atg cca aac tca tca ttc aag cga cca cag att aga tag
525

Leu Pro Met Pro Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg
165 170

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38

Met Glu Gly Lys Arg Ser Gln Gly Gln Gly Tyr Met Lys Lys Lys Ser
1 5 10 15

Tyr Leu Val Glu Glu Asp Met Glu Thr Asp Thr Asp Glu Glu Glu
20 25 30

Val Gly Arg Asp Arg Val Arg Gly Ser Arg Gly Ser Ile Asn Arg Gly
35 40 45

Gly Ser Leu Arg Leu Cys Gln Val Asp Arg Cys Thr Ala Asp Met Lys
50 55 60

Glu Ala Lys Leu Tyr His Arg Arg His Lys Val Cys Glu Val His Ala
65 70 75 80

Lys Ala Ser Ser Val Phe Leu Ser Gly Leu Asn Gln Arg Phe Cys Gln
85 90 95

Gln Cys Ser Arg Phe His Asp Leu Gln Glu Phe Asp Glu Ala Lys Arg
100 105 110

Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser
115 120 125

Ser Gly Glu Ser Thr Tyr Gly Glu Gly Ser Gly Arg Arg Gly Ile Asn
130 135 140

Gly Gln Val Val Met Gln Asn Gln Glu Arg Ser Arg Val Glu Met Thr
145 150 155 160

Leu Pro Met Pro Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg
165 170

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51

Met Glu Arg Glu Gln Glu Glu Ser Thr Met Arg Lys
1 5 10

aga agg cag cca cct caa gaa gaa gtg cct aac cac gtg gct aca agg
99

Arg Arg Gln Pro Pro Gln Glu Glu Val Pro Asn His Val Ala Thr Arg
15 20 25

aag ccg tac aga ggg ata cgg agg agg aag tgg ggc aag tgg gtg gct
147

Lys Pro Tyr Arg Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala
30 35 40

gag att cgt gag cct aac aaa cgc tca cgg ctt tgg ctt ggc tct tac
195

Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr
45 50 55 60

aca acc gat atc gcc gcc gct aga gcc tac gac gtg gcc gtc ttc tac
243

Thr Thr Asp Ile Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr
65 70 75

ctc cgt ggc ccc tcc gca cgt ctc aac ttc cct gat ctt ctc ttg caa
291

Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro Asp Leu Leu Leu Gln
80 85 90

gaa gag gac cat ctc tca gcc gcc acc acc gct gac atg ccc gca gct
339

Glu Glu Asp His Leu Ser Ala Ala Thr Thr Ala Asp Met Pro Ala Ala
95 100 105

ctt ata agg gaa aaa gcg gcg gag gtc ggc gcc aga gtc gac gct ctt
387

Leu Ile Arg Glu Lys Ala Ala Glu Val Gly Ala Arg Val Asp Ala Leu
110 115 120

cta gct tct gcc gct cct tcg atg gct cac tcc act ccg ccg gta ata
435

Leu Ala Ser Ala Ala Pro Ser Met Ala His Ser Thr Pro Pro Val Ile
125 130 135 140

aaa ccc gac ttg aat caa ata ccc gaa tcc gga gat ata tag
477

Lys Pro Asp Leu Asn Gln Ile Pro Glu Ser Gly Asp Ile
145 150

tcaatttata tacatgtagt ttgttttggt tgattagaag attacattta catacaagat
537

acacatagat actggaaaat ataggatatgt atacattcat aaattatctt atgtatcaaa
597

gaattttata gattctgatt agctttttgt ttttgttttt gataagaact ctgattagtt
657

gtccggagac aaaaccggct aagagcaatc catgagaagc tagcgagtgt ttttagttc
717

aagttgtaat ataatgcat attaattctt tagtaatttt gt
759

<210> 40 <211> 153 <212> PRT <213> Arabidopsis thaliana <400>
40

Met Glu Arg Glu Gln Glu Glu Ser Thr Met Arg Lys Arg Arg Gln Pro
1 5 10 15

Pro Gln Glu Glu Val Pro Asn His Val Ala Thr Arg Lys Pro Tyr Arg
20 25 30

Gly Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ala Glu Ile Arg Glu
35 40 45

Pro Asn Lys Arg Ser Arg Leu Trp Leu Gly Ser Tyr Thr Thr Asp Ile
50 55 60

Ala Ala Ala Arg Ala Tyr Asp Val Ala Val Phe Tyr Leu Arg Gly Pro

76

gaa gct cac ctt tgg gat aag agt acc tgg aac caa aac cag aac aag
 403
 Glu Ala His Leu Trp Asp Lys Ser Thr Trp Asn Gln Asn Gln Asn Lys
 85 90 95
 aag gga aaa caa gtt tat cta gga gca tat gat gat gaa gag gct gct
 451
 Lys Gly Lys Gln Val Tyr Leu Gly Ala Tyr Asp Asp Glu Glu Ala Ala
 100 105 110 115
 gct aga gct tac gac ctt gct gcc tta aaa tat tgg ggt cct ggg aca
 499
 Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Gly Thr
 120 125 130
 ctt ata aat ttt ccg gtg act gat tat acc agg gat tta gaa gaa atg
 547
 Leu Ile Asn Phe Pro Val Thr Asp Tyr Thr Arg Asp Leu Glu Glu Met
 135 140 145
 caa aat ctc tca agg gaa gaa tac ctt gca tct tta cgt aga tat ccc
 595
 Gln Asn Leu Ser Arg Glu Glu Tyr Leu Ala Ser Leu Arg Arg Tyr Pro
 150 155 160
 ttt ggc aga aaa agc agc ggt ttc tct agg gga ata gcg aaa tat cgt
 643
 Phe Gly Arg Lys Ser Ser Gly Phe Ser Arg Gly Ile Ala Lys Tyr Arg
 165 170 175
 gga ctt caa agc cga tgg gac gca tca gcc agt cgt atg cct gga cct
 691
 Gly Leu Gln Ser Arg Trp Asp Ala Ser Ala Ser Arg Met Pro Gly Pro
 180 185 190 195
 gaa tac ttc agt aac att cat tac ggg gca ggt gat gat cgt gga aca
 739
 Glu Tyr Phe Ser Asn Ile His Tyr Gly Ala Gly Asp Asp Arg Gly Thr
 200 205 210
 gaa ggt gac ttt cta ggt agc ttt tgt ctg gaa aga aag att gat cta
 787
 Glu Gly Asp Phe Leu Gly Ser Phe Cys Leu Glu Arg Lys Ile Asp Leu
 215 220 225
 aca gga tac ata aag tgg tgg gga gcc aac aag aac cgt caa cca gaa
 835
 Thr Gly Tyr Ile Lys Trp Trp Gly Ala Asn Lys Asn Arg Gln Pro Glu
 230 235 240
 tct tca tca aaa gca tca gag gat gca aac gtc gaa gat gct ggt act
 883
 Ser Ser Ser Lys Ala Ser Glu Asp Ala Asn Val Glu Asp Ala Gly Thr
 245 250 255
 gag ctt aaa aca ctg gaa cac aca tcc cat gca aca gaa cca tac aag
 931
 Glu Leu Lys Thr Leu Glu His Thr Ser His Ala Thr Glu Pro Tyr Lys
 260 265 270 275

gcg cca aac ctt ggc gtc ctt tgt gga act cag aga aaa gaa aaa gaa
 979
 Ala Pro Asn Leu Gly Val Leu Cys Gly Thr Gln Arg Lys Glu Lys Glu
 280 285 290

ata tca tca cca tca agc tct tct gct tta agc atc ttg tct cag tcg
 1027
 Ile Ser Ser Pro Ser Ser Ser Ser Ala Leu Ser Ile Leu Ser Gln Ser
 295 300 305

cct gcc ttc aag agc cta gag gag aaa gtg ttg aag atc caa gaa agc
 1075
 Pro Ala Phe Lys Ser Leu Glu Glu Lys Val Leu Lys Ile Gln Glu Ser
 310 315 320

tgc aat aat gaa aac gat gag aat gca aac cgt aac atc atc aat atg
 1123
 Cys Asn Asn Glu Asn Asp Glu Asn Ala Asn Arg Asn Ile Ile Asn Met
 325 330 335

gag aag aat aac ggc aag gca ata gag aaa cca gtt gtg agt cat gga
 1171
 Glu Lys Asn Asn Gly Lys Ala Ile Glu Lys Pro Val Val Ser His Gly
 340 345 350 355

gtt gct tta ggc ggt gct gct gct ttg tct ctt cag aaa agc atg tac
 1219
 Val Ala Leu Gly Gly Ala Ala Ala Leu Ser Leu Gln Lys Ser Met Tyr
 360 365 370

cca ctt acc tct ctc tta acg gct cca ttg ctc acc aac tac aat aca
 1267
 Pro Leu Thr Ser Leu Leu Thr Ala Pro Leu Leu Thr Asn Tyr Asn Thr
 375 380 385

ttg gat cct ctt gca gac cct att ctc tgg aca cca ttt ctt cct tca
 1315
 Leu Asp Pro Leu Ala Asp Pro Ile Leu Trp Thr Pro Phe Leu Pro Ser
 390 395 400

gga tcc tct ctt act tca gag gtg aca aag aca gag acc agc tgt tcc
 1363
 Gly Ser Ser Leu Thr Ser Glu Val Thr Lys Thr Glu Thr Ser Cys Ser
 405 410 415

acg tac agc tac ctc cca caa gag aaa tga gccgttcct ttagacttta
 1413
 Thr Tyr Ser Tyr Leu Pro Gln Glu Lys
 420 425

tgtatgtcag attctccttt ttgagatga attcgtcgac ttgacatctc ttgtctctt
 1473

ttatggagaa aaagtggga aaagtgtgac aatggtctga agcaggaatg tacaggtttt
 1533

gttagtgggt gtgttttttt tttccagtg tggaatatag aatcatgata ttttgtgtaa
 1593

aacagaaaaa agttatcatt atagtataga agtttgctct taaaaaaaaa aaaaaaa
 1650

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42

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1 5 10 15

Cys Ser Gly Gly Gly Gly Gly Glu Ser Ser Glu Thr Val Ala Ala Ser
20 25 30

Asp Gln Met Leu Leu Tyr Arg Gly Phe Lys Lys Ala Lys Lys Glu Arg
35 40 45

Gly Cys Thr Ala Lys Glu Arg Ile Ser Lys Met Pro Pro Cys Thr Ala
50 55 60

Gly Lys Arg Ser Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr
65 70 75 80

Gly Arg Tyr Glu Ala His Leu Trp Asp Lys Ser Thr Trp Asn Gln Asn
85 90 95

Gln Asn Lys Lys Gly Lys Gln Val Tyr Leu Gly Ala Tyr Asp Asp Glu
100 105 110

Glu Ala Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly
115 120 125

Pro Gly Thr Leu Ile Asn Phe Pro Val Thr Asp Tyr Thr Arg Asp Leu
130 135 140

Glu Glu Met Gln Asn Leu Ser Arg Glu Glu Tyr Leu Ala Ser Leu Arg
145 150 155 160

Arg Tyr Pro Phe Gly Arg Lys Ser Ser Gly Phe Ser Arg Gly Ile Ala
165 170 175

Lys Tyr Arg Gly Leu Gln Ser Arg Trp Asp Ala Ser Ala Ser Arg Met
180 185 190

Pro Gly Pro Glu Tyr Phe Ser Asn Ile His Tyr Gly Ala Gly Asp Asp
195 200 205

Arg Gly Thr Glu Gly Asp Phe Leu Gly Ser Phe Cys Leu Glu Arg Lys
210 215 220

Ile Asp Leu Thr Gly Tyr Ile Lys Trp Trp Gly Ala Asn Lys Asn Arg
225 230 235 240

Gln Pro Glu Ser Ser Ser Lys Ala Ser Glu Asp Ala Asn Val Glu Asp
245 250 255

Ala Gly Thr Glu Leu Lys Thr Leu Glu His Thr Ser His Ala Thr Glu
260 265 270

Pro Tyr Lys Ala Pro Asn Leu Gly Val Leu Cys Gly Thr Gln Arg Lys
275 280 285

Glu Lys Glu Ile Ser Ser Pro Ser Ser Ser Ser Ala Leu Ser Ile Leu
290 295 300

Ser Gln Ser Pro Ala Phe Lys Ser Leu Glu Glu Lys Val Leu Lys Ile
305 310 315 320

Gln Glu Ser Cys Asn Asn Glu Asn Asp Glu Asn Ala Asn Arg Asn Ile
325 330 335

Ile Asn Met Glu Lys Asn Asn Gly Lys Ala Ile Glu Lys Pro Val Val
340 345 350

Ser His Gly Val Ala Leu Gly Gly Ala Ala Ala Leu Ser Leu Gln Lys
355 360 365

Ser Met Tyr Pro Leu Thr Ser Leu Leu Thr Ala Pro Leu Leu Thr Asn
370 375 380

Tyr Asn Thr Leu Asp Pro Leu Ala Asp Pro Ile Leu Trp Thr Pro Phe
385 390 395 400

Leu Pro Ser Gly Ser Ser Leu Thr Ser Glu Val Thr Lys Thr Glu Thr
405 410 415

Ser Cys Ser Thr Tyr Ser Tyr Leu Pro Gln Glu Lys
420 425

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52

Met Thr Thr Glu Lys Glu Asn Val Thr Thr Ala
1 5 10

gtg gcc gtg aaa gac ggc gga gaa aag agt aag gaa gtg agt .gac aag
100

Val Ala Val Lys Asp Gly Gly Glu Lys Ser Lys Glu Val Ser Asp Lys
15 20 25

ggc gta aag aag aga aag aat gta act aag gcc ctg gcc gtg aat gac
148

Gly Val Lys Lys Arg Lys Asn Val Thr Lys Ala Leu Ala Val Asn Asp
30 35 40

ggc gga gaa aag agt aag gaa gtg cgt tac agg ggt gta agg agg aga
196

Gly Gly Glu Lys Ser Lys Glu Val Arg Tyr Arg Gly Val Arg Arg Arg
45 50 55

cca tgg ggg aga tat gct gcg gag atc cgt gat ccg gta aag aaa aaa
244

Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Val Lys Lys Lys
60 65 70 75

cgg gtc tgg ctc ggg tcc ttc aac acg ggg gag gaa gcc gcc aga gcc
292

Arg Val Trp Leu Gly Ser Phe Asn Thr Gly Glu Glu Ala Ala Arg Ala
80 85 90

tac gac tcc gct gcc ata agg ttt cga gga tcg aaa gct act act aac
340

Tyr Asp Ser Ala Ala Ile Arg Phe Arg Gly Ser Lys Ala Thr Thr Asn
95 100 105

ttc cct cta atc gga tac tat ggg att tct tcg gcg acg ccg gtg aac
388

Phe Pro Leu Ile Gly Tyr Tyr Gly Ile Ser Ser Ala Thr Pro Val Asn
110 115 120

aac aac ctt tcc gag acg gtg agt gat gga aat gcc aac ctc cct ctc
436

Asn Asn Leu Ser Glu Thr Val Ser Asp Gly Asn Ala Asn Leu Pro Leu
125 130 135

gtt gga gac gat ggg aat gct ttg gct tct ccg gtg aac aac acc ctt
484

Val Gly Asp Asp Gly Asn Ala Leu Ala Ser Pro Val Asn Asn Thr Leu
140 145 150 155

tcc gaa acg gcg cgt gat gga aca ctt cca tcg gat tgt cac gac atg
532

Ser Glu Thr Ala Arg Asp Gly Thr Leu Pro Ser Asp Cys His Asp Met
160 165 170

tta tct ccg ggg gtg gct gaa gcg gtt gct gga ttt ttc tta gat ctg
580

Leu Ser Pro Gly Val Ala Glu Ala Val Ala Gly Phe Phe Leu Asp Leu
175 180 185

cct gaa gtt att gcg ttg aaa gag gag ctt gat cga gtt tgt cct gac
628

Pro Glu Val Ile Ala Leu Lys Glu Glu Leu Asp Arg Val Cys Pro Asp
190 195 200

cag ttt gag tcc att gat atg ggg ttg act att ggt cct caa acc gcc
676

Gln Phe Glu Ser Ile Asp Met Gly Leu Thr Ile Gly Pro Gln Thr Ala
205 210 215

gtg gaa gag cct gag act tcc tcc gcc gtg gat tgt aag ctg cga atg
724

Val Glu Glu Pro Glu Thr Ser Ser Ala Val Asp Cys Lys Leu Arg Met
220 225 230 235

gaa ccg gat ctt gac ctc aac gca agt ccc taa agattgatct gatgttgtg
777

Glu Pro Asp Leu Asp Leu Asn Ala Ser Pro
240 245

tccttgaata agtttgttat cttgtcgtc ttctgattgt ctgtacttct attggttgat
837

tcgtgctttt ggaggacaaa acaaacattt ttttatgtat taaaaaagg taattgaact
897

attatcgaaa aaaaaaaaaa aaaaaaaaaa aaaaaa
933

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44

Met Thr Thr Glu Lys Glu Asn Val Thr Thr Ala Val Ala Val Lys Asp
1 5 10 15

Gly Gly Glu Lys Ser Lys Glu Val Ser Asp Lys Gly Val Lys Lys Arg
20 25 30

Lys Asn Val Thr Lys Ala Leu Ala Val Asn Asp Gly Gly Glu Lys Ser
35 40 45

Lys Glu Val Arg Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Arg Tyr
50 55 60

Ala Ala Glu Ile Arg Asp Pro Val Lys Lys Lys Arg Val Trp Leu Gly
65 70 75 80

Ser Phe Asn Thr Gly Glu Glu Ala Ala Arg Ala Tyr Asp Ser Ala Ala
85 90 95

Ile Arg Phe Arg Gly Ser Lys Ala Thr Thr Asn Phe Pro Leu Ile Gly
100 105 110

Tyr Tyr Gly Ile Ser Ser Ala Thr Pro Val Asn Asn Asn Leu Ser Glu
115 120 125

Thr Val Ser Asp Gly Asn Ala Asn Leu Pro Leu Val Gly Asp Asp Gly

130 135 140
 Asn Ala Leu Ala Ser Pro Val Asn Asn Thr Leu Ser Glu Thr Ala Arg
 145 150 155 160
 Asp Gly Thr Leu Pro Ser Asp Cys His Asp Met Leu Ser Pro Gly Val
 165 170 175
 Ala Glu Ala Val Ala Gly Phe Phe Leu Asp Leu Pro Glu Val Ile Ala
 180 185 190
 Leu Lys Glu Glu Leu Asp Arg Val Cys Pro Asp Gln Phe Glu Ser Ile
 195 200 205
 Asp Met Gly Leu Thr Ile Gly Pro Gln Thr Ala Val Glu Glu Pro Glu
 210 215 220
 Thr Ser Ser Ala Val Asp Cys Lys Leu Arg Met Glu Pro Asp Leu Asp
 225 230 235 240
 Leu Asn Ala Ser Pro
 245
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 tctgtagga tata atg cca ccc tct cct cct aaa tct cct ttt att agc
 110
 Met Pro Pro Ser Pro Pro Lys Ser Pro Phe Ile Ser
 1 5 10
 tct tca ctc aaa gga gct cat gaa gat cgc aaa ttt aaa tgc tat agg
 158
 Ser Ser Leu Lys Gly Ala His Glu Asp Arg Lys Phe Lys Cys Tyr Arg
 15 20 25
 ggt gtc cga aag agg tct tgg ggc aaa tgg gtg tct gaa atc aga gtt
 206
 Gly Val Arg Lys Arg Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Val
 30 35 40
 cca aag act gga cga cga ata tgg cta ggt tca tac gat gct cca gag
 254
 Pro Lys Thr Gly Arg Arg Ile Trp Leu Gly Ser Tyr Asp Ala Pro Glu
 45 50 55 60
 aag gca gct aga gcc tat gat gct gct ttg ttc tgt att agg ggt gag
 302
 Lys Ala Ala Arg Ala Tyr Asp Ala Ala Leu Phe Cys Ile Arg Gly Glu

65										70										75										
aag gga gtt tac aat ttt ccc act gat aaa aag ccg cag ctt cca gaa																														
350																														
Lys Gly Val Tyr Asn Phe Pro Thr Asp Lys Lys Pro Gln Leu Pro Glu																														
80	85	90																												
ggt tct gtc cgg cct ctg tcc aag ctc gac ata cag aca ata gca aca																														
398																														
Gly Ser Val Arg Pro Leu Ser Lys Leu Asp Ile Gln Thr Ile Ala Thr																														
95	100	105																												
aac tat gct tca tca gtt gtg cat gta cct tcc cat gcc acc aca ctc																														
446																														
Asn Tyr Ala Ser Ser Val Val His Val Pro Ser His Ala Thr Thr Leu																														
110	115	120																												
ccg gca aca acc cag gtt ccc tct gaa gtt cct gct tcc tct gat gtt																														
494																														
Pro Ala Thr Thr Gln Val Pro Ser Glu Val Pro Ala Ser Ser Asp Val																														
125	130	135	140																											
tct gct tct act gag att aca gag atg gtc gat gaa tat tat ctc cca																														
542																														
Ser Ala Ser Thr Glu Ile Thr Glu Met Val Asp Glu Tyr Tyr Leu Pro																														
145	150	155																												
acc gat gca act gca gaa tca ata ttc tca gtt gaa gac tta caa ctg																														
590																														
Thr Asp Ala Thr Ala Glu Ser Ile Phe Ser Val Glu Asp Leu Gln Leu																														
160	165	170																												
gac agt ttc ctc atg atg gac att gat tgg ata aac aat cta atc tga																														
638																														
Asp Ser Phe Leu Met Met Asp Ile Asp Trp Ile Asn Asn Leu Ile																														
175	180	185																												
tgtgtaacgt cacttgacgt gacatttaac atgggttaac tatcagttac ctgtctgctt																														
698																														
cttgtaaggg tatacttgga tccttgctt tgaacttggt ttatttagca tgcaaa																														
754																														
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46																														
Met Pro Pro Ser Pro Pro Lys Ser Pro Phe Ile Ser Ser Ser Leu Lys																														
1	5	10	15																											
Gly Ala His Glu Asp Arg Lys Phe Lys Cys Tyr Arg Gly Val Arg Lys																														
20	25	30																												
Arg Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro Lys Thr Gly																														
35	40	45																												
Arg Arg Ile Trp Leu Gly Ser Tyr Asp Ala Pro Glu Lys Ala Ala Arg																														
50	55	60																												

Ala Tyr Asp Ala Ala Leu Phe Cys Ile Arg Gly Glu Lys Gly Val Tyr
65 70 75 80

Asn Phe Pro Thr Asp Lys Lys Pro Gln Leu Pro Glu Gly Ser Val Arg
85 90 95

Pro Leu Ser Lys Leu Asp Ile Gln Thr Ile Ala Thr Asn Tyr Ala Ser
100 105 110

Ser Val Val His Val Pro Ser His Ala Thr Thr Leu Pro Ala Thr Thr
115 120 125

Gln Val Pro Ser Glu Val Pro Ala Ser Ser Asp Val Ser Ala Ser Thr
130 135 140

Glu Ile Thr Glu Met Val Asp Glu Tyr Tyr Leu Pro Thr Asp Ala Thr
145 150 155 160

Ala Glu Ser Ile Phe Ser Val Glu Asp Leu Gln Leu Asp Ser Phe Leu
165 170 175

Met Met Asp Ile Asp Trp Ile Asn Asn Leu Ile
180 185

<210> 47 <211> 914 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (37)..(672) <223> G147

<400> 47
aaatcatcag atagaaggaa atattctgat tgagag atg gct cgt gga aag att
54

Met Ala Arg Gly Lys Ile
1 5

cag ctt aag agg att gag aac ccg gtt cac aga caa gtg act ttt tgc
102

Gln Leu Lys Arg Ile Glu Asn Pro Val His Arg Gln Val Thr Phe Cys
10 15 20

aag agg aga act ggt ctt ctc aag aag gct aag gag ctc tct gtg ctc
150

Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala Lys Glu Leu Ser Val Leu
25 30 35

tgt gat gcc gag atc ggt gtt gtg atc ttc tct cct cag ggc aag ctc
198

Cys Asp Ala Glu Ile Gly Val Val Ile Phe Ser Pro Gln Gly Lys Leu
40 45 50

ttt gag ctc gct act aaa gga aca atg gag gga atg att gat aag tac
246

Phe Glu Leu Ala Thr Lys Gly Thr Met Glu Gly Met Ile Asp Lys Tyr

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55                               60                               65                               70
atg aag tgt act ggt ggt ggt cgt ggt tct tct tct gct act ttt act
294
Met Lys Cys Thr Gly Gly Gly Arg Gly Ser Ser Ser Ala Thr Phe Thr
              75                               80                               85

gct caa gaa caa ctt caa cca cca aat ctt gat ccg aaa gat gag atc
342
Ala Gln Glu Gln Leu Gln Pro Pro Asn Leu Asp Pro Lys Asp Glu Ile
              90                               95                               100

aac gtg ctt aag caa gag att gag atg ctt cag aaa ggg ata agc tat
390
Asn Val Leu Lys Gln Glu Ile Glu Met Leu Gln Lys Gly Ile Ser Tyr
              105                               110                               115

atg ttt gga gga gga gat ggg gct atg aat ctt gaa gaa ctt ctt ttg
438
Met Phe Gly Gly Gly Asp Gly Ala Met Asn Leu Glu Glu Leu Leu Leu
              120                               125                               130

ctt gag aag cat ctt gag tat tgg att tct cag att cgc tct gct aag
486
Leu Glu Lys His Leu Glu Tyr Trp Ile Ser Gln Ile Arg Ser Ala Lys
              135                               140                               145                               150

atg gat gtt atg ctt caa gaa att cag tca ttg agg aac aag gaa gga
534
Met Asp Val Met Leu Gln Glu Ile Gln Ser Leu Arg Asn Lys Glu Gly
              155                               160                               165

gtc ctc aaa aac acc aac aag tat ctc ctc gac aag ata gag gaa aac
582
Val Leu Lys Asn Thr Asn Lys Tyr Leu Leu Asp Lys Ile Glu Glu Asn
              170                               175                               180

aac aat agc ata tta gat gct aac ttc gca gtc atg gag aca aac tat
630
Asn Asn Ser Ile Leu Asp Ala Asn Phe Ala Val Met Glu Thr Asn Tyr
              185                               190                               195

tcc tat ccg cta aca atg cca agt gaa ata ttt cag ttc tag
672
Ser Tyr Pro Leu Thr Met Pro Ser Glu Ile Phe Gln Phe
              200                               205                               210

accatagggg atttgaagac tatgtctcac gaatttaaata aaccttggtta agtataatat
732

agtgttggtta aatcacacat aattaaaata aagcctgtgg aacttcgcta ggcagttgaa
792

aatctatccg tatgttttat cctcttggtt tacatttggt ggtgtgaaga tgaaatgact
852

gcaagtgtgg tgtgtactta taactctttc tactttctat ctatgttttg aatttatgga
912

tt
914

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Arg Gln Val Thr Phe Cys Lys Arg Arg Thr Gly Leu Leu Lys Lys Ala
20 25 30

Lys Glu Leu Ser Val Leu Cys Asp Ala Glu Ile Gly Val Val Ile Phe
35 40 45

Ser Pro Gln Gly Lys Leu Phe Glu Leu Ala Thr Lys Gly Thr Met Glu
50 55 60

Gly Met Ile Asp Lys Tyr Met Lys Cys Thr Gly Gly Gly Arg Gly Ser
65 70 75 80

Ser Ser Ala Thr Phe Thr Ala Gln Glu Gln Leu Gln Pro Pro Asn Leu
85 90 95

Asp Pro Lys Asp Glu Ile Asn Val Leu Lys Gln Glu Ile Glu Met Leu
100 105 110

Gln Lys Gly Ile Ser Tyr Met Phe Gly Gly Gly Asp Gly Ala Met Asn
115 120 125

Leu Glu Glu Leu Leu Leu Leu Glu Lys His Leu Glu Tyr Trp Ile Ser
130 135 140

Gln Ile Arg Ser Ala Lys Met Asp Val Met Leu Gln Glu Ile Gln Ser
145 150 155 160

Leu Arg Asn Lys Glu Gly Val Leu Lys Asn Thr Asn Lys Tyr Leu Leu
165 170 175

Asp Lys Ile Glu Glu Asn Asn Asn Ser Ile Leu Asp Ala Asn Phe Ala
180 185 190

Val Met Glu Thr Asn Tyr Ser Tyr Pro Leu Thr Met Pro Ser Glu Ile
195 200 205

Phe Gln Phe
210

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 120

agaagaagag attttgattt tggtttaata tatagttggg gattaacagg atg gga
 176

Met Gly
 1

agg gta aaa ttg aag ata aag aag tta gag aac aca aat gga cgc caa
 224
 Arg Val Lys Leu Lys Ile Lys Lys Leu Glu Asn Thr Asn Gly Arg Gln
 5 10 15

tct aca ttt gct aaa agg aaa aat ggg atc ttg aaa aag gct aat gag
 272
 Ser Thr Phe Ala Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala Asn Glu
 20 25 30

cta tct att ctt tgt gac att gat att gtt ctt ctt atg ttc tct cct
 320
 Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe Ser Pro
 35 40 45 50

act ggc aag gct gca ata tgt tgc ggt aca cga aga tgt ttc tct ttc
 368
 Thr Gly Lys Ala Ala Ile Cys Cys Gly Thr Arg Arg Cys Phe Ser Phe
 55 60 65

gaa agc tca gaa ctt gaa gaa aac ttt cca aaa gtt gga tca cga tgt
 416
 Glu Ser Ser Glu Leu Glu Glu Asn Phe Pro Lys Val Gly Ser Arg Cys
 70 75 80

aaa tat acg cga att tat agc ctc aag gac ttg agt act caa gca agg
 464
 Lys Tyr Thr Arg Ile Tyr Ser Leu Lys Asp Leu Ser Thr Gln Ala Arg
 85 90 95

att ctg cag gct cgg att tct gag ata cat gga aga tta agt tat tgg
 512
 Ile Leu Gln Ala Arg Ile Ser Glu Ile His Gly Arg Leu Ser Tyr Trp
 100 105 110

acg gaa cca gat aag att aac aat gtt gaa cac ttg gga cag ctc gaa
 560
 Thr Glu Pro Asp Lys Ile Asn Asn Val Glu His Leu Gly Gln Leu Glu
 115 120 125 130

att tcg att agg caa tcc ctt gat caa ttg cgt gca cac aag atg caa
 608
 Ile Ser Ile Arg Gln Ser Leu Asp Gln Leu Arg Ala His Lys Met Gln
 135 140 145

gat ggg att cag att cct tta gaa caa cag ctt caa tct atg tca tgg
 656
 Asp Gly Ile Gln Ile Pro Leu Glu Gln Gln Leu Gln Ser Met Ser Trp
 150 155 160

att ctt aat agc aac acc acc aac att gtc acc gag gaa cac aat tca
 704
 Ile Leu Asn Ser Asn Thr Thr Asn Ile Val Thr Glu Glu His Asn Ser
 165 170 175

atc ccg cag agg gaa gtc gag tgc tca gcg agt tct tca ttc ggg agc
 752
 Ile Pro Gln Arg Glu Val Glu Cys Ser Ala Ser Ser Ser Phe Gly Ser
 180 185 190

tat cca ggc tac ttt gga aca ggg aaa tct cct gaa atg aca att ccg
 800
 Tyr Pro Gly Tyr Phe Gly Thr Gly Lys Ser Pro Glu Met Thr Ile Pro
 195 200 205 210

ggt caa gaa aca agc ttt ctt gat gaa cta aac acc gga cag ctg aaa
 848
 Gly Gln Glu Thr Ser Phe Leu Asp Glu Leu Asn Thr Gly Gln Leu Lys
 215 220 225

cag gac aca agc tcg cag cag cag ttc act aat aat aat aat atc aca
 896
 Gln Asp Thr Ser Ser Gln Gln Gln Phe Thr Asn Asn Asn Asn Ile Thr
 230 235 240

gca tac aat ccc aat ctt cac aat gat atg aat cat cac caa acg ttg
 944
 Ala Tyr Asn Pro Asn Leu His Asn Asp Met Asn His His Gln Thr Leu
 245 250 255

cct cct cct cct ctt cct ctt act ctt ccg cat gct cag gtg tat att
 992
 Pro Pro Pro Pro Leu Pro Leu Thr Leu Pro His Ala Gln Val Tyr Ile
 260 265 270

cca atg aat cag aga gag tat cat atg aat gga ttc ttt gaa gca cca
 1040
 Pro Met Asn Gln Arg Glu Tyr His Met Asn Gly Phe Phe Glu Ala Pro
 275 280 285 290

cca cct gat tct tct gct tac aac gac aac acc aac caa acc agg ttt
 1088
 Pro Pro Asp Ser Ser Ala Tyr Asn Asp Asn Thr Asn Gln Thr Arg Phe
 295 300 305

ggt tct agc agc agc tcc ttg cct tgc tca atc tca atg ttc gac gaa
 1136
 Gly Ser Ser Ser Ser Ser Leu Pro Cys Ser Ile Ser Met Phe Asp Glu
 310 315 320

tac ttg ttt tcc cag atg cag cag ccg aac tga gagagatttg atgaatgatg
 1189
 Tyr Leu Phe Ser Gln Met Gln Gln Pro Asn
 325 330

ataaaacatc tcactgaaga aactcaaacc aatatttttt ttcagaaaca gcaagaaagc
1249

taaaactctg ccgatttctg aattgggtcc aagaagaaaa aaaccagtgg taatccctgg
1309

tagattgtgc aaccaaacca cacacaatac gtgttcattt attttttcta tatcttcaat
1369

agatgtcact taattctttt ctatacataa tttctcagtc agaat
1414

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Met Gly Arg Val Lys Leu Lys Ile Lys Lys Leu Glu Asn Thr Asn Gly
1 5 10 15

Arg Gln Ser Thr Phe Ala Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala
20 25 30

Asn Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe
35 40 45

Ser Pro Thr Gly Lys Ala Ala Ile Cys Cys Gly Thr Arg Arg Cys Phe
50 55 60

Ser Phe Glu Ser Ser Glu Leu Glu Glu Asn Phe Pro Lys Val Gly Ser
65 70 75 80

Arg Cys Lys Tyr Thr Arg Ile Tyr Ser Leu Lys Asp Leu Ser Thr Gln
85 90 95

Ala Arg Ile Leu Gln Ala Arg Ile Ser Glu Ile His Gly Arg Leu Ser
100 105 110

Tyr Trp Thr Glu Pro Asp Lys Ile Asn Asn Val Glu His Leu Gly Gln
115 120 125

Leu Glu Ile Ser Ile Arg Gln Ser Leu Asp Gln Leu Arg Ala His Lys
130 135 140

Met Gln Asp Gly Ile Gln Ile Pro Leu Glu Gln Gln Leu Gln Ser Met
145 150 155 160

Ser Trp Ile Leu Asn Ser Asn Thr Thr Asn Ile Val Thr Glu Glu His
165 170 175

Asn Ser Ile Pro Gln Arg Glu Val Glu Cys Ser Ala Ser Ser Ser Phe

180 185 190
 Gly Ser Tyr Pro Gly Tyr Phe Gly Thr Gly Lys Ser Pro Glu Met Thr
 195 200 205
 Ile Pro Gly Gln Glu Thr Ser Phe Leu Asp Glu Leu Asn Thr Gly Gln
 210 215 220
 Leu Lys Gln Asp Thr Ser Ser Gln Gln Gln Phe Thr Asn Asn Asn Asn
 225 230 235 240
 Ile Thr Ala Tyr Asn Pro Asn Leu His Asn Asp Met Asn His His Gln
 245 250 255
 Thr Leu Pro Pro Pro Pro Leu Pro Leu Thr Leu Pro His Ala Gln Val
 260 265 270
 Tyr Ile Pro Met Asn Gln Arg Glu Tyr His Met Asn Gly Phe Phe Glu
 275 280 285
 Ala Pro Pro Pro Asp Ser Ser Ala Tyr Asn Asp Asn Thr Asn Gln Thr
 290 295 300
 Arg Phe Gly Ser Ser Ser Ser Ser Leu Pro Cys Ser Ile Ser Met Phe
 305 310 315 320
 Asp Glu Tyr Leu Phe Ser Gln Met Gln Gln Pro Asn
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 ggt cgt cag aaa ata gag atg aaa aaa atg gaa aac gaa agc aac ctt
 103
 Gly Arg Gln Lys Ile Glu Met Lys Lys Met Glu Asn Glu Ser Asn Leu
 10 15 20

 cag gtt act ttc tca aaa aga aga ttc ggt ctt ttc aaa aaa gct agt
 151
 Gln Val Thr Phe Ser Lys Arg Arg Phe Gly Leu Phe Lys Lys Ala Ser
 25 30 35

 gaa ctt tgc aca tta agt ggt gca gag att ctg ttg att gtg ttc tct
 199
 Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile Leu Leu Ile Val Phe Ser

40	45	50
cct ggt ggg aaa gtg ttt tct ttt ggc cat cca agt gtt caa gaa ctc 247		
Pro Gly Gly Lys Val Phe Ser Phe Gly His Pro Ser Val Gln Glu Leu 55 60 65 70		
att cat cgc ttt tcg aat cct aac cat aat tct gcc att gtc cat cat 295		
Ile His Arg Phe Ser Asn Pro Asn His Asn Ser Ala Ile Val His His 75 80 85		
cag aac aac aat ctc caa ctt gtt gaa acc cgt ccg gat aga aat atc 343		
Gln Asn Asn Asn Leu Gln Leu Val Glu Thr Arg Pro Asp Arg Asn Ile 90 95 100		
caa tat ctc aac aat ata ctc act gag gtg ctg gca aac cag gaa aag 391		
Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val Leu Ala Asn Gln Glu Lys 105 110 115		
gag aaa cag aag aga atg gtt ttg gac cta ttg aaa gaa tcc aga gaa 439		
Glu Lys Gln Lys Arg Met Val Leu Asp Leu Leu Lys Glu Ser Arg Glu 120 125 130		
caa gta gga aac tgg tat gaa aaa gat gtg aaa gat ctc gac atg aat 487		
Gln Val Gly Asn Trp Tyr Glu Lys Asp Val Lys Asp Leu Asp Met Asn 135 140 145 150		
gaa acc aac cag ctg ata tct gct ctt caa gat gtg aaa aag aaa ctg 535		
Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln Asp Val Lys Lys Lys Leu 155 160 165		
gta aga gaa atg tct caa tat tct caa gta aat gtt tcg cag aat tac 583		
Val Arg Glu Met Ser Gln Tyr Ser Gln Val Asn Val Ser Gln Asn Tyr 170 175 180		
ttt ggt caa agt tct ggc gtg att ggt ggt ggt aat gtt ggc att gat 631		
Phe Gly Gln Ser Ser Gly Val Ile Gly Gly Gly Asn Val Gly Ile Asp 185 190 195		
ctt ttt gat caa aga aga aat gca ttc aac tat aat cca aac atg gtg 679		
Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn Tyr Asn Pro Asn Met Val 200 205 210		
ttt ccc aat cat aca cca cca atg ttt gga tac aac aat gat gga gtt 727		
Phe Pro Asn His Thr Pro Pro Met Phe Gly Tyr Asn Asn Asp Gly Val 215 220 225 230		
ctc gtt ccg ata tcc aac atg aac tac atg tca agt tac aac ttc aac 775		
Leu Val Pro Ile Ser Asn Met Asn Tyr Met Ser Ser Tyr Asn Phe Asn 235 240 245		

cag agc tag agtctgaagc tagaagaaca tcctaatacaa tatttgcgtt
824
Gln Ser

atattggcta tggttactgt taggattggt cttgtattgt gagacttaag tttgtttttt
884

cttttaattt gtttcagttg gttgggtttt cattttattc gtcgtttggt ttcctttggt
944

tttgatatt tttgtatccc agaataaatt tatttatcct ttaaaaa
991

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52

Met Val Arg Ser Thr Lys Gly Arg Gln Lys Ile Glu Met Lys Lys Met
1 5 10 15

Glu Asn Glu Ser Asn Leu Gln Val Thr Phe Ser Lys Arg Arg Phe Gly
20 25 30

Leu Phe Lys Lys Ala Ser Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile
35 40 45

Leu Leu Ile Val Phe Ser Pro Gly Gly Lys Val Phe Ser Phe Gly His
50 55 60

Pro Ser Val Gln Glu Leu Ile His Arg Phe Ser Asn Pro Asn His Asn
65 70 75 80

Ser Ala Ile Val His His Gln Asn Asn Asn Leu Gln Leu Val Glu Thr
85 90 95

Arg Pro Asp Arg Asn Ile Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val
100 105 110

Leu Ala Asn Gln Glu Lys Glu Lys Gln Lys Arg Met Val Leu Asp Leu
115 120 125

Leu Lys Glu Ser Arg Glu Gln Val Gly Asn Trp Tyr Glu Lys Asp Val
130 135 140

Lys Asp Leu Asp Met Asn Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln
145 150 155 160

Asp Val Lys Lys Lys Leu Val Arg Glu Met Ser Gln Tyr Ser Gln Val
165 170 175

Asn Val Ser Gln Asn Tyr Phe Gly Gln Ser Ser Gly Val Ile Gly Gly
 180 185 190

Gly Asn Val Gly Ile Asp Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn
 195 200 205

Tyr Asn Pro Asn Met Val Phe Pro Asn His Thr Pro Pro Met Phe Gly
 210 215 220

Tyr Asn Asn Asp Gly Val Leu Val Pro Ile Ser Asn Met Asn Tyr Met
 225 230 235 240

Ser Ser Tyr Asn Phe Asn Gln Ser
 245

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 56

Met
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aac ttc ctc gtt cct ttt gaa gaa acc aat gtc tta acc ttt ttc tct
 104
 Asn Phe Leu Val Pro Phe Glu Glu Thr Asn Val Leu Thr Phe Phe Ser
 5 10 15

tct tct tct tcc tct tct ctt tct tct cct tct ttc ccc att cac aac
 152
 Ser Ser Ser Ser Ser Ser Leu Ser Ser Pro Ser Phe Pro Ile His Asn
 20 25 30

tct tcc tcc act act act act cat gca cct cta ggg ttt tct aat aat
 200
 Ser Ser Ser Thr Thr Thr Thr His Ala Pro Leu Gly Phe Ser Asn Asn
 35 40 45

ctt cag ggt gga gga ccc ttg gga tca aag gtg gtt aat gat gat cag
 248
 Leu Gln Gly Gly Gly Pro Leu Gly Ser Lys Val Val Asn Asp Asp Gln
 50 55 60 65

gag aat ttt gga ggt gga act aac aat gat gct cat tct aat tct tgg
 296
 Glu Asn Phe Gly Gly Gly Thr Asn Asn Asp Ala His Ser Asn Ser Trp
 70 75 80

tgg aga tca aat agt gga agt gga gat atg aag aac aaa gtg aag ata
 344
 Trp Arg Ser Asn Ser Gly Ser Gly Asp Met Lys Asn Lys Val Lys Ile
 85 90 95

agg agg aaa cta aga gag cca aga ttc tgt ttc caa acc aaa agc gat
392

Arg Arg Lys Leu Arg Glu Pro Arg Phe Cys Phe Gln Thr Lys Ser Asp
100 105 110

gtt gat gtt ctt gac gat ggc tac aaa tgg cgt aaa tat ggt cag aaa
440

Val Asp Val Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln Lys
115 120 125

gtc gtc aag aac agc ctt cac ccc agg agt tat tac aga tgc aca cac
488

Val Val Lys Asn Ser Leu His Pro Arg Ser Tyr Tyr Arg Cys Thr His
130 135 140 145

aac aac tgt agg gtg aaa aag aga gtg gag cga cta tcg gaa gat tgt
536

Asn Asn Cys Arg Val Lys Lys Arg Val Glu Arg Leu Ser Glu Asp Cys
150 155 160

aga atg gtg att act act tac gaa ggt cgt cac aac cac att ccc tct
584

Arg Met Val Ile Thr Thr Tyr Glu Gly Arg His Asn His Ile Pro Ser
165 170 175

gat gac tcc act tct cct gac cat gat tgt ctc tct tcc ttt taa
629

Asp Asp Ser Thr Ser Pro Asp His Asp Cys Leu Ser Ser Phe
180 185 190

catctctttc tatatatcta tatatagaca gttatatgtg cacatataga tgtgtgatat
689

attgcatatt tgatattgca tgtgtttttc aagagtatgt catcagatgt tatgcatata
749

ttcttgactt gttgcttata gtatacatat gtaataatat atattgacat tggtagttca
809

tttctgttca aacaaaaaaaa aaaaaaaaa
837

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54

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1 5 10 15

Ser Ser Ser Ser Ser Ser Ser Leu Ser Ser Pro Ser Phe Pro Ile His
20 25 30

Asn Ser Ser Ser Thr Thr Thr Thr His Ala Pro Leu Gly Phe Ser Asn
35 40 45

Asn Leu Gln Gly Gly Gly Pro Leu Gly Ser Lys Val Val Asn Asp Asp
50 55 60

Gln Glu Asn Phe Gly Gly Gly Thr Asn Asn Asp Ala His Ser Asn Ser
65 70 75 80

Trp Trp Arg Ser Asn Ser Gly Ser Gly Asp Met Lys Asn Lys Val Lys
85 90 95

Ile Arg Arg Lys Leu Arg Glu Pro Arg Phe Cys Phe Gln Thr Lys Ser
100 105 110

Asp Val Asp Val Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Gln
115 120 125

Lys Val Val Lys Asn Ser Leu His Pro Arg Ser Tyr Tyr Arg Cys Thr
130 135 140

His Asn Asn Cys Arg Val Lys Lys Arg Val Glu Arg Leu Ser Glu Asp
145 150 155 160

Cys Arg Met Val Ile Thr Thr Tyr Glu Gly Arg His Asn His Ile Pro
165 170 175

Ser Asp Asp Ser Thr Ser Pro Asp His Asp Cys Leu Ser Ser Phe
180 185 190

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Met Asp Arg Glu Asp Ile Asn Pro Met Leu Ser Arg Leu Asp Val
1 5 10 15

gaa aac aac aac acc ttc tct tcc ttt gta gac aaa acc cta atg atg
97
Glu Asn Asn Asn Thr Phe Ser Ser Phe Val Asp Lys Thr Leu Met Met
20 25 30

atg cct cca tca aca ttt tcc ggt gaa gtg gaa cct tca tct tct tct
145
Met Pro Pro Ser Thr Phe Ser Gly Glu Val Glu Pro Ser Ser Ser Ser
35 40 45

tct tgg tat cca gaa agc ttt cat gtg cat gcg ccg cca tta cca cct
193
Ser Trp Tyr Pro Glu Ser Phe His Val His Ala Pro Pro Leu Pro Pro
50 55 60

gag aat gat caa ata ggt gag aaa ggg aag gag ctg aaa gag aag aga
241
Glu Asn Asp Gln Ile Gly Glu Lys Gly Lys Glu Leu Lys Glu Lys Arg
65 70 75

tcg agg aaa gtt cca agg att gcg ttt cat acg agg agc gat gat gat
289

Ser Arg Lys Val Pro Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp
80 85 90 95

gtt ctt gat gat ggt tat cgt tgg cga aaa tat ggg cag aaa tct gtc
337

Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val
100 105 110

aag cac aat gct cat ccc agg agc tat tac aga tgt acg tac cac aca
385

Lys His Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr
115 120 125

tgc aac gtg aag aaa caa gtg cag aga ttg gca aaa gat cca aac gtc
433

Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val
130 135 140

gtc gta acg acc tac gaa ggc gtt cat aac cat cct tgt gag aag ctc
481

Val Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu
145 150 155

atg gag act ctt aat cct ctt ctc agg caa ctc cag ttc ctc tcc agt
529

Met Glu Thr Leu Asn Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Ser
160 165 170 175

ttc tct aat ctt tga atatataatg gcttaattaa tgggtgtaatt acttaaaggt
584

Phe Ser Asn Leu

gattaaggtg ttaatcacc cactgaccgt ttgacgaccc acatctccca agtgacaagt
644

cacaagtgtag tagatcagat tttaaacc aa tgtaacagtt acgacttttt acaaatgttt
704

ctgaatttta tcccctgatt tctggttaat gatcggttta cgccgatgat ttgacaaata
764

ccagacaaaa caagtttagt tacatatgta agtatgaaaa ggtagtttcc tctaacttca
824

ttaaaaaaaa aaaaaaaaaa
844

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1 5 10 15

Asn Asn Asn Thr Phe Ser Ser Phe Val Asp Lys Thr Leu Met Met Met
20 25 30

Pro Pro Ser Thr Phe Ser Gly Glu Val Glu Pro Ser Ser Ser Ser
 35 40 45
 Trp Tyr Pro Glu Ser Phe His Val His Ala Pro Pro Leu Pro Pro Glu
 50 55 60
 Asn Asp Gln Ile Gly Glu Lys Gly Lys Glu Leu Lys Glu Lys Arg Ser
 65 70 75 80
 Arg Lys Val Pro Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp Val
 85 90 95
 Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys
 100 105 110
 His Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr Cys
 115 120 125
 Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val Val
 130 135 140
 Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu Met
 145 150 155 160
 Glu Thr Leu Asn Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Ser Phe
 165 170 175
 Ser Asn Leu

<210> 57 <211> 1974 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (327)..(1937) <223> G184

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ataaccacat aatttaataca aactctttct ctctctttct aagatctttt gctttgctct
 120

ttctcttttt gatcttccta tatatggaga agcaccaaaa cggtacttac tatacgatac
 180

tgtacggatc catcaaactg gattaattat caaaacgtac atttttatct tacctggcaa
 240

gttacattcc tagggttttg gagaatccaa tcaacaacaa agaaaataat catcgttaca
 300

ataatcagta tcacgcacag acttag atg ttc cgg ttt cca gtg agt cta ggc
353

Met Phe Arg Phe Pro Val Ser Leu Gly
1 5

ggt tca cgt gac gaa gac cgt cac gat cag atc aca ccg ttg gat gac
401

Gly Ser Arg Asp Glu Asp Arg His Asp Gln Ile Thr Pro Leu Asp Asp
10 15 20 25

cat cgt gtg gtg gtt gat gag gtt gac ttc ttc tca gag aag aga gat
449

His Arg Val Val Val Asp Glu Val Asp Phe Phe Ser Glu Lys Arg Asp
30 35 40

agg gtt tca cgt gag aac atc aac gac gac gac gac gaa ggc aat aag
497

Arg Val Ser Arg Glu Asn Ile Asn Asp Asp Asp Asp Glu Gly Asn Lys
45 50 55

gtt ctc atc aaa atg gag ggt tca cga gtt gaa gaa aac gat cgt tcc
545

Val Leu Ile Lys Met Glu Gly Ser Arg Val Glu Glu Asn Asp Arg Ser
60 65 70

aga gat gtc aat atc ggt ctg aat ctt ctg acc gcg aat acg gga agc
593

Arg Asp Val Asn Ile Gly Leu Asn Leu Leu Thr Ala Asn Thr Gly Ser
75 80 85

gat gag tca acg gtg gat gat gga cta tca atg gat atg gaa gat aaa
641

Asp Glu Ser Thr Val Asp Asp Gly Leu Ser Met Asp Met Glu Asp Lys
90 95 100 105

cgt gca aag att gag aac gca caa cta caa gaa gag ctc aag aag atg
689

Arg Ala Lys Ile Glu Asn Ala Gln Leu Gln Glu Glu Leu Lys Lys Met
110 115 120

aaa ata gag aat caa agg cta aga gat atg ttg agc caa gcg acg acc
737

Lys Ile Glu Asn Gln Arg Leu Arg Asp Met Leu Ser Gln Ala Thr Thr
125 130 135

aac ttc aat gcc tta caa atg caa ctt gtt gcc gtc atg agg caa caa
785

Asn Phe Asn Ala Leu Gln Met Gln Leu Val Ala Val Met Arg Gln Gln
140 145 150

gaa caa cgt aac tct tca caa gat cat ctc ctg gag agc aaa gca gaa
833

Glu Gln Arg Asn Ser Ser Gln Asp His Leu Leu Glu Ser Lys Ala Glu
155 160 165

gga agg aaa cgg cag gaa ctg caa atc atg gtg cca agg cag ttc atg
881

Gly Arg Lys Arg Gln Glu Leu Gln Ile Met Val Pro Arg Gln Phe Met
170 175 180 185

gac ctt ggg ccg tcg tct gga gca gca gag cat gga gcc gaa gtg tca
 929
 Asp Leu Gly Pro Ser Ser Gly Ala Ala Glu His Gly Ala Glu Val Ser
 190 195 200
 tct gaa gag agg aca acg gtt cgt tca ggt tct cct cct tcg ctt cta
 977
 Ser Glu Glu Arg Thr Thr Val Arg Ser Gly Ser Pro Pro Ser Leu Leu
 205 210 215
 gaa agt tcc aat ccc cga gag aac gga aag agg ttg ctt gga aga gaa
 1025
 Glu Ser Ser Asn Pro Arg Glu Asn Gly Lys Arg Leu Leu Gly Arg Glu
 220 225 230
 gaa agc tca gag gaa tca gag tct aac gcc tgg gga aac cct aac aaa
 1073
 Glu Ser Ser Glu Glu Ser Glu Ser Asn Ala Trp Gly Asn Pro Asn Lys
 235 240 245
 gtc ccc aaa cat aat cca tcc tct agc aat agc aat gga aac aga aac
 1121
 Val Pro Lys His Asn Pro Ser Ser Ser Asn Ser Asn Gly Asn Arg Asn
 250 255 260 265
 gga aat gtt att gat cag tcg gcc gca gaa gcc acc atg cgg aaa gcc
 1169
 Gly Asn Val Ile Asp Gln Ser Ala Ala Glu Ala Thr Met Arg Lys Ala
 270 275 280
 cgt gtc tca gtt cgt gcc cga tct gaa gct gcc atg ata agc gat gga
 1217
 Arg Val Ser Val Arg Ala Arg Ser Glu Ala Ala Met Ile Ser Asp Gly
 285 290 295
 tgt caa tgg aga aag tac gga caa aaa atg gct aaa gga aac ccg tgt
 1265
 Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met Ala Lys Gly Asn Pro Cys
 300 305 310
 ccg cgg gct tat tat cgt tgc aca atg gcc ggt gga tgt cca gtt cgc
 1313
 Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala Gly Gly Cys Pro Val Arg
 315 320 325
 aag caa gtg cag cgt tgc gca gaa gac aga tct att ctc ata acc acc
 1361
 Lys Gln Val Gln Arg Cys Ala Glu Asp Arg Ser Ile Leu Ile Thr Thr
 330 335 340 345
 tac gaa gga aac cac aac cat cca ctc cca cca gcc gct acg gcc atg
 1409
 Tyr Glu Gly Asn His Asn His Pro Leu Pro Pro Ala Ala Thr Ala Met
 350 355 360
 gcc tca aca acc acc gca gct gca agc atg ctc ctc tcg ggc tca atg
 1457
 Ala Ser Thr Thr Thr Ala Ala Ala Ser Met Leu Leu Ser Gly Ser Met
 365 370 375

tcg agt caa gac ggt tta atg aac cca aca aac ctc cta gct cga gct
1505

Ser Ser Gln Asp Gly Leu Met Asn Pro Thr Asn Leu Leu Ala Arg Ala
380 385 390

atc ttg cct tgc tcc tca agc atg gct aca atc tca gcc tcc gca cca
1553

Ile Leu Pro Cys Ser Ser Ser Met Ala Thr Ile Ser Ala Ser Ala Pro
395 400 405

ttc cca acc atc aca ttg gac ctc acc aat tca ccc aac ggt aac aac
1601

Phe Pro Thr Ile Thr Leu Asp Leu Thr Asn Ser Pro Asn Gly Asn Asn
410 415 420 425

cct aat atg acc act aat aac ccg ttg atg cag ttc gct caa cgg ccc
1649

Pro Asn Met Thr Thr Asn Asn Pro Leu Met Gln Phe Ala Gln Arg Pro
430 435 440

ggt ttc aac ccg gca gtt ttg cct caa gtg gtt ggt caa gct atg tac
1697

Gly Phe Asn Pro Ala Val Leu Pro Gln Val Val Gly Gln Ala Met Tyr
445 450 455

aat aac caa caa cag tcc aag ttt tct ggt tta cag tta ccg gct cag
1745

Asn Asn Gln Gln Gln Ser Lys Phe Ser Gly Leu Gln Leu Pro Ala Gln
460 465 470

cca ctg cag atc gcg gcc act tcc tcg gtg gcc gag agc gtt agt gct
1793

Pro Leu Gln Ile Ala Ala Thr Ser Ser Val Ala Glu Ser Val Ser Ala
475 480 485

gcc agt gca gca att gcg tcc gat cca aac ttt gcg gcg gct cta gcg
1841

Ala Ser Ala Ala Ile Ala Ser Asp Pro Asn Phe Ala Ala Ala Leu Ala
490 495 500 505

gca gcg atc acg tcc att atg aac ggt tcc agt cat caa aat aat aac
1889

Ala Ala Ile Thr Ser Ile Met Asn Gly Ser Ser His Gln Asn Asn Asn
510 515 520

acc aat aat aat aat gtg gct acg agc aac aat gac agt agg caa taa
1937

Thr Asn Asn Asn Asn Val Ala Thr Ser Asn Asn Asp Ser Arg Gln
525 530 535

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1974

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 20 25 30
 Val Asp Phe Phe Ser Glu Lys Arg Asp Arg Val Ser Arg Glu Asn Ile
 35 40 45
 Asn Asp Asp Asp Asp Glu Gly Asn Lys Val Leu Ile Lys Met Glu Gly
 50 55 60
 Ser Arg Val Glu Glu Asn Asp Arg Ser Arg Asp Val Asn Ile Gly Leu
 65 70 75 80
 Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Thr Val Asp Asp
 85 90 95
 Gly Leu Ser Met Asp Met Glu Asp Lys Arg Ala Lys Ile Glu Asn Ala
 100 105 110
 Gln Leu Gln Glu Glu Leu Lys Lys Met Lys Ile Glu Asn Gln Arg Leu
 115 120 125
 Arg Asp Met Leu Ser Gln Ala Thr Thr Asn Phe Asn Ala Leu Gln Met
 130 135 140
 Gln Leu Val Ala Val Met Arg Gln Gln Glu Gln Arg Asn Ser Ser Gln
 145 150 155 160
 Asp His Leu Leu Glu Ser Lys Ala Glu Gly Arg Lys Arg Gln Glu Leu
 165 170 175
 Gln Ile Met Val Pro Arg Gln Phe Met Asp Leu Gly Pro Ser Ser Gly
 180 185 190
 Ala Ala Glu His Gly Ala Glu Val Ser Ser Glu Glu Arg Thr Thr Val
 195 200 205
 Arg Ser Gly Ser Pro Pro Ser Leu Leu Glu Ser Ser Asn Pro Arg Glu
 210 215 220
 Asn Gly Lys Arg Leu Leu Gly Arg Glu Glu Ser Ser Glu Glu Ser Glu
 225 230 235 240
 Ser Asn Ala Trp Gly Asn Pro Asn Lys Val Pro Lys His Asn Pro Ser
 245 250 255
 Ser Ser Asn Ser Asn Gly Asn Arg Asn Gly Asn Val Ile Asp Gln Ser

260	265	270
Ala Ala Glu Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg		
275	280	285
Ser Glu Ala Ala Met Ile Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly		
290	295	300
Gln Lys Met Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys		
305	310	315
Thr Met Ala Gly Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala		
	325	330
Glu Asp Arg Ser Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His		
	340	345
Pro Leu Pro Pro Ala Ala Thr Ala Met Ala Ser Thr Thr Thr Ala Ala		
	355	360
Ala Ser Met Leu Leu Ser Gly Ser Met Ser Ser Gln Asp Gly Leu Met		
370	375	380
Asn Pro Thr Asn Leu Leu Ala Arg Ala Ile Leu Pro Cys Ser Ser Ser		
385	390	395
Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp		
	405	410
Leu Thr Asn Ser Pro Asn Gly Asn Asn Pro Asn Met Thr Thr Asn Asn		
	420	425
Pro Leu Met Gln Phe Ala Gln Arg Pro Gly Phe Asn Pro Ala Val Leu		
435	440	445
Pro Gln Val Val Gly Gln Ala Met Tyr Asn Asn Gln Gln Gln Ser Lys		
450	455	460
Phe Ser Gly Leu Gln Leu Pro Ala Gln Pro Leu Gln Ile Ala Ala Thr		
465	470	475
Ser Ser Val Ala Glu Ser Val Ser Ala Ala Ser Ala Ala Ile Ala Ser		
	485	490
Asp Pro Asn Phe Ala Ala Ala Leu Ala Ala Ala Ile Thr Ser Ile Met		
500	505	510

Asn Gly Ser Ser His Gln Asn Asn Asn Thr Asn Asn Asn Asn Val Ala
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Thr Ser Asn Asn Asp Ser Arg Gln
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ccactctttg aacgta atg gag aag aac cat agt agt gga gag tgg gag aag
 112

Met Glu Lys Asn His Ser Ser Gly Glu Trp Glu Lys
 1 5 10

atg aag aac gag atc aac gag cta atg ata gaa gga aga gac tat gca
 160

Met Lys Asn Glu Ile Asn Glu Leu Met Ile Glu Gly Arg Asp Tyr Ala
 15 20 25

cac cag ttt gga tca gct tca tct caa gaa aca cgt gaa cat tta gcc
 208

His Gln Phe Gly Ser Ala Ser Ser Gln Glu Thr Arg Glu His Leu Ala
 30 35 40

aaa aag att ctt caa tct tac cac aag tct ctc acc atc atg aac tac
 256

Lys Lys Ile Leu Gln Ser Tyr His Lys Ser Leu Thr Ile Met Asn Tyr
 45 50 55 60

tcc ggc gaa ctt gac caa gtt tct cag ggt gga gga agc ccc aag agc
 304

Ser Gly Glu Leu Asp Gln Val Ser Gln Gly Gly Ser Pro Lys Ser
 65 70 75

gat gat tcc gat caa gaa cca ctt gtc atc aag agt tcg aag aag tca
 352

Asp Asp Ser Asp Gln Glu Pro Leu Val Ile Lys Ser Ser Lys Lys Ser
 80 85 90

atg cca agg tgg agt tca aaa gtc aga att gcc cct gga gct ggt gtt
 400

Met Pro Arg Trp Ser Ser Lys Val Arg Ile Ala Pro Gly Ala Gly Val
 95 100 105

gat aga acg ctg gac gat gga ttc agt tgg aga aag tac ggc cag aag
 448

Asp Arg Thr Leu Asp Asp Gly Phe Ser Trp Arg Lys Tyr Gly Gln Lys
 110 115 120

gat att ctc gga gcc aaa ttt cca aga gga tac tat aga tgc acg tat
 496

Asp Ile Leu Gly Ala Lys Phe Pro Arg Gly Tyr Tyr Arg Cys Thr Tyr
 125 130 135 140

aga aag tct caa gga tgt gaa gcc act aaa caa gtc caa aga tct gat
544
Arg Lys Ser Gln Gly Cys Glu Ala Thr Lys Gln Val Gln Arg Ser Asp
145 150 155

gaa aat cag atg ctc ctt gag atc agt tac cga gga ata cat tct tgc
592
Glu Asn Gln Met Leu Leu Glu Ile Ser Tyr Arg Gly Ile His Ser Cys
160 165 170

tct caa gct gca aat gtc ggt aca aca atg ccg ata caa aac ctc gaa
640
Ser Gln Ala Ala Asn Val Gly Thr Thr Met Pro Ile Gln Asn Leu Glu
175 180 185

ccg aac cag acc caa gaa cac gga aat ctt gac atg gta aag gaa agt
688
Pro Asn Gln Thr Gln Glu His Gly Asn Leu Asp Met Val Lys Glu Ser
190 195 200

gta gac aac tac aat cac caa gca cat ttg cat cac aac ctt cac tat
736
Val Asp Asn Tyr Asn His Gln Ala His Leu His His Asn Leu His Tyr
205 210 215 220

cca ttg tca tct acc cca aat cta gag aat aac aat gcc tat atg ctt
784
Pro Leu Ser Ser Thr Pro Asn Leu Glu Asn Asn Asn Ala Tyr Met Leu
225 230 235

caa atg cga gat caa aac atc gaa tat ttt gga tct acg agc ttc tct
832
Gln Met Arg Asp Gln Asn Ile Glu Tyr Phe Gly Ser Thr Ser Phe Ser
240 245 250

agt gat cta gga act agt atc aac tac aat ttt cca gca tct ggc tcg
880
Ser Asp Leu Gly Thr Ser Ile Asn Tyr Asn Phe Pro Ala Ser Gly Ser
255 260 265

gct tct cac tca gca tca aac tct ccg tcc acc gtc cct ttg gaa tcc
928
Ala Ser His Ser Ala Ser Asn Ser Pro Ser Thr Val Pro Leu Glu Ser
270 275 280

ccg ttt gaa agc tat gat cca aat cat cca tat gga gga ttt ggt ggg
976
Pro Phe Glu Ser Tyr Asp Pro Asn His Pro Tyr Gly Gly Phe Gly Gly
285 290 295 300

ttc tat tct tag ttatctactt aaggaggga cggaactttt tacatgacct
1028
Phe Tyr Ser

cttgattaaa gagagagttt tcataatagc taatcaattt cctattcaaa tatccgagtt
1088

ttttttctaa tcatgtttat caattgtctt attacagaag gcttattttc aggtctatgt
1148

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1205

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Ile Asn Glu Leu Met Ile Glu Gly Arg Asp Tyr Ala His Gln Phe Gly
20 25 30

Ser Ala Ser Ser Gln Glu Thr Arg Glu His Leu Ala Lys Lys Ile Leu
35 40 45

Gln Ser Tyr His Lys Ser Leu Thr Ile Met Asn Tyr Ser Gly Glu Leu
50 55 60

Asp Gln Val Ser Gln Gly Gly Gly Ser Pro Lys Ser Asp Asp Ser Asp
65 70 75 80

Gln Glu Pro Leu Val Ile Lys Ser Ser Lys Lys Ser Met Pro Arg Trp
85 90 95

Ser Ser Lys Val Arg Ile Ala Pro Gly Ala Gly Val Asp Arg Thr Leu
100 105 110

Asp Asp Gly Phe Ser Trp Arg Lys Tyr Gly Gln Lys Asp Ile Leu Gly
115 120 125

Ala Lys Phe Pro Arg Gly Tyr Tyr Arg Cys Thr Tyr Arg Lys Ser Gln
130 135 140

Gly Cys Glu Ala Thr Lys Gln Val Gln Arg Ser Asp Glu Asn Gln Met
145 150 155 160

Leu Leu Glu Ile Ser Tyr Arg Gly Ile His Ser Cys Ser Gln Ala Ala
165 170 175

Asn Val Gly Thr Thr Met Pro Ile Gln Asn Leu Glu Pro Asn Gln Thr
180 185 190

Gln Glu His Gly Asn Leu Asp Met Val Lys Glu Ser Val Asp Asn Tyr
195 200 205

Asn His Gln Ala His Leu His His Asn Leu His Tyr Pro Leu Ser Ser

210 215 220
 Thr Pro Asn Leu Glu Asn Asn Asn Ala Tyr Met Leu Gln Met Arg Asp
 225 230 235 240
 Gln Asn Ile Glu Tyr Phe Gly Ser Thr Ser Phe Ser Ser Asp Leu Gly
 245 250 255
 Thr Ser Ile Asn Tyr Asn Phe Pro Ala Ser Gly Ser Ala Ser His Ser
 260 265 270
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 Met Ser
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 cat gaa atc aat gat ctt aac aac tat cac tac act tca tcg tat aat
 104
 His Glu Ile Lys Asp Leu Asn Asn Tyr His Tyr Thr Ser Ser Tyr Asn
 5 10 15
 cat tac aat atc aac aac caa aat atg att aat ctc cct tac gtt tct
 152
 His Tyr Asn Ile Asn Asn Gln Asn Met Ile Asn Leu Pro Tyr Val Ser
 20 25 30
 ggt cca tct gct tat aat gca aac atg atc tca tca tca caa gta ggt
 200
 Gly Pro Ser Ala Tyr Asn Ala Asn Met Ile Ser Ser Ser Gln Val Gly
 35 40 45 50
 ttt gat cta ccc tcg aag aac ttg agt cct caa gga gcc ttc gag ttg
 248
 Phe Asp Leu Pro Ser Lys Asn Leu Ser Pro Gln Gly Ala Phe Glu Leu
 55 60 65
 ggt ttc gag ctt tct cca tct tct tct gac ttt ttt aat cct tcc ctc
 296
 Gly Phe Glu Leu Ser Pro Ser Ser Ser Asp Phe Phe Asn Pro Ser Leu
 70 75 80
 gat caa gag aac ggt ttg tat aat gct tat aat tat aat agt agt caa
 344
 Asp Gln Glu Asn Gly Leu Tyr Asn Ala Tyr Asn Tyr Asn Ser Ser Gln
 85 90 95

aag agt cat gaa gtt gtc ggt gat ggt tgt gca acc att aag agt gaa
 392
 Lys Ser His Glu Val Val Gly Asp Gly Cys Ala Thr Ile Lys Ser Glu
 100 105 110

gtt agg gtt tca gca tct cct tct tca agt gag gcc gat cat cat cca
 440
 Val Arg Val Ser Ala Ser Pro Ser Ser Ser Glu Ala Asp His His Pro
 115 120 125 130

gga gaa gat tcc ggc aag atc cgg aag aaa aga gaa gtt cgc gat gga
 488
 Gly Glu Asp Ser Gly Lys Ile Arg Lys Lys Arg Glu Val Arg Asp Gly
 135 140 145

gga gaa gat gat caa cgc tct cag aaa gta gtt aaa aca aag aag aaa
 536
 Gly Glu Asp Asp Gln Arg Ser Gln Lys Val Val Lys Thr Lys Lys Lys
 150 155 160

gag gag aag aaa aaa gag cca cga gtc tcg ttc atg act aag acc gaa
 584
 Glu Glu Lys Lys Lys Glu Pro Arg Val Ser Phe Met Thr Lys Thr Glu
 165 170 175

gtt gat cat ctc gaa gac ggc tat cgt tgg aga aag tat ggc caa aaa
 632
 Val Asp His Leu Glu Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys
 180 185 190

gca gtc aaa aac agt cct tat ccg agg agt tac tat aga tgc acg act
 680
 Ala Val Lys Asn Ser Pro Tyr Pro Arg Ser Tyr Tyr Arg Cys Thr Thr
 195 200 205 210

cag aag tgc aac gtg aag aag aga gtg gag aga tct tac caa gac cca
 728
 Gln Lys Cys Asn Val Lys Lys Arg Val Glu Arg Ser Tyr Gln Asp Pro
 215 220 225

acg gtc gtc atc aca acc tac gag agt caa cac aac cat ccg atc ccg
 776
 Thr Val Val Ile Thr Thr Tyr Glu Ser Gln His Asn His Pro Ile Pro
 230 235 240

acc aat cgt cgg aca gca atg ttc tct gga acc acc gca tct gat tat
 824
 Thr Asn Arg Arg Thr Ala Met Phe Ser Gly Thr Thr Ala Ser Asp Tyr
 245 250 255

aac cca tca tcg tct cca ata ttc tcc gat ctc atc atc aat act cca
 872
 Asn Pro Ser Ser Ser Pro Ile Phe Ser Asp Leu Ile Ile Asn Thr Pro
 260 265 270

aga agc ttc tca aat gat gat ctc ttc cgt gtg cca tac gct agt gtg
 920
 Arg Ser Phe Ser Asn Asp Asp Leu Phe Arg Val Pro Tyr Ala Ser Val
 275 280 285 290

aac gtg aac cct agt tat cat caa cag caa cat gga ttt cat caa cag
 968
 Asn Val Asn Pro Ser Tyr His Gln Gln Gln His Gly Phe His Gln Gln
 295 300 305

gag agt gag ttc gag ctc ttg aag gag atg ttt cct tcg gtt ttc ttc
 1016
 Glu Ser Glu Phe Glu Leu Leu Lys Glu Met Phe Pro Ser Val Phe Phe
 310 315 320

aaa caa gag cct tga tgatataata taatatagaa acaatttttt ttctgctaag
 1071
 Lys Gln Glu Pro
 325

aaatatagaa caaaacttgg atgcataata agtgatgata gtgttattta ttttttgcac
 1131

gtatatatta tacatgtttt gttactagc tataggatat actggtagta attaagcata
 1191

aatatggagc ccttcgactt attacaataa tttttggtat ggaaaaaatt
 1241

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Met Ser His Glu Ile Lys Asp Leu Asn Asn Tyr His Tyr Thr Ser Ser
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Tyr Asn His Tyr Asn Ile Asn Asn Gln Asn Met Ile Asn Leu Pro Tyr
 20 25 30

Val Ser Gly Pro Ser Ala Tyr Asn Ala Asn Met Ile Ser Ser Ser Gln
 35 40 45

Val Gly Phe Asp Leu Pro Ser Lys Asn Leu Ser Pro Gln Gly Ala Phe
 50 55 60

Glu Leu Gly Phe Glu Leu Ser Pro Ser Ser Ser Asp Phe Phe Asn Pro
 65 70 75 80

Ser Leu Asp Gln Glu Asn Gly Leu Tyr Asn Ala Tyr Asn Tyr Asn Ser
 85 90 95

Ser Gln Lys Ser His Glu Val Val Gly Asp Gly Cys Ala Thr Ile Lys
 100 105 110

Ser Glu Val Arg Val Ser Ala Ser Pro Ser Ser Ser Glu Ala Asp His
 115 120 125

His Pro Gly Glu Asp Ser Gly Lys Ile Arg Lys Lys Arg Glu Val Arg

130 135 140
 Asp Gly Gly Glu Asp Asp Gln Arg Ser Gln Lys Val Val Lys Thr Lys
 145 150 155 160
 Lys Lys Glu Glu Lys Lys Lys Glu Pro Arg Val Ser Phe Met Thr Lys
 165 170 175
 Thr Glu Val Asp His Leu Glu Asp Gly Tyr Arg Trp Arg Lys Tyr Gly
 180 185 190
 Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg Ser Tyr Tyr Arg Cys
 195 200 205
 Thr Thr Gln Lys Cys Asn Val Lys Lys Arg Val Glu Arg Ser Tyr Gln
 210 215 220
 Asp Pro Thr Val Val Ile Thr Thr Tyr Glu Ser Gln His Asn His Pro
 225 230 235 240
 Ile Pro Thr Asn Arg Arg Thr Ala Met Phe Ser Gly Thr Thr Ala Ser
 245 250 255
 Asp Tyr Asn Pro Ser Ser Ser Pro Ile Phe Ser Asp Leu Ile Ile Asn
 260 265 270
 Thr Pro Arg Ser Phe Ser Asn Asp Asp Leu Phe Arg Val Pro Tyr Ala
 275 280 285
 Ser Val Asn Val Asn Pro Ser Tyr His Gln Gln Gln His Gly Phe His
 290 295 300
 Gln Gln Glu Ser Glu Phe Glu Leu Leu Lys Glu Met Phe Pro Ser Val
 305 310 315 320
 Phe Phe Lys Gln Glu Pro
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 99
 Glu Asp Glu Gln Leu Arg Arg Met Val Glu Lys Tyr Gly Pro Arg Asn
 15 20 25
 tgg tct gcg att agc aaa tcg att cca ggt cga tct ggt aaa tcg tgt
 147
 Trp Ser Ala Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys
 30 35 40
 aga tta cgt tgg tgt aat cag tta tct ccg gag gtt gag cat cgt cct
 195
 Arg Leu Arg Trp Cys Asn Gln Leu Ser Pro Glu Val Glu His Arg Pro
 45 50 55 60
 ttc tcg ccg gag gaa gat gag act att gta acc gcc cgt gct cag ttt
 243
 Phe Ser Pro Glu Glu Asp Glu Thr Ile Val Thr Ala Arg Ala Gln Phe
 65 70 75
 ggt aac aag tgg gcg acg att gct cgt ctt ctt aac ggt cgt acg gat
 291
 Gly Asn Lys Trp Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp
 80 85 90
 aac gcc gtt aaa aat cac tgg aac tct acg ctt aag agg aaa tgc agc
 339
 Asn Ala Val Lys Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Ser
 95 100 105
 gga ggt gtg gcg gtt acg acg gtg acg gag acg gag gaa gat cag gat
 387
 Gly Gly Val Ala Val Thr Thr Val Thr Glu Thr Glu Glu Asp Gln Asp
 110 115 120
 cgg ccg aag aag agg aga tct gtt agc ttt gat cct gct ttt gct ccg
 435
 Arg Pro Lys Lys Arg Arg Ser Val Ser Phe Asp Pro Ala Phe Ala Pro
 125 130 135 140
 gtg gat act gga ttg tac atg agt cct gag agt cct aac gga atc gat
 483
 Val Asp Thr Gly Leu Tyr Met Ser Pro Glu Ser Pro Asn Gly Ile Asp
 145 150 155
 gtt agt gat tct agc acg att ccg tca ccg tcg tct cct gtt gct cag
 531
 Val Ser Asp Ser Ser Thr Ile Pro Ser Pro Ser Ser Pro Val Ala Gln
 160 165 170
 ctg ttt aaa cca atg ccg att tcc ggc ggt ttt acg gtg gtt ccg cag
 579
 Leu Phe Lys Pro Met Pro Ile Ser Gly Gly Phe Thr Val Val Pro Gln
 175 180 185
 ccg tta ccg gtt gaa atg tct tcg tct tcg gag gat cca cct act tcg
 627
 Pro Leu Pro Val Glu Met Ser Ser Ser Ser Glu Asp Pro Pro Thr Ser
 190 195 200

ttg agt ttg tca cta cct gga gct gag aac acg agt tcg agc cat aac
675

Leu Ser Leu Ser Leu Pro Gly Ala Glu Asn Thr Ser Ser Ser His Asn
205 210 215 220

aat aac aac aac gcg ttg atg ttt ccg aga ttt gag agt cag atg aag
723

Asn Asn Asn Asn Ala Leu Met Phe Pro Arg Phe Glu Ser Gln Met Lys
225 230 235

att aat gta gag gag aga gga gga gga gga gaa gga cgt aga ggt gag
771

Ile Asn Val Glu Glu Arg Gly Gly Gly Glu Gly Arg Arg Gly Glu
240 245 250

ttt atg acg gtg gtg cag gag atg ata aaa gct gaa gtg agg agt tac
819

Phe Met Thr Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr
255 260 265

atg gcg gaa atg cag aaa aca agt ggt gga ttc gtc gtc gga ggt tta
867

Met Ala Glu Met Gln Lys Thr Ser Gly Gly Phe Val Val Gly Gly Leu
270 275 280

tac gaa tcc ggc ggc aat ggt ggt ttt agg gat tgt gga gta ata aca
915

Tyr Glu Ser Gly Gly Asn Gly Gly Phe Arg Asp Cys Gly Val Ile Thr
285 290 295 300

cct aag gtt gag tag ttttggttta ggggttaaaac ttgaatcgat tggggatttt
970

Pro Lys Val Glu

caagagcatt catttttggg gtttatggta aaattfaaaaa caaaaacaaa atgtacagag
1030

gaattaaaaat ttctatggaa taatcttaaaa tctcaaatat ttgttacttg ttttggat
1090

tcataaccaa aatcaaa
1107

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Leu Arg Arg Met Val Glu Lys Tyr Gly Pro Arg Asn Trp Ser Ala Ile
20 25 30

Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
35 40 45

Cys Asn Gln Leu Ser Pro Glu Val Glu His Arg Pro Phe Ser Pro Glu

50		55		60
Glu Asp Glu Thr Ile Val Thr Ala Arg Ala Gln Phe Gly Asn Lys Trp				
65		70		75
				80
Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys				
	85		90	95
Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Ser Gly Gly Val Ala				
	100		105	110
Val Thr Thr Val Thr Glu Thr Glu Glu Asp Gln Asp Arg Pro Lys Lys				
	115		120	125
Arg Arg Ser Val Ser Phe Asp Pro Ala Phe Ala Pro Val Asp Thr Gly				
	130		135	140
Leu Tyr Met Ser Pro Glu Ser Pro Asn Gly Ile Asp Val Ser Asp Ser				
145		150		155
				160
Ser Thr Ile Pro Ser Pro Ser Ser Pro Val Ala Gln Leu Phe Lys Pro				
	165		170	175
Met Pro Ile Ser Gly Gly Phe Thr Val Val Pro Gln Pro Leu Pro Val				
	180		185	190
Glu Met Ser Ser Ser Ser Glu Asp Pro Pro Thr Ser Leu Ser Leu Ser				
	195		200	205
Leu Pro Gly Ala Glu Asn Thr Ser Ser Ser His Asn Asn Asn Asn Asn				
	210		215	220
Ala Leu Met Phe Pro Arg Phe Glu Ser Gln Met Lys Ile Asn Val Glu				
225		230		235
				240
Glu Arg Gly Gly Gly Gly Glu Gly Arg Arg Gly Glu Phe Met Thr Val				
	245		250	255
Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr Met Ala Glu Met				
	260		265	270
Gln Lys Thr Ser Gly Gly Phe Val Val Gly Gly Leu Tyr Glu Ser Gly				
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Gly Asn Gly Gly Phe Arg Asp Cys Gly Val Ile Thr Pro Lys Val Glu				
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 103
 Cys Cys Glu Lys Val Gly Ile Lys Arg Gly Arg Trp Thr Ala Glu Glu
 10 15 20
 gac cag att ctc tcc aac tac att caa tcc aat ggt gaa ggt tct tgg
 151
 Asp Gln Ile Leu Ser Asn Tyr Ile Gln Ser Asn Gly Glu Gly Ser Trp
 25 30 35
 aga tct ctc ccc aaa aat gcc gga tta aaa agg tgt gga aag agc tgt
 199
 Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys
 40 45 50
 aga ttg aga tgg ata aac tat cta aga tca gac ctc aag cgt gga aac
 247
 Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp Leu Lys Arg Gly Asn
 55 60 65
 ata act cca gaa gaa gaa gaa ctc gtt gtt aaa ttg cat tcc act ttg
 295
 Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys Leu His Ser Thr Leu
 70 75 80 85
 gga aac agg tgg tca cta atc gcg ggt cat cta cca ggg aga aca gac
 343
 Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu Pro Gly Arg Thr Asp
 90 95 100
 aac gaa ata aaa aat tat tgg aac tct cat ctc agc cgt aaa ctc cac
 391
 Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys Leu His
 105 110 115
 aac ttc att agg aag cca tcc atc tct caa gac gtc tcc gcc gta atc
 439
 Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp Val Ser Ala Val Ile
 120 125 130
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 487
 Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro Gln Ala Lys Arg Arg
 135 140 145
 ctt ggg aga acg agt agg tcc gct atg aaa cca aaa atc cgc aga aca
 535
 Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro Lys Ile Arg Arg Thr
 150 155 160 165

aaa act cgt aaa acg aag aaa acg tct gca cca ccg gag cct aac gcc
 583
 Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro Pro Glu Pro Asn Ala
 170 175 180

gat gta gct ggg gct gat aaa gaa gca tta atg gtg gag tca agt gga
 631
 Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met Val Glu Ser Ser Gly
 185 190 195

gcc gag gct gag cta gga cga cca tgt gac tac tat gga gat gat tgt
 679
 Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr Tyr Gly Asp Asp Cys
 200 205 210

aac aaa aat ctc atg agc att aat ggc gat aat gga gtt tta acg ttt
 727
 Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn Gly Val Leu Thr Phe
 215 220 225

gat gat gat atc atc gat ctt ttg ttg gac gag tca gat cct ggc cac
 775
 Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu Ser Asp Pro Gly His
 230 235 240 245

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 823
 Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Glu Leu His Asn Ile
 250 255 260

aga gac tct gaa gga gcc aga ggg ttc tcg gat act tgg aac caa ggg
 871
 Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp Thr Trp Asn Gln Gly
 265 270 275

aat ctc gac tgt ctt ctt cag tct tgt cca tct gtg gag tcg ttt ctc
 919
 Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser Val Glu Ser Phe Leu
 280 285 290

aac tac gac cac caa gtt aac gac gcg tcg acg gat gag ttt atc gat
 967
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 295 300 305

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 1015
 Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn Asn Leu Trp His Glu
 310 315 320 325

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 1063
 Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu Leu Asp Gly Asp Asp
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 1111
 Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn Phe Gly Glu Pro Leu
 345 350 355

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1156

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1209

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Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp
50 55 60

Leu Lys Arg Gly Asn Ile Thr Pro Glu Glu Glu Leu Val Val Lys
65 70 75 80

Leu His Ser Thr Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
100 105 110

Ser Arg Lys Leu His Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp
115 120 125

Val Ser Ala Val Ile Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro
130 135 140

Gln Ala Lys Arg Arg Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro
145 150 155 160

Lys Ile Arg Arg Thr Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro
165 170 175

Pro Glu Pro Asn Ala Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met
180 185 190

Val Glu Ser Ser Gly Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr

195 200 205
 Tyr Gly Asp Asp Cys Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn
 210 215 220
 Gly Val Leu Thr Phe Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu
 225 230 235 240
 Ser Asp Pro Gly His Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Gly
 245 250 255
 Glu Leu His Asn Ile Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp
 260 265 270
 Thr Trp Asn Gln Gly Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser
 275 280 285
 Val Glu Ser Phe Leu Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr
 290 295 300
 Asp Glu Phe Ile Asp Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn
 305 310 315 320
 Asn Leu Trp His Glu Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu
 325 330 335
 Leu Asp Gly Asp Asp Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn
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 110
 Met Ala Asp Arg Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Glu
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 cag ctt cgt agg ctt gtt gtt aaa tac ggt cca aga aac tgg aca gtg
 158

Gln Leu Arg Arg Leu Val Val Lys Tyr Gly Pro Arg Asn Trp Thr Val
 20 25 30
 att agc aaa tct att ccc ggt aga tcg ggg aaa tcg tgt cgt tta cgg
 206
 Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg
 35 40 45
 tgg tgc aac cag ctt tcg ccg caa gtt gag cat cgg ccg ttt tcg gct
 254
 Trp Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala
 50 55 60
 gag gaa gac gag acg atc gca cgt gct cac gct cag ttc ggg aat aaa
 302
 Glu Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys
 65 70 75
 tgg gcg acg att gct cgt ctt ctc aac ggt cgt acg gac aac gcc gtg
 350
 Trp Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val
 80 85 90 95
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 398
 Lys Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp
 100 105 110
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 446
 His Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser
 115 120 125
 gtg agt gcg gga tct cca cct gtt gtt act ggg ctt tac atg agc cca
 494
 Val Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro
 130 135 140
 gga agc cca act gga tct gat gtc agt gat tca agt act atc ccg ata
 542
 Gly Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile
 145 150 155
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 590
 Leu Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Val
 160 165 170 175
 gtg cta ccg ctt cct atc gaa acg tcg tct ttt tcc gat gat cca ccg
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 180 185 190
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 686
 Thr Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser
 195 200 205
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 734
 Asn Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg

210 215 220
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 225 230 235
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 Arg Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly
 240 245 250 255
 gag ttt atg gcg gtg gtg caa gag atg att aag gcg gaa gtg agg agt
 878
 Glu Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser
 260 265 270
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 926
 Tyr Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly
 275 280 285
 ttc att gat aat ggc atg att ccg atg agt caa att gga gtt ggg aga
 974
 Phe Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg
 290 295 300
 atc gag tag acaaagt gag attattagga aactgttttaa attggagaag
 1023
 Ile Glu
 305
 aagaaaaatg ctctgttttt ttctcctttg gattaggcct aagaattttg ggttttaagg
 1083
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 35 40 45
 Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala Glu
 50 55 60

Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys Trp
 65 70 75 80

Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys
 85 90 95

Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp His
 100 105 110

Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser Val
 115 120 125

Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro Gly
 130 135 140

Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile Leu
 145 150 155 160

Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Val Val
 165 170 175

Leu Pro Leu Pro Ile Glu Thr Ser Ser Phe Ser Asp Asp Pro Pro Thr
 180 185 190

Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser Asn
 195 200 205

Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg His
 210 215 220

Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser Gly Gly Phe Arg
 225 230 235 240

Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly Glu
 245 250 255

Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr
 260 265 270

Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly Phe
 275 280 285

Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg Ile
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Glu

305

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 96
 Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr Val Arg Thr His
 20 25 30
 ggc cag ggc cac tgg aac cgc atc gcc aag aaa act ggg ctc aag aga
 144
 Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg
 35 40 45
 tgt ggg aaa agc,tgt agg ttg aga tgg atg aac tac tta agc cct aat
 192
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn
 50 55 60
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 240
 Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg
 65 70 75 80
 ctc cac aag ctc ctc ggc aac aga tgg tgg ttg ata gcg aaa aga gtt
 288
 Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val
 85 90 95
 ccg gga aga aca gac aac caa gta aag aat tac tgg aac aca cat ctc
 336
 Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu
 100 105 110
 agc aag aaa ctt ggt ctc gga gat cat tca act gcc gtc aaa gcc gca
 384
 Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala
 115 120 125
 tgc ggt gta gag tct cca ccg tct atg gcc ctt ata acc aca acg tcc
 432
 Cys Gly Val Glu Ser Pro Pro Ser Met Ala Leu Ile Thr Thr Thr Ser
 130 135 140
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 480
 Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe
 145 150 155 160
 gac act tta gtt gac gaa tcc aaa ctc aaa cca aaa tcc aaa cta gtc
 528
 Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val
 165 170 175

cac gca aca cca act gac gta gaa gtt gca gct acg gtt cca aat ctg
576

His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu
180 185 190

ttc gat acc ttt tgg gtt ctt gaa gac gac ttc gag ctt agt tca ctc
624

Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu
195 200 205

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660

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210 215

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Gly Gln Gly His Trp Asn Arg Ile Ala Lys Lys Thr Gly Leu Lys Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn
50 55 60

Val Asn Arg Gly Asn Phe Thr Asp Gln Glu Glu Asp Leu Ile Ile Arg
65 70 75 80

Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val
85 90 95

Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Thr His Leu
100 105 110

Ser Lys Lys Leu Gly Leu Gly Asp His Ser Thr Ala Val Lys Ala Ala
115 120 125

Cys Gly Val Glu Ser Pro Pro Ser Met Ala Leu Ile Thr Thr Thr Ser
130 135 140

Ser Ser His Gln Glu Ile Ser Gly Gly Lys Asn Ser Thr Leu Arg Phe
145 150 155 160

Asp Thr Leu Val Asp Glu Ser Lys Leu Lys Pro Lys Ser Lys Leu Val

165 170 175
 His Ala Thr Pro Thr Asp Val Glu Val Ala Ala Thr Val Pro Asn Leu
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 Phe Asp Thr Phe Trp Val Leu Glu Asp Asp Phe Glu Leu Ser Ser Leu
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 101
 Ser Ala Ser Val Ser Gly Gly Glu Gly Ala Gly Gly Pro Ala Pro Phe
 10 15 20
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 149
 Leu Val Lys Thr Tyr Glu Met Val Asp Asp Ser Ser Thr Asp Gln Ile
 25 30 35 40
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 197
 Val Ser Trp Ser Ala Asn Asn Asn Ser Phe Ile Val Trp Asn His Ala
 45 50 55
 gaa ttt tca cgc ctc ctt ctt cca acc tac ttc aaa cac aat aac ttc
 245
 Glu Phe Ser Arg Leu Leu Leu Pro Thr Tyr Phe Lys His Asn Asn Phe
 60 65 70
 tct tcc ttc att cgt cag ctc aat acc tat ggg ttt agg aag att gat
 293
 Ser Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Asp
 75 80 85
 cca gag agg tgg gag ttt ttg aat gat gat ttt att aag gat cag aag
 341
 Pro Glu Arg Trp Glu Phe Leu Asn Asp Asp Phe Ile Lys Asp Gln Lys
 90 95 100
 cat ctt ctc aag aat ata cat aga agg aaa cct ata cac agc cac agt
 389
 His Leu Leu Lys Asn Ile His Arg Arg Lys Pro Ile His Ser His Ser
 105 110 115 120
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 437

His Pro Pro Ala Ser Ser Thr Asp Gln Glu Arg Ala Val Leu Gln Glu
 125 130 135
 caa atg gac aag ctt tca cgt gag aaa gct gca att gaa gct aag ctt
 485
 Gln Met Asp Lys Leu Ser Arg Glu Lys Ala Ala Ile Glu Ala Lys Leu
 140 145 150
 tta aag ttc aaa caa cag aag gtt gta gca aag cat cag ttt gaa gaa
 533
 Leu Lys Phe Lys Gln Gln Lys Val Val Ala Lys His Gln Phe Glu Glu
 155 160 165
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 581
 Met Thr Glu His Val Asp Asp Met Glu Asn Arg Gln Lys Lys Leu Leu
 170 175 180
 aat ttt ttg gaa act gcg att cgg aat cct act ttt gtt aag aat ttt
 629
 Asn Phe Leu Glu Thr Ala Ile Arg Asn Pro Thr Phe Val Lys Asn Phe
 185 190 195 200
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 725
 Arg Leu Pro Glu Val Glu Gln Ser Lys Pro Pro Ser Glu Asp Ser His
 220 225 230
 ctg gat aat agt agt ggt agc tcg aga cgc gag tct gga aac att ttt
 773
 Leu Asp Asn Ser Ser Gly Ser Ser Arg Arg Glu Ser Gly Asn Ile Phe
 235 240 245
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 821
 His Gln Asn Phe Ser Asn Lys Leu Arg Leu Glu Leu Ser Pro Ala Asp
 250 255 260
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 869
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 265 270 275 280
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 917
 Gly Ala Ser Pro Lys Gly Ile Leu Ser Gly Gly Asp Pro Asn Thr Thr
 285 290 295
 cta aca aaa aga gaa ggc cta cca ttt gca cct gaa gct cta gag ctt
 965
 Leu Thr Lys Arg Glu Gly Leu Pro Phe Ala Pro Glu Ala Leu Glu Leu
 300 305 310
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315 320 325
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 330 335 340
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 1109
 Gly Ser Phe Ser Cys His Leu Asn Leu Thr Leu Ala Ser Ala Pro Leu
 345 350 355 360
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 1157
 Pro Asp Lys Thr Ala Ser Gln Ile Ala Lys Thr Thr Leu Lys Ser Gln
 365 370 375
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 1205
 Glu Leu Asn Phe Asn Ser Ile Glu Thr Ser Ala Ser Glu Lys Asn Arg
 380 385 390
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 1253
 Gly Arg Gln Glu Ile Ala Val Gly Gly Ser Gln Ala Asn Ala Ala Pro
 395 400 405
 cca gca aga gtg aat gat gta ttc tgg gaa cag ttc cta aca gaa agg
 1301
 Pro Ala Arg Val Asn Asp Val Phe Trp Glu Gln Phe Leu Thr Glu Arg
 410 415 420
 cca ggg tct tca gat aat gag gag gca agt tcg act tat aga ggt aac
 1349
 Pro Gly Ser Ser Asp Asn Glu Glu Ala Ser Ser Thr Tyr Arg Gly Asn
 425 430 435 440
 cca tac gaa gag caa gag gag aaa aga aac ggg agt atg atg tta cgt
 1397
 Pro Tyr Glu Glu Gln Glu Glu Lys Arg Asn Gly Ser Met Met Leu Arg
 445 450 455
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 1450
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 460 465
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Pro	Ala	Pro	Phe
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Tyr	Glu	Met	Val
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Thr	Asp	Gln	Ile
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Val	Ser	Trp	Ser
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	45		
Ser	Phe	Ile	Val
	50		
Trp	Asn	His	Ala
			55
Glu	Phe	Ser	Arg
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Leu	Leu	Leu	Pro
Thr	Tyr	Phe	Lys
	65		
His	Asn	Asn	Phe
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Ser	Ser	Phe	Ile
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Arg	Gln	Leu	Asn
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Thr	Tyr	Gly	Phe
Arg	Lys	Ile	Asp
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Pro	Glu	Arg	Trp
	90		
Glu	Phe	Leu	Asn
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Asp	Asp	Phe	Ile
Lys	Asp	Gln	Lys
	100		
His	Leu	Leu	Lys
Asn	Ile	His	Arg
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Arg	Lys	Pro	Ile
	115		
His	Ser	His	Ser
His	Pro	Pro	Ala
	120		
Ser	Ser	Thr	Asp
			125
Gln	Glu	Arg	Ala
	130		
Val	Leu	Gln	Glu
Met	Asp	Lys	Leu
Ser	Arg	Glu	
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Lys	Ala	Ala	Ile
Glu	Ala	Lys	Leu
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Leu	Lys	Phe	Lys
Gln	Gln	Lys	Val
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Val	Ala	Lys	His
Gln	Phe	Glu	Glu
	165		
Met	Thr	Glu	His
Val	Asp	Asp	Met
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Glu	Asn	Arg	Gln
Lys	Lys	Leu	Leu
Asn	Phe	Leu	Glu
Thr	Ala	Ile	Arg
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Thr	Ala	Ile	Arg
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Thr	Ala	Ile	Arg
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Val	Lys	Asn	Phe
Gly	Lys	Lys	Val
Glu	Gln	Leu	Asp
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Arg	Leu	Pro	Glu
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Gln	Ser		
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Leu	Asp	Asn	Ser
Ser	Ser	Gly	Ser
Ser			
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Arg	Arg	Glu	Ser
Gly	Asn	Ile	Phe
His	Gln	Asn	Phe
Ser	Asn	Lys	Leu
Leu			
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Arg	Arg	Glu	Ser
Gly	Asn	Ile	Phe
His	Gln	Asn	Phe
Ser	Asn	Lys	Leu
Leu			
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His	Gln	Asn	Phe
Ser	Asn	Lys	Leu
Leu			
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Phe Ala Pro Glu Ala Leu Glu Leu Ala Asp Thr Gly Thr Cys Pro Arg
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 325 330 335

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 340 345 350

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Ala Lys Thr Thr Leu Lys Ser Gln Glu Leu Asn Phe Asn Ser Ile Glu
 370 375 380

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Gly Ser Gln Ala Asn Ala Ala Pro Pro Ala Arg Val Asn Asp Val Phe
 405 410 415

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Ala Ser Ser Thr Tyr Arg Gly Asn Pro Tyr Glu Glu Gln Glu Glu Lys
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Thr Leu
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 Met Asp Thr Thr Ile Asp Gly
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 Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp
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 Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr
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 Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser
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 Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp
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 Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys
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 Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val
 120 125 130 135
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 545
 Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala
 140 145 150
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 155 160 165
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Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile
 170 175 180
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 Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val Val Ile
 185 190 195
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 Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala
 200 205 210 215
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 Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn
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 Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys
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 881
 Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val
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 265 270 275
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 Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro
 315 320 325
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 345 350 355
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Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile
          395          400          405
cct aga gat gtt cct ccc tct ttt gca gtg gcg gcc gat gaa ttg aag
1361
Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys
          410          415          420
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1409
Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu
          425          430          435
ttt cca acg gaa gca caa gct gca atg gag atc gcc gaa atg aag gga
1457
Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly
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Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly
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Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu
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gaa gag cat caa agt aga cta aaa gcg ctt tct aaa acc gtg gaa ctc
1601
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1649
Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met
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aac tgt gag gac ttg act caa ctg gct tgc gga gaa gac gac act gct
1697
Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp Asp Thr Ala
          520          525          530          535
gag aaa cga cta caa aag aag caa agg tac atg gaa ata caa gag aca
1745
Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr
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cta aag aag gcc ttt agt gag gac aat ttg gaa tta gga aat tcg tcc
1793
Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly Asn Ser Ser
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Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr Gly Gly Lys Arg
570 575 580

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1894

Ser Asn Arg Lys Leu Ser His Arg Arg Arg
585 590

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1954

tggcgtcata tagtttcgct ctctgttttg catcctgtgt attattgctg caggtgtgct
2014

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Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His
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Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala
85 90 95

Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu
100 105 110

Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val
115 120 125

Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro
130 135 140

Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys
 145 150 155 160

Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile
 165 170 175

Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp
 180 185 190

Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu
 195 200 205

Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys
 210 215 220

Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser
 225 230 235 240

Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu
 245 250 255

Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys
 260 265 270

Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Lys Glu
 275 280 285

Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala
 290 295 300

Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala
 305 310 315 320

Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala
 325 330 335

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 340 345 350

Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile
 355 360 365

Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln
 370 375 380

Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln
385 390 395 400

Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala
405 410 415

Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg
420 425 430

Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met
435 440 445

Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu
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465 470 475 480

Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala
485 490 495

Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser
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Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala
515 520 525

Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg
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Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn
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216

Glu Asn Asn Ile Leu Pro Val Glu Pro Thr Asp Ser Ala Ser Asp Ser
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264

Ile Phe His Tyr Asp Asp Ala Ser Gln Ala Lys Ile Gln Gln Glu Lys
35 40 45

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312

Pro Trp Ala Ser Asp Pro Asn Tyr Phe Lys Arg Val His Ile Ser Ala
50 55 60

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360

Leu Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile
65 70 75

gag atc atg ggt ctt atg cag ggt aaa acc gag ggt gat aca atc atc
408

Glu Ile Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile
80 85 90 95

gtt atg gat gct ttt gct ttg cct gtt gaa ggt act gag act agg gtt
456

Val Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val
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504

Asn Ala Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr
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552

Ser Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser
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600

His Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln
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648

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 744
 Thr Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr
 195 200 205

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 840
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 225 230 235

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 His Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser
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 260 265 270

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 Asp Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser
 275 280 285

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 290 295 300

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 1080
 Glu Pro Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val
 305 310 315

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 Glu Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe
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 Asn Ser Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro
 340 345 350

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 Glu Pro Met Ile Thr Ser
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Ala Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser
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Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His
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Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met
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Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln
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Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln
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 225 230 235 240

Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser
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Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp
 260 265 270

Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg
 275 280 285

Tyr Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu
 290 295 300

Pro Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu
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Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn
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Trp Leu Ser Gln Phe Val Asp Asp Ser Phe Ala Asp Phe Pro Ala Asn		
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336		
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115	120	125
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480		
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576		
Gly Met Arg Arg Cys Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp		
180	185	190
agg aca gga cca ctt gga cct aaa aca cta tgt aac gct tgt gga gtc		
624		
Arg Thr Gly Pro Leu Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val		
195	200	205
cgg ttt aaa tcc ggt aga ctt gta ccg gaa tat aga ccg gct tcg agt		
672		
Arg Phe Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser		
210	215	220
cct act ttt gtt ttg act cag cat tca aac tct cac ccg aaa gtg atg		
720		
Pro Thr Phe Val Leu Thr Gln His Ser Asn Ser His Arg Lys Val Met		
225	230	235
240		

gag ctt cga cgg cag aaa gaa gtt atg aga caa cca caa caa gtt caa
 768
 Glu Leu Arg Arg Gln Lys Glu Val Met Arg Gln Pro Gln Gln Val Gln
 245 250 255

ctt cat cac cac cac cac ccg ttt tag
 795
 Leu His His His His His Pro Phe
 260

<210> 78 <211> 264 <212> PRT <213> Arabidopsis thaliana <400>
 78

Met Asp Val Tyr Gly Leu Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
 1 5 10 15

Leu Leu Asp Phe Ser Asn Glu Asp Ile Phe Ser Ala Ser Ser Ser Gly
 20 25 30

Gly Ser Thr Ala Ala Thr Ser Ser Ser Ser Phe Pro Pro Pro Gln Asn
 35 40 45

Pro Ser Phe His His His His Leu Pro Ser Ser Ala Asp His His Ser
 50 55 60

Phe Leu His Asp Ile Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu
 65 70 75 80

Trp Leu Ser Gln Phe Val Asp Asp Ser Phe Ala Asp Phe Pro Ala Asn
 85 90 95

Pro Leu Gly Gly Thr Met Thr Ser Val Lys Thr Glu Thr Ser Phe Pro
 100 105 110

Gly Lys Pro Arg Ser Lys Arg Ser Arg Ala Pro Ala Pro Phe Ala Gly
 115 120 125

Thr Trp Ser Pro Met Pro Leu Glu Ser Glu His Gln Gln Leu His Ser
 130 135 140

Ala Ala Lys Phe Lys Pro Lys Lys Glu Gln Ser Gly Gly Gly Gly Gly
 145 150 155 160

Gly Gly Gly Arg His Gln Ser Ser Ser Ser Glu Thr Thr Glu Gly Gly
 165 170 175

Gly Met Arg Arg Cys Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp
 180 185 190

Arg Thr Gly Pro Leu Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val
 195 200 205

Arg Phe Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser
 210 215 220

Pro Thr Phe Val Leu Thr Gln His Ser Asn Ser His Arg Lys Val Met
 225 230 235 240

Glu Leu Arg Arg Gln Lys Glu Val Met Arg Gln Pro Gln Gln Val Gln
 245 250 255

Leu His His His His His Pro Phe
 260

<210> 79 <211> 727 <212> DNA <213> Arabidopsis thaliana <220>
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 60

atcatcatca tcagaagaaa a atg gtt gcg ata tcg gag atc aag tcg acg
 111

Met Val Ala Ile Ser Glu Ile Lys Ser Thr
 1 5 10

gtg gat gtc acg gcg gcg aat tgt ttg atg ctt tta tct aga gtt gga
 159

Val Asp Val Thr Ala Ala Asn Cys Leu Met Leu Leu Ser Arg Val Gly
 15 20 25

caa gaa aac gtt gac ggt ggc gat caa aaa cgc gtt ttc aca tgt aaa
 207

Gln Glu Asn Val Asp Gly Gly Asp Gln Lys Arg Val Phe Thr Cys Lys
 30 35 40

acg tgt ttg aag cag ttt cat tcg ttc caa gcc tta gga ggt cac cgt
 255

Thr Cys Leu Lys Gln Phe His Ser Phe Gln Ala Leu Gly Gly His Arg
 45 50 55

gcg agt cac aag aag cct aac aac gac gct ttg tcg tct gga ttg atg
 303

Ala Ser His Lys Lys Pro Asn Asn Asp Ala Leu Ser Ser Gly Leu Met
 60 65 70

aag aag gtg aaa acg tcg tcg cat cct tgt ccc ata tgt gga gtg gag
 351

Lys Lys Val Lys Thr Ser Ser His Pro Cys Pro Ile Cys Gly Val Glu
 75 80 85 90

ttt ccg atg gga caa gct ttg gga gga cac atg agg aga cac agg aac
 399

Phe Pro Met Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Asn
 95 100 105
 gag agt ggg gct gct ggt ggc gcg ttg gtt aca cgc gct ttg ttg ccg
 447
 Glu Ser Gly Ala Ala Gly Gly Ala Leu Val Thr Arg Ala Leu Leu Pro
 110 115 120
 gag ccc acg gtg act acg ttg aag aaa tct agc agt ggg aag aga gtg
 495
 Glu Pro Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val
 125 130 135
 gct tgt ttg gat ctg agt cta ggg atg gtg gac aat ttg aat ctc aag
 543
 Ala Cys Leu Asp Leu Ser Leu Gly Met Val Asp Asn Leu Asn Leu Lys
 140 145 150
 ttg gag ctt gga aga aca gtt tat tga ttttatttat tttccttaaa
 590
 Leu Glu Leu Gly Arg Thr Val Tyr
 155 160
 ttttctgaat atatttggtt ctctcattct ttgaattttt cttaatatc tagattatac
 650
 atacatccgc agatttagga aactttcata gagtgaatc ttttctttct gtaaaaatat
 710
 attttacttg tagcaaa
 727
 <210> 80 <211> 162 <212> PRT <213> Arabidopsis thaliana <400>
 80
 Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala Ala
 1 5 10 15
 Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp Gly
 20 25 30
 Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln Phe
 35 40 45
 His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Pro
 50 55 60
 Asn Asn Asp Ala Leu Ser Ser Gly Leu Met Lys Lys Val Lys Thr Ser
 65 70 75 80
 Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala
 85 90 95
 Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Gly Ala Ala Gly
 141

100 105 110
 Gly Ala Leu Val Thr Arg Ala Leu Leu Pro Glu Pro Thr Val Thr Thr
 115 120 125
 Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu Asp Leu Ser
 130 135 140
 Leu Gly Met Val Asp Asn Leu Asn Leu Lys Leu Glu Leu Gly Arg Thr
 145 150 155 160
 Val Tyr

<210> 81 <211> 628 <212> DNA <213> Arabidopsis thaliana <220>
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<400> 81
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 53

Met Val Ala Arg Ser Glu Glu Ile Val
 1 5

ata gtg gaa gaa gat acg act gcg aaa tgt ttg atg ttg tta tca aga
 101
 Ile Val Glu Glu Asp Thr Thr Ala Lys Cys Leu Met Leu Leu Ser Arg
 10 15 20 25

gtc gga gaa tgc ggc ggc ggc tgc ggg gga gat gaa cgt gtt ttc cga
 149
 Val Gly Glu Cys Gly Gly Gly Cys Gly Gly Asp Glu Arg Val Phe Arg
 30 35 40

tgc aag act tgt ctt aaa gag ttc tca tcg ttt caa gct ttg gga ggt
 197
 Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser Phe Gln Ala Leu Gly Gly
 45 50 55

cat cgt gca agc cac aag aaa ctt atc aac agt gac aat cca tca ctt
 245
 His Arg Ala Ser His Lys Lys Leu Ile Asn Ser Asp Asn Pro Ser Leu
 60 65 70

ctt gga tcc ttg tcc aac aag aaa act aaa acg tct cat cct tgt ccg
 293
 Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys Thr Ser His Pro Cys Pro
 75 80 85

ata tgt gga gtg aag ttt ccg atg gga caa gct ctt ggt ggt cac atg
 341
 Ile Cys Gly Val Lys Phe Pro Met Gly Gln Ala Leu Gly Gly His Met
 90 95 100 105

agg aga cat agg aac gag aaa gtc tca ggc tcg ttg gtt aca cgt tct
 389
 Arg Arg His Arg Asn Glu Lys Val Ser Gly Ser Leu Val Thr Arg Ser

110 115 120
 ttt cta ccg gag acg acg acg gtg acg gct ttg aag aaa ttt agt agt
 437
 Phe Leu Pro Glu Thr Thr Thr Val Thr Ala Leu Lys Lys Phe Ser Ser
 125 130 135
 ggg aag aga gtg gct tgt ttg gat ttg gac tta gat tcg atg gag agt
 485
 Gly Lys Arg Val Ala Cys Leu Asp Leu Asp Leu Asp Ser Met Glu Ser
 140 145 150
 ttg gtc aat tgg aag ttg gag ttg gga aga acg att tct tgg agt taa
 533
 Leu Val Asn Trp Lys Leu Glu Leu Gly Arg Thr Ile Ser Trp Ser
 155 160 165
 gtttttgggt tgtatacagt ttcacatgat tttgtaattct ttgttgatcc aattatcgta
 593
 ccgatcgatg tgaatattat ttgatacaa taaaa
 628
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 82
 Met Val Ala Arg Ser Glu Glu Ile Val Ile Val Glu Glu Asp Thr Thr
 1 5 10 15
 Ala Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly
 20 25 30
 Cys Gly Gly Asp Glu Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu
 35 40 45
 Phe Ser Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys
 50 55 60
 Leu Ile Asn Ser Asp Asn Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys
 65 70 75 80
 Lys Thr Lys Thr Ser His Pro Cys Pro Ile Cys Gly Val Lys Phe Pro
 85 90 95
 Met Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Asn Glu Lys
 100 105 110
 Val Ser Gly Ser Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
 115 120 125
 Val Thr Ala Leu Lys Lys Phe Ser Ser Gly Lys Arg Val Ala Cys Leu
 130 135 140

Asp Leu Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu
 145 150 155 160

Leu Gly Arg Thr Ile Ser Trp Ser
 165

<210> 83 <211> 615 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(615) <223> G357

<400> 83
 atg cag aac aaa cac aaa tgc aag ctc tgt tcc aag agt ttc tgt aat
 48
 Met Gln Asn Lys His Lys Cys Lys Leu Cys Ser Lys Ser Phe Cys Asn
 1 5 10 15
 ggc aga gca ctt ggt ggt cac atg aag tct cac ttg gtc tca tct cag
 96
 Gly Arg Ala Leu Gly Gly His Met Lys Ser His Leu Val Ser Ser Gln
 20 25 30
 tct tca gct cgg aag aaa cta ggt gac tcg gtc tat tct tct tct tcc
 144
 Ser Ser Ala Arg Lys Lys Leu Gly Asp Ser Val Tyr Ser Ser Ser Ser
 35 40 45
 tct tcc tcc gat ggt aaa gcg ctc gcc tac ggg tta cga gag aac ccg
 192
 Ser Ser Ser Asp Gly Lys Ala Leu Ala Tyr Gly Leu Arg Glu Asn Pro
 50 55 60
 agg aag agt ttc cgg gtc ttt aat ccg gat cct gag tca tcc aca att
 240
 Arg Lys Ser Phe Arg Val Phe Asn Pro Asp Pro Glu Ser Ser Thr Ile
 65 70 75 80
 tac aac agt gag aca gag acc gaa cct gaa tcc gga gac ccg gtt aag
 288
 Tyr Asn Ser Glu Thr Glu Thr Glu Pro Glu Ser Gly Asp Pro Val Lys
 85 90 95
 aaa cgg gtc aga gga gat gtt tca aag aag aag aag aag gca aag
 336
 Lys Arg Val Arg Gly Asp Val Ser Lys Lys Lys Lys Lys Ala Lys
 100 105 110
 agt aag aga gtg ttt gag aac tcg aag aag caa aag aca att cac gag
 384
 Ser Lys Arg Val Phe Glu Asn Ser Lys Lys Gln Lys Thr Ile His Glu
 115 120 125
 tca cca gaa cca gcg agt tct gtc tct gat ggt tct cct gaa caa gat
 432
 Ser Pro Glu Pro Ala Ser Ser Val Ser Asp Gly Ser Pro Glu Gln Asp
 130 135 140
 tta gct atg tgc ttg atg atg ctg tca aga gat tca agg gag ctc gag
 480

Leu Ala Met Cys Leu Met Met Leu Ser Arg Asp Ser Arg Glu Leu Glu
 145 150 155 160

att aaa ctg aaa aaa ccg gag gaa gag agg aag ccg gaa aaa aga cat
 528

Ile Lys Leu Lys Lys Pro Glu Glu Glu Arg Lys Pro Glu Lys Arg His
 165 170 175

ttc cct gag ctc cgt cgc tgt atg ata gat ctg aat ctt cct ccg ccg
 576

Phe Pro Glu Leu Arg Arg Cys Met Ile Asp Leu Asn Leu Pro Pro Pro
 180 185 190

caa gaa gct gaa gct gtc acc gtc gtt tca gcc ata taa
 615

Gln Glu Ala Glu Ala Val Thr Val Val Ser Ala Ile
 195 200

<210> 84 <211> 204 <212> PRT <213> Arabidopsis thaliana <400>
 84

Met Gln Asn Lys His Lys Cys Lys Leu Cys Ser Lys Ser Phe Cys Asn
 1 5 10 15

Gly Arg Ala Leu Gly Gly His Met Lys Ser His Leu Val Ser Ser Gln
 20 25 30

Ser Ser Ala Arg Lys Lys Leu Gly Asp Ser Val Tyr Ser Ser Ser Ser
 35 40 45

Ser Ser Ser Asp Gly Lys Ala Leu Ala Tyr Gly Leu Arg Glu Asn Pro
 50 55 60

Arg Lys Ser Phe Arg Val Phe Asn Pro Asp Pro Glu Ser Ser Thr Ile
 65 70 75 80

Tyr Asn Ser Glu Thr Glu Thr Glu Pro Glu Ser Gly Asp Pro Val Lys
 85 90 95

Lys Arg Val Arg Gly Asp Val Ser Lys Lys Lys Lys Lys Lys Ala Lys
 100 105 110

Ser Lys Arg Val Phe Glu Asn Ser Lys Lys Gln Lys Thr Ile His Glu
 115 120 125

Ser Pro Glu Pro Ala Ser Ser Val Ser Asp Gly Ser Pro Glu Gln Asp
 130 135 140

Leu Ala Met Cys Leu Met Met Leu Ser Arg Asp Ser Arg Glu Leu Glu
 145 150 155 160

Ile Lys Leu Lys Lys Pro Glu Glu Glu Arg Lys Pro Glu Lys Arg His
 165 170 175

Phe Pro Glu Leu Arg Arg Cys Met Ile Asp Leu Asn Leu Pro Pro Pro
 180 185 190

Gln Glu Ala Glu Ala Val Thr Val Val Ser Ala Ile
 195 200

<210> 85 <211> .728 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (64)..(516) <223> G364

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 60

ggt atg gac tac cag cca aac aca tcc cta cgt cta agc cta cca agt
 108

Met Asp Tyr Gln Pro Asn Thr Ser Leu Arg Leu Ser Leu Pro Ser
 1 5 10 15

tac aag aac cac caa cta aac cta gaa ctt gtt ctc gag cct tct tcc
 156

Tyr Lys Asn His Gln Leu Asn Leu Glu Leu Val Leu Glu Pro Ser Ser
 20 25 30

atg tct tct tct tca tct tct tcc acg aac tca tca tca tgt ttg gag
 204

Met Ser Ser Ser Ser Ser Ser Ser Thr Asn Ser Ser Ser Cys Leu Glu
 35 40 45

cag cct agg gta ttc tca tgt aac tat tgt caa aga aag ttt tac agc
 252

Gln Pro Arg Val Phe Ser Cys Asn Tyr Cys Gln Arg Lys Phe Tyr Ser
 50 55 60

tct caa gct ctt ggt ggt cat caa aac gct cat aag ctt gag aga acc
 300

Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys Leu Glu Arg Thr
 65 70 75

tta gcc aag aag agt cga gaa ctc ttt aga tcc tca aac act gtt gat
 348

Leu Ala Lys Lys Ser Arg Glu Leu Phe Arg Ser Ser Asn Thr Val Asp
 80 85 90 95

tct gat cag cct tac ccg ttc tcc ggt cgc ttt gag ctt tac ggc cgt
 396

Ser Asp Gln Pro Tyr Pro Phe Ser Gly Arg Phe Glu Leu Tyr Gly Arg
 100 105 110

ggc tac caa gga ttt ctc gaa agt ggc ggc tcg agg gac ttc tcc gcc
 444

Gly Tyr Gln Gly Phe Leu Glu Ser Gly Gly Ser Arg Asp Phe Ser Ala
 115 120 125

cgc cgt gtg ccg gag agt ggt ctt gat cag gat cag gag aag agt cac

492

Arg Arg Val Pro Glu Ser Gly Leu Asp Gln Asp Gln Glu Lys Ser His

130

135

140

ctt gac tta tcc tta agg ctc taa aagaatctta tattttgtta gtctatatat

546

Leu Asp Leu Ser Leu Arg Leu

145

150

tatcatatca attgttaatc ttaaaattga ttgttttact tattagtcac ttcctattat

606

ctgaaagttt tctttgtaag ttgtaactat ggtcctaaat tcaaatacaa atttgatttt

666

ggaagatggc acctaatac gtagttaaat aagttaaaaa aatgaaggat ctataattct

726

ct

728

<210> 86 <211> 150 <212> PRT <213> Arabidopsis thaliana <400>
86

Met Asp Tyr Gln Pro Asn Thr Ser Leu Arg Leu Ser Leu Pro Ser Tyr

1

5

10

15

Lys Asn His Gln Leu Asn Leu Glu Leu Val Leu Glu Pro Ser Ser Met

20

25

30

Ser Ser Ser Ser Ser Ser Ser Thr Asn Ser Ser Ser Cys Leu Glu Gln

35

40

45

Pro Arg Val Phe Ser Cys Asn Tyr Cys Gln Arg Lys Phe Tyr Ser Ser

50

55

60

Gln Ala Leu Gly Gly His Gln Asn Ala His Lys Leu Glu Arg Thr Leu

65

70

75

80

Ala Lys Lys Ser Arg Glu Leu Phe Arg Ser Ser Asn Thr Val Asp Ser

85

90

95

Asp Gln Pro Tyr Pro Phe Ser Gly Arg Phe Glu Leu Tyr Gly Arg Gly

100

105

110

Tyr Gln Gly Phe Leu Glu Ser Gly Gly Ser Arg Asp Phe Ser Ala Arg

115

120

125

Arg Val Pro Glu Ser Gly Leu Asp Gln Asp Gln Glu Lys Ser His Leu

130

135

140

Asp Leu Ser Leu Arg Leu
145 150

<210> 87 <211> 2217 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (37)..(2202) <223> G385

<400> 87
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54

Met Phe Glu Pro Asn Met
1 5

ctg ctt gcg gct atg aac aac gca gac agc aat aac cac aac tac aac
102

Leu Leu Ala Ala Met Asn Asn Ala Asp Ser Asn Asn His Asn Tyr Asn
10 15 20

cac gaa gac aac aat aat gaa gga ttt ctt cgg gac gat gaa ttc gac
150

His Glu Asp Asn Asn Asn Glu Gly Phe Leu Arg Asp Asp Glu Phe Asp
25 30 35

agt ccg aat act aaa tcg gga agt gag aat caa gaa gga gga tca gga
198

Ser Pro Asn Thr Lys Ser Gly Ser Glu Asn Gln Glu Gly Gly Ser Gly
40 45 50

aac gac caa gat cct ctt cat cct aac aag aag aaa cga tat cat cga
246

Asn Asp Gln Asp Pro Leu His Pro Asn Lys Lys Lys Arg Tyr His Arg
55 60 65 70

cac acc caa ctt cag atc cag gag atg gaa gcg ttc ttc aaa gag tgt
294

His Thr Gln Leu Gln Ile Gln Glu Met Glu Ala Phe Phe Lys Glu Cys
75 80 85

cct cac cca gat gac aag caa agg aaa cag cta agc cgt gaa ttg aat
342

Pro His Pro Asp Asp Lys Gln Arg Lys Gln Leu Ser Arg Glu Leu Asn
90 95 100

ttg gaa cct ctt cag gtc aaa ttc tgg ttc caa aac aaa cgt acc caa
390

Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn Lys Arg Thr Gln
105 110 115

atg aag aat cat cac gag cgg cat gag aac tca cat ctt cgg gcg gag
438

Met Lys Asn His His Glu Arg His Glu Asn Ser His Leu Arg Ala Glu
120 125 130

aac gaa aag ctt cga aac gac aac cta aga tat cga gag gct ctt gca
486

Asn Glu Lys Leu Arg Asn Asp Asn Leu Arg Tyr Arg Glu Ala Leu Ala
135 140 145 150

aat gct tcg tgt cct aat tgt ggt ggt cca aca gct atc gga gaa atg
534

Asn Ala Ser Cys Pro Asn Cys Gly Gly Pro Thr Ala Ile Gly Glu Met
 155 160 165
 tca ttc gac gaa cac caa ctc cgt ctc gaa aat gct cga tta agg gaa
 582
 Ser Phe Asp Glu His Gln Leu Arg Leu Glu Asn Ala Arg Leu Arg Glu
 170 175 180
 gag atc gac cgt ata tcc gca atc gca gct aaa tac gta ggc aag cca
 630
 Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr Val Gly Lys Pro
 185 190 195
 gtc tca aac tat cca ctt atg tct cct cct cct ctt cct cca cgt cca
 678
 Val Ser Asn Tyr Pro Leu Met Ser Pro Pro Pro Leu Pro Pro Arg Pro
 200 205 210
 cta gaa ctc gcc atg gga aat att gga gga gaa gct tat gga aac aat
 726
 Leu Glu Leu Ala Met Gly Asn Ile Gly Gly Glu Ala Tyr Gly Asn Asn
 215 220 225 230
 cca aac gat ctc ctt aag tcc atc act gca cca aca gaa tct gac aaa
 774
 Pro Asn Asp Leu Leu Lys Ser Ile Thr Ala Pro Thr Glu Ser Asp Lys
 235 240 245
 cct gtc atc atc gac tta tcc gtg gct gca atg gaa gag ctc atg agg
 822
 Pro Val Ile Ile Asp Leu Ser Val Ala Ala Met Glu Glu Leu Met Arg
 250 255 260
 atg gtt caa gta gac gag cct ctg tgg aag agt ttg gct tta gac gaa
 870
 Met Val Gln Val Asp Glu Pro Leu Trp Lys Ser Leu Ala Leu Asp Glu
 265 270 275
 gaa gaa tat gca agg acc ttt cct aga ggg atc gga cct aga ccg gct
 918
 Glu Glu Tyr Ala Arg Thr Phe Pro Arg Gly Ile Gly Pro Arg Pro Ala
 280 285 290
 gga tat aga tca gaa gct tcg cga gaa agc gcg gtt gtg atc atg aat
 966
 Gly Tyr Arg Ser Glu Ala Ser Arg Glu Ser Ala Val Val Ile Met Asn
 295 300 305 310
 cat gtt aac atc gtt gag att ctc atg gat gtg aat caa tgg tcg acg
 1014
 His Val Asn Ile Val Glu Ile Leu Met Asp Val Asn Gln Trp Ser Thr
 315 320 325
 att ttc gcg ggg atg gtt tct aga gca atg aca tta gcg gtt tta tcg
 1062
 Ile Phe Ala Gly Met Val Ser Arg Ala Met Thr Leu Ala Val Leu Ser
 330 335 340
 aca gga gtt gca gga aac tat aat gga gct ctt caa gtg atg agc gca
 1110
 Thr Gly Val Ala Gly Asn Tyr Asn Gly Ala Leu Gln Val Met Ser Ala

345	350	355
gag ttt caa gtt cca tct cca tta gtc cca aca cgt gaa acc tat ttc		
1158		
Glu Phe Gln Val Pro Ser Pro Leu Val Pro Thr Arg Glu Thr Tyr Phe		
360	365	370
gca cgt tac tgt aaa caa caa gga gat ggt tcg tgg gcg gtt gtc gat		
1206		
Ala Arg Tyr Cys Lys Gln Gln Gly Asp Gly Ser Trp Ala Val Val Asp		
375	380	385
att tcg ttg gat agt ctc caa cca aat ccc ccg gct aga tgc agg cgg		
1254		
Ile Ser Leu Asp Ser Leu Gln Pro Asn Pro Pro Ala Arg Cys Arg Arg		
395	400	405
cga gct tca gga tgt ttg att caa gaa ttg cca aat gga tat tct aag		
1302		
Arg Ala Ser Gly Cys Leu Ile Gln Glu Leu Pro Asn Gly Tyr Ser Lys		
410	415	420
gtg act tgg gtg gag cat gtg gaa gtt gat gac aga gga gtt cat aac		
1350		
Val Thr Trp Val Glu His Val Glu Val Asp Asp Arg Gly Val His Asn		
425	430	435
tta tac aaa cac atg gtt agt act ggt cat gcc ttc ggt gct aaa cgc		
1398		
Leu Tyr Lys His Met Val Ser Thr Gly His Ala Phe Gly Ala Lys Arg		
440	445	450
tgg gta gcc att ctt gac cgc caa tgc gag cgg tta gct agt gtc atg		
1446		
Trp Val Ala Ile Leu Asp Arg Gln Cys Glu Arg Leu Ala Ser Val Met		
455	460	465
gct aca aac att tcc tct gga gaa gtt ggc gtg ata acc aac caa gaa		
1494		
Ala Thr Asn Ile Ser Ser Gly Glu Val Gly Val Ile Thr Asn Gln Glu		
475	480	485
ggg agg agg agt atg ctg aaa ttg gca gag cgg atg gtt ata agc ttt		
1542		
Gly Arg Arg Ser Met Leu Lys Leu Ala Glu Arg Met Val Ile Ser Phe		
490	495	500
tgt gca gga gtg agt gct tca acc gct cac acg tgg act aca ttg tcc		
1590		
Cys Ala Gly Val Ser Ala Ser Thr Ala His Thr Trp Thr Thr Leu Ser		
505	510	515
ggt aca gga gct gaa gat gtt aga gtg atg act agg aag agt gtg gat		
1638		
Gly Thr Gly Ala Glu Asp Val Arg Val Met Thr Arg Lys Ser Val Asp		
520	525	530
gat cca gga agg tct cct ggt att gtt ctt agt gca gcc act tct ttt		
1686		
Asp Pro Gly Arg Ser Pro Gly Ile Val Leu Ser Ala Ala Thr Ser Phe		
535	540	545
550		

tgg atc cct gtt cct cca aag cga gtc ttt gac ttc ctc aga gac gag
1734

Trp Ile Pro Val Pro Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu
555 560 565

aat tca aga aat gag tgg gat att ctg tct aat gga gga gtt gtg caa
1782

Asn Ser Arg Asn Glu Trp Asp Ile Leu Ser Asn Gly Gly Val Val Gln
570 575 580

gaa atg gca cat att gct aac ggg agg gat acc gga aac tgt gtt tct
1830

Glu Met Ala His Ile Ala Asn Gly Arg Asp Thr Gly Asn Cys Val Ser
585 590 595

ctt ctt cgg gta aat agt gca aac tct agc cag agc aat atg ctg atc
1878

Leu Leu Arg Val Asn Ser Ala Asn Ser Ser Gln Ser Asn Met Leu Ile
600 605 610

cta caa gag agc tgc att gat cct aca gct tcc ttt gtg atc tat gct
1926

Leu Gln Glu Ser Cys Ile Asp Pro Thr Ala Ser Phe Val Ile Tyr Ala
615 620 625 630

cca gtc gat att gta gct atg aac ata gtg ctt aat gga ggt gat cca
1974

Pro Val Asp Ile Val Ala Met Asn Ile Val Leu Asn Gly Gly Asp Pro
635 640 645

gac tat gtg gct ctg ctt cca tca ggt ttt gct att ctt cct gat ggt
2022

Asp Tyr Val Ala Leu Leu Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly
650 655 660

aat gcc aat agt gga gcc cct gga gga gat gga ggg tcg ctc ttg act
2070

Asn Ala Asn Ser Gly Ala Pro Gly Gly Asp Gly Gly Ser Leu Leu Thr
665 670 675

gtt gct ttt cag att ctg gtt gac tca gtt cct acg gct aag ctg tct
2118

Val Ala Phe Gln Ile Leu Val Asp Ser Val Pro Thr Ala Lys Leu Ser
680 685 690

ctt ggc tct gtt gca act gtc aat aat cta ata gct tgc act gtt gag
2166

Leu Gly Ser Val Ala Thr Val Asn Asn Leu Ile Ala Cys Thr Val Glu
695 700 705 710

aga atc aaa gct tca atg tct tgt gag act gct tga aaaccatcca ttagc
2217

Arg Ile Lys Ala Ser Met Ser Cys Glu Thr Ala
715 720

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88

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 260 265 270

Ser Leu Ala Leu Asp Glu Glu Glu Tyr Ala Arg Thr Phe Pro Arg Gly
 275 280 285

Ile Gly Pro Arg Pro Ala Gly Tyr Arg Ser Glu Ala Ser Arg Glu Ser
 290 295 300

Ala Val Val Ile Met Asn His Val Asn Ile Val Glu Ile Leu Met Asp
 305 310 315 320

Val Asn Gln Trp Ser Thr Ile Phe Ala Gly Met Val Ser Arg Ala Met
 325 330 335

Thr Leu Ala Val Leu Ser Thr Gly Val Ala Gly Asn Tyr Asn Gly Ala
 340 345 350

Leu Gln Val Met Ser Ala Glu Phe Gln Val Pro Ser Pro Leu Val Pro
 355 360 365

Thr Arg Glu Thr Tyr Phe Ala Arg Tyr Cys Lys Gln Gln Gly Asp Gly
 370 375 380

Ser Trp Ala Val Val Asp Ile Ser Leu Asp Ser Leu Gln Pro Asn Pro
 385 390 395 400

Pro Ala Arg Cys Arg Arg Arg Ala Ser Gly Cys Leu Ile Gln Glu Leu
 405 410 415

Pro Asn Gly Tyr Ser Lys Val Thr Trp Val Glu His Val Glu Val Asp
 420 425 430

Asp Arg Gly Val His Asn Leu Tyr Lys His Met Val Ser Thr Gly His
 435 440 445

Ala Phe Gly Ala Lys Arg Trp Val Ala Ile Leu Asp Arg Gln Cys Glu
 450 455 460

Arg Leu Ala Ser Val Met Ala Thr Asn Ile Ser Ser Gly Glu Val Gly
 465 470 475 480

Val Ile Thr Asn Gln Glu Gly Arg Arg Ser Met Leu Lys Leu Ala Glu
 485 490 495

Arg Met Val Ile Ser Phe Cys Ala Gly Val Ser Ala Ser Thr Ala His
 500 505 510
 Thr Trp Thr Thr Leu Ser Gly Thr Gly Ala Glu Asp Val Arg Val Met
 515 520 525
 Thr Arg Lys Ser Val Asp Asp Pro Gly Arg Ser Pro Gly Ile Val Leu
 530 535 540
 Ser Ala Ala Thr Ser Phe Trp Ile Pro Val Pro Pro Lys Arg Val Phe
 545 550 555 560
 Asp Phe Leu Arg Asp Glu Asn Ser Arg Asn Glu Trp Asp Ile Leu Ser
 565 570 575
 Asn Gly Gly Val Val Gln Glu Met Ala His Ile Ala Asn Gly Arg Asp
 580 585 590
 Thr Gly Asn Cys Val Ser Leu Leu Arg Val Asn Ser Ala Asn Ser Ser
 595 600 605
 Gln Ser Asn Met Leu Ile Leu Gln Glu Ser Cys Ile Asp Pro Thr Ala
 610 615 620
 Ser Phe Val Ile Tyr Ala Pro Val Asp Ile Val Ala Met Asn Ile Val
 625 630 635 640
 Leu Asn Gly Gly Asp Pro Asp Tyr Val Ala Leu Leu Pro Ser Gly Phe
 645 650 655
 Ala Ile Leu Pro Asp Gly Asn Ala Asn Ser Gly Ala Pro Gly Gly Asp
 660 665 670
 Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val Asp Ser Val
 675 680 685
 Pro Thr Ala Lys Leu Ser Leu Gly Ser Val Ala Thr Val Asn Asn Leu
 690 695 700
 Ile Ala Cys Thr Val Glu Arg Ile Lys Ala Ser Met Ser Cys Glu Thr
 705 710 715 720
 Ala

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 1 5 10 15
 agt caa caa aaa gaa cca tct ctg agg ttg aat ctt atg ccg ttg aca
 96
 Ser Gln Gln Lys Glu Pro Ser Leu Arg Leu Asn Leu Met Pro Leu Thr
 20 25 30
 act tct tct tct tct tct tcg ttt caa cac atg cac aat cag aat aac
 144
 Thr Ser Ser Ser Ser Ser Ser Phe Gln His Met His Asn Gln Asn Asn
 35 40 45
 aat agc cat ccc cag aag att cat aac atc tct tgg act cat ctg ttt
 192
 Asn Ser His Pro Gln Lys Ile His Asn Ile Ser Trp Thr His Leu Phe
 50 55 60
 caa tct tct ggg att aaa cgt aca act gca gag aga aac tcc gac gcc
 240
 Gln Ser Ser Gly Ile Lys Arg Thr Thr Ala Glu Arg Asn Ser Asp Ala
 65 70 75 80
 ggg tca ttt cta aga ggt ttc aac gtg aac aga gct cag tct tcg gtg
 288
 Gly Ser Phe Leu Arg Gly Phe Asn Val Asn Arg Ala Gln Ser Ser Val
 85 90 95
 gcg gta gtg gac ttg gaa gaa gaa gcc gcc gtc gtc tcg tct cca aac
 336
 Ala Val Val Asp Leu Glu Glu Glu Ala Ala Val Val Ser Ser Pro Asn
 100 105 110
 agc gcc gtt tcg agt ctg agt gga aat aaa agg gat ctt gcg gtg gcg
 384
 Ser Ala Val Ser Ser Leu Ser Gly Asn Lys Arg Asp Leu Ala Val Ala
 115 120 125
 aga gga gga gat gaa aac gag gcg gag aga gct tct tgc tca cgc gga
 432
 Arg Gly Gly Asp Glu Asn Glu Ala Glu Arg Ala Ser Cys Ser Arg Gly
 130 135 140
 ggg gga agc ggt ggt agc gac gat gaa gac ggc gga aac ggc gac gga
 480
 Gly Gly Ser Gly Gly Ser Asp Asp Glu Asp Gly Gly Asn Gly Asp Gly
 145 150 155 160
 tca agg aag aaa cta cgg tta tcg aag gat caa gct ctt gtt ctc gag
 528
 Ser Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ala Leu Val Leu Glu
 165 170 175
 gag act ttt aaa gaa cat agc act ctt aat ccg aag caa aag ctg gct
 576

Glu Thr Phe Lys Glu His Ser Thr Leu Asn Pro Lys Gln Lys Leu Ala
 180 185 190
 cta gca aaa cag ttg aat cta agg gca aga caa gtt gaa gtg tgg ttt
 624
 Leu Ala Lys Gln Leu Asn Leu Arg Ala Arg Gln Val Glu Val Trp Phe
 195 200 205
 cag aac cgt agg gca agg acg aag ctg aaa caa acg gag gtt gat tgt
 672
 Gln Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys
 210 215 220
 gag tat tta aag aga tgt tgc gat aat ctg acc gag gag aat cga cgg
 720
 Glu Tyr Leu Lys Arg Cys Cys Asp Asn Leu Thr Glu Glu Asn Arg Arg
 225 230 235 240
 ctg cag aaa gaa gtg tcg gag ctg agg gcg ttg aag ttg tct cca cat
 768
 Leu Gln Lys Glu Val Ser Glu Leu Arg Ala Leu Lys Leu Ser Pro His
 245 250 255
 ctc tac atg cac atg act cct cct act act ctc acc atg tgc cct tct
 816
 Leu Tyr Met His Met Thr Pro Pro Thr Thr Leu Thr Met Cys Pro Ser
 260 265 270
 tgc gaa cgt gtc tcc tcc tct gcc gcc act gtg acc gct gct cct tcc
 864
 Cys Glu Arg Val Ser Ser Ser Ala Ala Thr Val Thr Ala Ala Pro Ser
 275 280 285
 act act act act cct acg gtg gtg ggg cgg cca agt cca cag cga tta
 912
 Thr Thr Thr Thr Pro Thr Val Val Gly Arg Pro Ser Pro Gln Arg Leu
 290 295 300
 act cct tgg act gct att tct ctc cag caa aaa tca ggt cgc tag
 957
 Thr Pro Trp Thr Ala Ile Ser Leu Gln Gln Lys Ser Gly Arg
 305 310 315
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 Met Gly Glu Arg Asp Asp Gly Leu Gly Leu Ser Leu Ser Leu Gly Asn
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 Ser Gln Gln Lys Glu Pro Ser Leu Arg Leu Asn Leu Met Pro Leu Thr
 20 25 30
 Thr Ser Ser Ser Ser Ser Ser Phe Gln His Met His Asn Gln Asn Asn
 35 40 45
 Asn Ser His Pro Gln Lys Ile His Asn Ile Ser Trp Thr His Leu Phe
 50 55 60

Gln Ser Ser Gly Ile Lys Arg Thr Thr Ala Glu Arg Asn Ser Asp Ala
 65 70 75 80

Gly Ser Phe Leu Arg Gly Phe Asn Val Asn Arg Ala Gln Ser Ser Val
 85 90 95

Ala Val Val Asp Leu Glu Glu Glu Ala Ala Val Val Ser Ser Pro Asn
 100 105 110

Ser Ala Val Ser Ser Leu Ser Gly Asn Lys Arg Asp Leu Ala Val Ala
 115 120 125

Arg Gly Gly Asp Glu Asn Glu Ala Glu Arg Ala Ser Cys Ser Arg Gly
 130 135 140

Gly Gly Ser Gly Gly Ser Asp Asp Glu Asp Gly Gly Asn Gly Asp Gly
 145 150 155 160

Ser Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ala Leu Val Leu Glu
 165 170 175

Glu Thr Phe Lys Glu His Ser Thr Leu Asn Pro Lys Gln Lys Leu Ala
 180 185 190

Leu Ala Lys Gln Leu Asn Leu Arg Ala Arg Gln Val Glu Val Trp Phe
 195 200 205

Gln Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys
 210 215 220

Glu Tyr Leu Lys Arg Cys Cys Asp Asn Leu Thr Glu Glu Asn Arg Arg
 225 230 235 240

Leu Gln Lys Glu Val Ser Glu Leu Arg Ala Leu Lys Leu Ser Pro His
 245 250 255

Leu Tyr Met His Met Thr Pro Pro Thr Thr Leu Thr Met Cys Pro Ser
 260 265 270

Cys Glu Arg Val Ser Ser Ser Ala Ala Thr Val Thr Ala Ala Pro Ser
 275 280 285

Thr Thr Thr Thr Pro Thr Val Val Gly Arg Pro Ser Pro Gln Arg Leu
 290 295 300

Thr Pro Trp Thr Ala Ile Ser Leu Gln Gln Lys Ser Gly Arg
 305 310 315

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 120

tatacaa atg gca atg gct tta aac atg aat gct tac gta gac gag ttc
 169

Met Ala Met Ala Leu Asn Met Asn Ala Tyr Val Asp Glu Phe
 1 5 10

atg gaa gct ctt gaa cca ttc atg aag gta act tca tct tct tct act
 217

Met Glu Ala Leu Glu Pro Phe Met Lys Val Thr Ser Ser Ser Ser Thr
 15 20 25 30

tcg aat tca tca aat cca aaa cca tta act cct aat ttc atc cct aat
 265

Ser Asn Ser Ser Asn Pro Lys Pro Leu Thr Pro Asn Phe Ile Pro Asn
 35 40 45

aat gac caa gtc tta ccg gta tct aac caa acc ggt ccg att ggg cta
 313

Asn Asp Gln Val Leu Pro Val Ser Asn Gln Thr Gly Pro Ile Gly Leu
 50 55 60

aac cag ctc act cca aca caa atc ctc caa att cag aca gag tta cat
 361

Asn Gln Leu Thr Pro Thr Gln Ile Leu Gln Ile Gln Thr Glu Leu His
 65 70 75

ctc cgg caa aac caa tct cgt cgt cgc gct ggt agt cat ctt ctc acc
 409

Leu Arg Gln Asn Gln Ser Arg Arg Arg Ala Gly Ser His Leu Leu Thr
 80 85 90

gct aaa cca acc tca atg aag aaa atc gac gta gca act aaa ccg gtt
 457

Ala Lys Pro Thr Ser Met Lys Lys Ile Asp Val Ala Thr Lys Pro Val
 95 100 105 110

aaa cta tac cga ggc gta aga cag agg caa tgg ggt aaa tgg gta gct
 505

Lys Leu Tyr Arg Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala
 115 120 125

gag att cgg cta cct aaa aac cga acc cgg tta tgg ctc ggt acg ttc
 553

Glu Ile Arg Leu Pro Lys Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe
 130 135 140

gaa acg gct caa gaa gct gca tta gct tac gat caa gca gct cat aag
 601
 Glu Thr Ala Gln Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala His Lys
 145 150 155

atc aga gga gac aac gct cgt ctc aat ttc cca gac att gtt cgt caa
 649
 Ile Arg Gly Asp Asn Ala Arg Leu Asn Phe Pro Asp Ile Val Arg Gln
 160 165 170

gga cac tat aaa cag ata ttg tct ccg tct atc aac gca aag atc gaa
 697
 Gly His Tyr Lys Gln Ile Leu Ser Pro Ser Ile Asn Ala Lys Ile Glu
 175 180 185 190

tcc atc tgc aat agt tct gat ctt cca ctg cct cag atc gag aaa cag
 745
 Ser Ile Cys Asn Ser Ser Asp Leu Pro Leu Pro Gln Ile Glu Lys Gln
 195 200 205

aac aaa aca gag gag gtg ctc tct ggt ttt tcc aaa ccg gag aaa gaa
 793
 Asn Lys Thr Glu Glu Val Leu Ser Gly Phe Ser Lys Pro Glu Lys Glu
 210 215 220

ccg gaa ttt ggg gag ata tac gga tgc gga tac tcg ggc tca tct cct
 841
 Pro Glu Phe Gly Glu Ile Tyr Gly Cys Gly Tyr Ser Gly Ser Ser Pro
 225 230 235

gag tcg gat ata acg ttg ttg gat ttc tca agc gac tgt gtg aaa gaa
 889
 Glu Ser Asp Ile Thr Leu Leu Asp Phe Ser Ser Asp Cys Val Lys Glu
 240 245 250

gat gag agt ttc ttg atg ggt ttg cac aag tat cct tct ttg gag att
 937
 Asp Glu Ser Phe Leu Met Gly Leu His Lys Tyr Pro Ser Leu Glu Ile
 255 260 265 270

gat tgg gac gct ata gag aaa ctc ttc tga atccatttta tctttttgat
 987
 Asp Trp Asp Ala Ile Glu Lys Leu Phe
 275

tcatttgtct ctaaattgta gaattttatt ttcagagctt tgtaaggga gttcttgaat
 1047

gagagttgca gaggactagt ggaacctaac tctgttttct tttgtaagta ttgtttataa
 1107

tgggccgttg aatgggcctt attgatttaa acagcccaag tttttaaaaa aaaaaaaaaa
 1167

aaaaaaaaaa
 1177

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20 25 30

Ser Ser Asn Pro Lys Pro Leu Thr Pro Asn Phe Ile Pro Asn Asn Asp
35 40 45

Gln Val Leu Pro Val Ser Asn Gln Thr Gly Pro Ile Gly Leu Asn Gln
50 55 60

Leu Thr Pro Thr Gln Ile Leu Gln Ile Gln Thr Glu Leu His Leu Arg
65 70 75 80

Gln Asn Gln Ser Arg Arg Arg Ala Gly Ser His Leu Leu Thr Ala Lys
85 90 95

Pro Thr Ser Met Lys Lys Ile Asp Val Ala Thr Lys Pro Val Lys Leu
100 105 110

Tyr Arg Gly Val Arg Gln Arg Gln Trp Gly Lys Trp Val Ala Glu Ile
115 120 125

Arg Leu Pro Lys Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe Glu Thr
130 135 140

Ala Gln Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala His Lys Ile Arg
145 150 155 160

Gly Asp Asn Ala Arg Leu Asn Phe Pro Asp Ile Val Arg Gln Gly His
165 170 175

Tyr Lys Gln Ile Leu Ser Pro Ser Ile Asn Ala Lys Ile Glu Ser Ile
180 185 190

Cys Asn Ser Ser Asp Leu Pro Leu Pro Gln Ile Glu Lys Gln Asn Lys
195 200 205

Thr Glu Glu Val Leu Ser Gly Phe Ser Lys Pro Glu Lys Glu Pro Glu
210 215 220

Phe Gly Glu Ile Tyr Gly Cys Gly Tyr Ser Gly Ser Ser Pro Glu Ser
225 230 235 240

Asp Ile Thr Leu Leu Asp Phe Ser Ser Asp Cys Val Lys Glu Asp Glu

161

gtt ggt ata ggc aga aaa gtg gat atg aga gct cat tcg tct tac gaa
 487
 Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala His Ser Ser Tyr Glu
 135 140 145
 aac ttg gct cag acg ctt gag gaa atg ttc ttt gga atg aca ggt act
 535
 Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe Gly Met Thr Gly Thr
 150 155 160 165
 act tgt cga gaa aag gtt aaa cct tta agg ctt tta gat gga tca tca
 583
 Thr Cys Arg Glu Lys Val Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser
 170 175 180
 gac ttt gta ctc act tat gaa gat aag gaa ggg gat tgg atg ctt gtt
 631
 Asp Phe Val Leu Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val
 185 190 195
 gga gat gtt cca tgg aga atg ttt atc aac tcg gtg aaa agg ctt cgg
 679
 Gly Asp Val Pro Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg
 200 205 210
 atc atg gga acc tca gaa gct agt gga cta gct cca aga cgt caa gag
 727
 Ile Met Gly Thr Ser Glu Ala Ser Gly Leu Ala Pro Arg Arg Gln Glu
 215 220 225
 cag aag gat aga caa aga aac aac cct gtt tag cttcccttcc aaagctggca
 780
 Gln Lys Asp Arg Gln Arg Asn Asn Pro Val
 230 235
 ttgtttatgt attgtttgag gtttgcaatt tactcgatac tttttgaaga aagtattttg
 840
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 900
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 992

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Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala
 20 25 30

Trp Lys Glu Arg Gly Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val
 35 40 45

Gly Ser Lys Arg Ser Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro
50 55 60

Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Leu His Arg
65 70 75 80

Met Asn Ser Leu Val Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu
85 90 95

Glu Gly Asp Gly Glu Lys Lys Val Val Lys Asn Asp Glu Leu Lys Asp
100 105 110

Val Ser Met Lys Val Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys
115 120 125

Val Asn Met Asp Gly Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala
130 135 140

His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe
145 150 155 160

Gly Met Thr Gly Thr Thr Cys Arg Glu Lys Val Lys Pro Leu Arg Leu
165 170 175

Leu Asp Gly Ser Ser Asp Phe Val Leu Thr Tyr Glu Asp Lys Glu Gly
180 185 190

Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn Ser
195 200 205

Val Lys Arg Leu Arg Ile Met Gly Thr Ser Glu Ala Ser Gly Leu Ala
210 215 220

Pro Arg Arg Gln Glu Gln Lys Asp Arg Gln Arg Asn Asn Pro Val
225 230 235

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<221> CDS <222> (1)..(1218) <223> G477

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Met Asp Ser Trp Ser Tyr Gly Arg Ser Val Phe Met Ser Asn Glu Thr
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ctt tta cct tgt gat act ttt gct aag aat aga aga ttt gaa cag aga
96

Leu Leu Pro Cys Asp Thr Phe Ala Lys Asn Arg Arg Phe Glu Gln Arg
 20 25 30
 ctc tct aat aat gat gat gtg ttg att tct gac atg gct ggt aac tcc
 144
 Leu Ser Asn Asn Asp Asp Val Leu Ile Ser Asp Met Ala Gly Asn Ser
 35 40 45
 aat gga ttc agt gct gtt tct att act aaa gtt gtt cct gaa gag gaa
 192
 Asn Gly Phe Ser Ala Val Ser Ile Thr Lys Val Val Pro Glu Glu Glu
 50 55 60
 gat gag gag aac ata tct tct tct tca aag ttc tct agt cag gaa ttg
 240
 Asp Glu Glu Asn Ile Ser Ser Ser Ser Lys Phe Ser Ser Gln Glu Leu
 65 70 75 80
 aat agg ata gat ttc aaa ctt agg agc ttt ttg gat tta gga aat gat
 288
 Asn Arg Ile Asp Phe Lys Leu Arg Ser Phe Leu Asp Leu Gly Asn Asp
 85 90 95
 gat gat gat aca tcc tct aga ggt ttt gct ctg cca tct aaa aag tct
 336
 Asp Asp Asp Thr Ser Ser Arg Gly Phe Ala Leu Pro Ser Lys Lys Ser
 100 105 110
 cga gct tca aac ttg tgc tct cag aat ccc ttg tgt caa gtt tat ggg
 384
 Arg Ala Ser Asn Leu Cys Ser Gln Asn Pro Leu Cys Gln Val Tyr Gly
 115 120 125
 tgt agt aag gat ctg agc tct tcg aaa gat tac cac aaa agg cat aga
 432
 Cys Ser Lys Asp Leu Ser Ser Ser Lys Asp Tyr His Lys Arg His Arg
 130 135 140
 gtt tgc gag gct cat tcg aaa act tct gtg gtc ata gtt aat ggt ctt
 480
 Val Cys Glu Ala His Ser Lys Thr Ser Val Val Ile Val Asn Gly Leu
 145 150 155 160
 gaa cag agg ttt tgt caa cag tgc agc agg ttt cat ttc ctc tca gag
 528
 Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Phe Leu Ser Glu
 165 170 175
 ttt gat gat ggc aaa aga agt tgc aga agg cga tta gcc ggt cac aat
 576
 Phe Asp Asp Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn
 180 185 190
 gaa cga aga agg aaa cct gca ttc tat ttc cta ccg ggt aag cgc cat
 624
 Glu Arg Arg Arg Lys Pro Ala Phe Tyr Phe Leu Pro Gly Lys Arg His
 195 200 205
 aag ctt ctt cgc acc tct caa gat gta gta ggc aac aag ttt ctg gag
 672
 Lys Leu Leu Arg Thr Ser Gln Asp Val Val Gly Asn Lys Phe Leu Glu

210	215	220
aat tca tca ttg gta ttg cca gag tca ttt cct ggt agt ctc tta tac 720		
Asn Ser Ser Leu Val Leu Pro Glu Ser Phe Pro Gly Ser Leu Leu Tyr 225 230 235 240		
aga gta ata gat gaa gac gac cac cgt aca agt aga ctc gtg agt ttc 768		
Arg Val Ile Asp Glu Asp Asp His Arg Thr Ser Arg Leu Val Ser Phe 245 250 255		
aaa gat gaa cct act tgt tcc atg ttt cct act aat gag caa aac agc 816		
Lys Asp Glu Pro Thr Cys Ser Met Phe Pro Thr Asn Glu Gln Asn Ser 260 265 270		
agc aga act tat gaa tct aaa cca gca att tat tcc acg gaa gta tcc 864		
Ser Arg Thr Tyr Glu Ser Lys Pro Ala Ile Tyr Ser Thr Glu Val Ser 275 280 285		
tcc att tgg gac tta cat gag acg gcg gca tca cgc tct act cgt gct 912		
Ser Ile Trp Asp Leu His Glu Thr Ala Ala Ser Arg Ser Thr Arg Ala 290 295 300		
ctc tct ctt ctg tca gct cag tcc caa caa cac ttg tct aag ttt cca 960		
Leu Ser Leu Leu Ser Ala Gln Ser Gln Gln His Leu Ser Lys Phe Pro 305 310 315 320		
aac aca acg ttc tca atc acc caa ccc aac caa aat ctc aat cac tca 1008		
Asn Thr Thr Phe Ser Ile Thr Gln Pro Asn Gln Asn Leu Asn His Ser 325 330 335		
tca tca act gac tat cat cag atg gaa caa ccg ttg tgg atc gat cct 1056		
Ser Ser Thr Asp Tyr His Gln Met Glu Gln Pro Leu Trp Ile Asp Pro 340 345 350		
ggc aag acc aat tct gct ggt tct agt tct tgt aaa gga aaa gga aca 1104		
Gly Lys Thr Asn Ser Ala Gly Ser Ser Ser Cys Lys Gly Lys Gly Thr 355 360 365		
tcc acg gtt gat cta ctg caa ctg tca tca cat ctt caa aga atc gag 1152		
Ser Thr Val Asp Leu Leu Gln Leu Ser Ser His Leu Gln Arg Ile Glu 370 375 380		
caa cag agg aat tac act ggt gat gtg aag cag gaa tat aat gag ctt 1200		
Gln Gln Arg Asn Tyr Thr Gly Asp Val Lys Gln Glu Tyr Asn Glu Leu 385 390 395 400		
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Tyr Phe Pro Gly Ser 405		

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Met Asp Ser Trp Ser Tyr Gly Arg Ser Val Phe Met Ser Asn Glu Thr
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20 25 30

Leu Ser Asn Asn Asp Asp Val Leu Ile Ser Asp Met Ala Gly Asn Ser
35 40 45

Asn Gly Phe Ser Ala Val Ser Ile Thr Lys Val Val Pro Glu Glu Glu
50 55 60

Asp Glu Glu Asn Ile Ser Ser Ser Ser Lys Phe Ser Ser Gln Glu Leu
65 70 75 80

Asn Arg Ile Asp Phe Lys Leu Arg Ser Phe Leu Asp Leu Gly Asn Asp
85 90 95

Asp Asp Asp Thr Ser Ser Arg Gly Phe Ala Leu Pro Ser Lys Lys Ser
100 105 110

Arg Ala Ser Asn Leu Cys Ser Gln Asn Pro Leu Cys Gln Val Tyr Gly
115 120 125

Cys Ser Lys Asp Leu Ser Ser Ser Lys Asp Tyr His Lys Arg His Arg
130 135 140

Val Cys Glu Ala His Ser Lys Thr Ser Val Val Ile Val Asn Gly Leu
145 150 155 160

Glu Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Phe Leu Ser Glu
165 170 175

Phe Asp Asp Gly Lys Arg Ser Cys Arg Arg Arg Leu Ala Gly His Asn
180 185 190

Glu Arg Arg Arg Lys Pro Ala Phe Tyr Phe Leu Pro Gly Lys Arg His
195 200 205

Lys Leu Leu Arg Thr Ser Gln Asp Val Val Gly Asn Lys Phe Leu Glu
210 215 220

Asn Ser Ser Leu Val Leu Pro Glu Ser Phe Pro Gly Ser Leu Leu Tyr
 225 230 235 240

Arg Val Ile Asp Glu Asp Asp His Arg Thr Ser Arg Leu Val Ser Phe
 245 250 255

Lys Asp Glu Pro Thr Cys Ser Met Phe Pro Thr Asn Glu Gln Asn Ser
 260 265 270

Ser Arg Thr Tyr Glu Ser Lys Pro Ala Ile Tyr Ser Thr Glu Val Ser
 275 280 285

Ser Ile Trp Asp Leu His Glu Thr Ala Ala Ser Arg Ser Thr Arg Ala
 290 295 300

Leu Ser Leu Leu Ser Ala Gln Ser Gln Gln His Leu Ser Lys Phe Pro
 305 310 315 320

Asn Thr Thr Phe Ser Ile Thr Gln Pro Asn Gln Asn Leu Asn His Ser
 325 330 335

Ser Ser Thr Asp Tyr His Gln Met Glu Gln Pro Leu Trp Ile Asp Pro
 340 345 350

Gly Lys Thr Asn Ser Ala Gly Ser Ser Ser Cys Lys Gly Lys Gly Thr
 355 360 365

Ser Thr Val Asp Leu Leu Gln Leu Ser Ser His Leu Gln Arg Ile Glu
 370 375 380

Gln Gln Arg Asn Tyr Thr Gly Asp Val Lys Gln Glu Tyr Asn Glu Leu
 385 390 395 400

Tyr Phe Pro Gly Ser
 405

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 48
 Met Arg Arg Pro Lys Ser Ser His Val Arg Met Glu Pro Val Ala Pro
 1 5 10 15
 cgt tca cat aac acg atg cca atg ctt gat caa ttt cga tct aat cat
 96
 Arg Ser His Asn Thr Met Pro Met Leu Asp Gln Phe Arg Ser Asn His
 20 25 30

cct gaa aca agc aag atc gag ggg gtc tct tcg ttg gac aca gct ctg
144

Pro Glu Thr Ser Lys Ile Glu Gly Val Ser Ser Leu Asp Thr Ala Leu
35 40 45

aag gtg ttt tgg aat aat caa agg gag cag cta gga aac ttt gca ggc
192

Lys Val Phe Trp Asn Asn Gln Arg Glu Gln Leu Gly Asn Phe Ala Gly
50 55 60

caa act cat ttg ccg cta tct agg gtc aga aag att ttg aaa tct gat
240

Gln Thr His Leu Pro Leu Ser Arg Val Arg Lys Ile Leu Lys Ser Asp
65 70 75 80

cct gaa gtc aag aag ata agc tgt gat gtt cct gct ttg ttt tcg aaa
288

Pro Glu Val Lys Lys Ile Ser Cys Asp Val Pro Ala Leu Phe Ser Lys
85 90 95

gcc tgt gaa tac ttc att cta gag gta aca tta cga gct tgg atg cat
336

Ala Cys Glu Tyr Phe Ile Leu Glu Val Thr Leu Arg Ala Trp Met His
100 105 110

act caa tca tgc act cgt gag acc atc cgg cgt tgt gat atc ttc cag
384

Thr Gln Ser Cys Thr Arg Glu Thr Ile Arg Arg Cys Asp Ile Phe Gln
115 120 125

gcc gta aag aac tca gga act tat gat ttc ctg att gat cgt gtc cct
432

Ala Val Lys Asn Ser Gly Thr Tyr Asp Phe Leu Ile Asp Arg Val Pro
130 135 140

ttt gga ccg cac tgt gtc acc cat cag ggt gtg caa cct cct gct gaa
480

Phe Gly Pro His Cys Val Thr His Gln Gly Val Gln Pro Pro Ala Glu
145 150 155 160

atg att ttg ccg gat atg aat gtt cca atc gat atg gac cag att gag
528

Met Ile Leu Pro Asp Met Asn Val Pro Ile Asp Met Asp Gln Ile Glu
165 170 175

gag gag aat atg atg gaa gag cgc tct gtc ggg ttt gac ctc aac tgt
576

Glu Glu Asn Met Met Glu Glu Arg Ser Val Gly Phe Asp Leu Asn Cys
180 185 190

gat ctc cag tga

588

Asp Leu Gln
195

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 105
 Ala Leu Glu Ala Leu Thr Ser Pro Arg Leu Ala Ser Pro Ile Pro Pro
 5 10 15

ttg ttc gaa gat tct tca gtc ttc cat gga gtc gag cac tgg aca aag
 153
 Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr Lys
 20 25 30

ggt aag cga tct aag aga tca aga tcc gat ttc cac cac caa aac ctc
 201
 Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn Leu
 35 40 45

act gag gaa gag tat cta gct ttt tgc ctc atg ctt ctc gct cgc gac
 249
 Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg Asp
 50 55 60 65

aac cgt cag cct cct cct cct ccg gcg gtg gag aag ttg agc tac aag
 297
 Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr Lys
 70 75 80

tgt agc gtc tgc gac aag acg ttc tct tct tac caa gct ctc ggt ggt
 345
 Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly Gly
 85 90 95

cac aag gca agc cac cgt aag aac tta tca cag act ctc tcc ggc gga
 393
 His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly Gly
 100 105 110

gga gat gat cat tca acc tcg tcg gcg aca acc aca tcc gcc gtg act
 441
 Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val Thr
 115 120 125

act gga agt ggg aaa tca cac gtt tgc acc atc tgt aac aag tct ttt
 489
 Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser Phe
 130 135 140 145

cct tcc ggt caa gct ctc ggc gga cac aag cgg tgc cac tac gaa gga
 537
 Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly
 150 155 160

aac aac aac atc aac act agt agc gtg tcc aac tcc gaa ggt gcg ggg
 585
 Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala Gly
 165 170 175

tcc act agc cac gtt agc agt agc cac cgt ggg ttt gac ctc aac atc
 633
 Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn Ile
 180 185 190

cct ccg atc cct gaa ttc tcg atg gtc aac gga gac gac gaa gtc atg
681
Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val Met
195 200 205

agc cct atg ccg gcg aag aag cct cgg ttt gac ttt ccg gtc aaa ctt
729
Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys Leu
210 215 220 225

caa ctt taa ggaaatttac ttagacgata agatttcggt tgtatactgt
778
Gln Leu

tgagagttgt gtaggaattt gttgactgta cataccaaat tggactttga ctgattccaa
838

ttctttctgt tctttcattt taaaaattat taaaccgatt ctttaccaca aa
890

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100.

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1 5 10 15

Pro Leu Phe Glu Asp Ser Ser Val Phe His Gly Val Glu His Trp Thr
20 25 30

Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn
35 40 45

Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg
50 55 60

Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr
65 70 75 80

Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly
85 90 95

Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly
100 105 110.

Gly Gly Asp Asp His Ser Thr Ser Ser Ala Thr Thr Thr Ser Ala Val
115 120 125

Thr Thr Gly Ser Gly Lys Ser His Val Cys Thr Ile Cys Asn Lys Ser
130 135 140

Phe Pro Ser Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu
145 150 155 160

Gly Asn Asn Asn Ile Asn Thr Ser Ser Val Ser Asn Ser Glu Gly Ala
165 170 175

Gly Ser Thr Ser His Val Ser Ser Ser His Arg Gly Phe Asp Leu Asn
180 185 190

Ile Pro Pro Ile Pro Glu Phe Ser Met Val Asn Gly Asp Asp Glu Val
195 200 205

Met Ser Pro Met Pro Ala Lys Lys Pro Arg Phe Asp Phe Pro Val Lys
210 215 220

Leu Gln Leu
225

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60

ttctttccaa gttcttctgt aaatcccaag tcccgtctt ttcctcttta tccttttcac
120

cagcttcgct actaagacaa caaatcttcc cctctctctc tcgcctgac gatcttcaaa
180

gagtaagaaa a atg cag gaa caa gcg act agc tct tta gct gca agc tct
230

Met Gln Glu Gln Ala Thr Ser Ser Leu Ala Ala Ser Ser
1 5 10

tta cca tca agc agc gag agg tca tca agc tct gct cca cat ttg gag
278

Leu Pro Ser Ser Ser Glu Arg Ser Ser Ser Ser Ala Pro His Leu Glu
15 20 25

atc aaa gaa gga att gaa agc gat gag gag ata cgg cga gtg ccg gag
326

Ile Lys Glu Gly Ile Glu Ser Asp Glu Glu Ile Arg Arg Val Pro Glu
30 35 40 45

ttt gga gga gaa gct gtc gga aaa gaa act tcc ggt aga gaa tct gga
374

Phe Gly Gly Glu Ala Val Gly Lys Glu Thr Ser Gly Arg Glu Ser Gly
50 55 60

tcg gcg acc ggt cag gag cgg aca cag gcg act gtc gga gaa agt caa
422

Ser Ala Thr Gly Gln Glu Arg Thr Gln Ala Thr Val Gly Glu Ser Gln
65 70 75

agg aag cga ggg agg aca ccg gcg gag aaa gag aac aag cgg ctg aag
470

Arg Lys Arg Gly Arg Thr Pro Ala Glu Lys Glu Asn Lys Arg Leu Lys
80 85 90

agg ttg ttg agg aac aga gtt tca gct cag caa gca aga gag agg aaa
518

Arg Leu Leu Arg Asn Arg Val Ser Ala Gln Gln Ala Arg Glu Arg Lys
95 100 105

aag gct tac ttg agc gag ttg gaa aac aga gtg aaa gac ttg gag aac
566

Lys Ala Tyr Leu Ser Glu Leu Glu Asn Arg Val Lys Asp Leu Glu Asn
110 115 120 125

aaa aac tct gaa ctt gaa gag cga ctc tct act ctt cag aac gag aac
614

Lys Asn Ser Glu Leu Glu Glu Arg Leu Ser Thr Leu Gln Asn Glu Asn
130 135 140

cag atg ctt aga cat att ctg aag aac aca aca gga aac aag aga gga
662

Gln Met Leu Arg His Ile Leu Lys Asn Thr Thr Gly Asn Lys Arg Gly
145 150 155

ggt ggt ggt ggt tct aat gct gat gca agc ctt tga tctccttctt
708

Gly Gly Gly Gly Ser Asn Ala Asp Ala Ser Leu
160 165

cttcttgtgt tatatttttg tggataaaat ttacagagaa ttgtatcaat aattatcatg
768

ttaaaattat atgggatgtg agagctaata ttgcaattgt agaccaagtt ctcttaaaaa
828

aaaaaaaaaa aaaa
842

<210> 102 <211> 168 <212> PRT <213> Arabidopsis thaliana <400>
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Met Gln Glu Gln Ala Thr Ser Ser Leu Ala Ala Ser Ser Leu Pro Ser
1 5 10 15

Ser Ser Glu Arg Ser Ser Ser Ser Ala Pro His Leu Glu Ile Lys Glu
20 25 30

Gly Ile Glu Ser Asp Glu Glu Ile Arg Arg Val Pro Glu Phe Gly Gly
35 40 45

Glu Ala Val Gly Lys Glu Thr Ser Gly Arg Glu Ser Gly Ser Ala Thr
50 55 60

Gly Gln Glu Arg Thr Gln Ala Thr Val Gly Glu Ser Gln Arg Lys Arg

Leu Val Thr Met Glu Glu Val Trp Asn Asp Ile Asn Leu Ala Ser Ile
60 65 70 75

cac cac cta aac cga cac agc cct cat cca caa cac aac cac gag cca
 413
 His His Leu Asn Arg His Ser Pro His Pro Gln His Asn His Glu Pro
 80 85 90
 agg ttc agg ggc caa aac cac cac aac caa aac cct aac tca atc ttc
 461
 Arg Phe Arg Gly Gln Asn His His Asn Gln Asn Pro Asn Ser Ile Phe
 95 100 105
 caa gat ttt ctc aaa gga tct ttg aac cag gaa cca gca ccc aca agc
 509
 Gln Asp Phe Leu Lys Gly Ser Leu Asn Gln Glu Pro Ala Pro Thr Ser
 110 115 120
 cag acc acg ggt tct gcg cct aat ggc gat tcc acc acg gtc act gtt
 557
 Gln Thr Thr Gly Ser Ala Pro Asn Gly Asp Ser Thr Thr Val Thr Val
 125 130 135
 ctt tac agc tct cct ttt cca cct cct gca act gtt ctg agc ttg aat
 605
 Leu Tyr Ser Ser Pro Phe Pro Pro Pro Ala Thr Val Leu Ser Leu Asn
 140 145 150 155
 tcc ggc gct ggc ttc gag ttt ctc gat aac caa gat cct ctt gtt acc
 653
 Ser Gly Ala Gly Phe Glu Phe Leu Asp Asn Gln Asp Pro Leu Val Thr
 160 165 170
 tca aac tct aat ctt cat acc cac cat cac ctc tca aac gct cat gcc
 701
 Ser Asn Ser Asn Leu His Thr His His His Leu Ser Asn Ala His Ala
 175 180 185
 ttc aac acc tct ttc gag gct ctg gtt cca tcc agt tct ttt ggt aag
 749
 Phe Asn Thr Ser Phe Glu Ala Leu Val Pro Ser Ser Ser Phe Gly Lys
 190 195 200
 aaa aga ggc caa gat tcc aat gaa ggt tca ggg aat aga aga cat aag
 797
 Lys Arg Gly Gln Asp Ser Asn Glu Gly Ser Gly Asn Arg Arg His Lys
 205 210 215
 cgt atg atc aag aac aga gaa tct gca gct cgt tcc cgc gct agg aaa
 845
 Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys
 220 225 230 235
 cag gct tat aca aac gag tta gaa ctt gaa gtt gct cac ttg cag gca
 893
 Gln Ala Tyr Thr Asn Glu Leu Glu Leu Glu Val Ala His Leu Gln Ala
 240 245 250
 gaa aat gca aga ctc aag aga caa caa gat caa aaa atg gct gca gca
 941
 Glu Asn Ala Arg Leu Lys Arg Gln Gln Asp Gln Lys Met Ala Ala Ala
 255 260 265

att cag caa ccc aaa aag aac aca ctt caa cgg tct tcc aca gct cca
989

Ile Gln Gln Pro Lys Lys Asn Thr Leu Gln Arg Ser Ser Thr Ala Pro
270 275 280

ttt tga gaaatctaca agtccttggt tctcttttgg ggattgagat tgtctcatga
1045
Phe

agaagtga aaatggcaaa agtttgtagc cttttttatt agctataagt ataactaagc
1105

ctaaaattgt agaactaaga tattgttaggg gaaaaaagaa gatgtaaaac aaaagacccg
1165

gaaagagaaa aggatctttc aatttcctaa ggcacaggaa cacctgtcct gggtcctctc
1225

ttaatgttct gtcgttttcc tatgcaaacc cttttttcac ttctgtacta acttatactt
1285

gtattcttg
1294

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104

Met Leu Ser Ser Ala Lys His Gln Arg Asn His Arg Leu Ser Ala Thr
1 5 10 15

Asn Lys Asn Gln Thr Leu Thr Lys Val Ser Ser Ile Ser Ser Ser Ser
20 25 30

Pro Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Ser Pro Leu
35 40 45

Pro Ser Gln Asp Ser Gln Ala Gln Lys Arg Ser Leu Val Thr Met Glu
50 55 60

Glu Val Trp Asn Asp Ile Asn Leu Ala Ser Ile His His Leu Asn Arg
65 70 75 80

His Ser Pro His Pro Gln His Asn His Glu Pro Arg Phe Arg Gly Gln
85 90 95

Asn His His Asn Gln Asn Pro Asn Ser Ile Phe Gln Asp Phe Leu Lys
100 105 110

Gly Ser Leu Asn Gln Glu Pro Ala Pro Thr Ser Gln Thr Thr Gly Ser
115 120 125

Ala Pro Asn Gly Asp Ser Thr Thr Val Thr Val Leu Tyr Ser Ser Pro
 130 135 140

Phe Pro Pro Pro Ala Thr Val Leu Ser Leu Asn Ser Gly Ala Gly Phe
 145 150 155 160

Glu Phe Leu Asp Asn Gln Asp Pro Leu Val Thr Ser Asn Ser Asn Leu
 165 170 175

His Thr His His His Leu Ser Asn Ala His Ala Phe Asn Thr Ser Phe
 180 185 190

Glu Ala Leu Val Pro Ser Ser Ser Phe Gly Lys Lys Arg Gly Gln Asp
 195 200 205

Ser Asn Glu Gly Ser Gly Asn Arg Arg His Lys Arg Met Ile Lys Asn
 210 215 220

Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Asn
 225 230 235 240

Glu Leu Glu Leu Glu Val Ala His Leu Gln Ala Glu Asn Ala Arg Leu
 245 250 255

Lys Arg Gln Gln Asp Gln Lys Met Ala Ala Ala Ile Gln Gln Pro Lys
 260 265 270

Lys Asn Thr Leu Gln Arg Ser Ser Thr Ala Pro Phe
 275 280

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gca aag cat aat aag atc aac aac cat agt gcc ttt tca att tcc tct
 102

Ala Lys His Asn Lys Ile Asn Asn His Ser Ala Phe Ser Ile Ser Ser
 5 10 15 20

tca tca tca tca tta tca aca tca tcc tcc cta ggc cat aac aaa tct
 150

Ser Ser Ser Ser Leu Ser Thr Ser Ser Ser Leu Gly His Asn Lys Ser
 25 30 35

caa gtc acc atg gaa gaa gta tgg aaa gaa atc aac ctt ggt tca ctt
 198

Gln Val Thr Met Glu Glu Val Trp Lys Glu Ile Asn Leu Gly Ser Leu
 40 45 50
 cac tac cat cgg caa cta aac att ggt cat gaa cca atg tta aag aac
 246
 His Tyr His Arg Gln Leu Asn Ile Gly His Glu Pro Met Leu Lys Asn
 55 60 65
 caa aac cct aat aac tcc atc ttt caa gat ttc ctc aac atg cct ctg
 294
 Gln Asn Pro Asn Asn Ser Ile Phe Gln Asp Phe Leu Asn Met Pro Leu
 70 75 80
 aat caa cca cca cca cca cca cca cct tcc tct tcc acc att gtc
 342
 Asn Gln Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser Ser Thr Ile Val
 85 90 95 100
 act gct ctc tat ggc tct ctg cct ctt ccg cct cct gcc act gtc ctc
 390
 Thr Ala Leu Tyr Gly Ser Leu Pro Leu Pro Pro Pro Ala Thr Val Leu
 105 110 115
 agc tta aac tcc ggt gtt gga ttc gag ttt ctt gat acc aca gaa aat
 438
 Ser Leu Asn Ser Gly Val Gly Phe Glu Phe Leu Asp Thr Thr Glu Asn
 120 125 130
 ctt ctt gct tct aac cct cgc tcc ttt gag gaa tct gca aag ttt ggt
 486
 Leu Leu Ala Ser Asn Pro Arg Ser Phe Glu Glu Ser Ala Lys Phe Gly
 135 140 145
 tgt ctt ggt aag aaa aga ggc caa gat tct gat gat act aga gga gac
 534
 Cys Leu Gly Lys Lys Arg Gly Gln Asp Ser Asp Asp Thr Arg Gly Asp
 150 155 160
 aga agg tat aag cgt atg atc aag aac aga gaa tct gct gct cgt tca
 582
 Arg Arg Tyr Lys Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg Ser
 165 170 175 180
 agg gct agg aag cag gca tat aca aac gaa ctt gag ctt gaa att gct
 630
 Arg Ala Arg Lys Gln Ala Tyr Thr Asn Glu Leu Glu Leu Glu Ile Ala
 185 190 195
 cac ttg cag aca gag aat gca aga ctc aag ata caa caa gag cag ctg
 678
 His Leu Gln Thr Glu Asn Ala Arg Leu Lys Ile Gln Gln Glu Gln Leu
 200 205 210
 aaa ata gcc gaa gca act caa aac caa gta aag aaa aca cta caa cgg
 726
 Lys Ile Ala Glu Ala Thr Gln Asn Gln Val Lys Lys Thr Leu Gln Arg
 215 220 225
 tct tcc aca gct cca ttt tga gaaaaatcta ctatttcttt ttgggggagt
 777
 Ser Ser Thr Ala Pro Phe

230

ttcaagtgtt tcttatgaag atgagaaaaa cagaaaaagt ttgtacattt tagctaagtt
837

aaatttgtgg tggttaagtaa tgtaaaagaa aagtgtgtgt agaagaaaag tgtctagaaa
897

aagaaagcaa ctaactttct tcttcttctc tggtttccta tcaactcttt tgacttttgt
957

actttttttc ttctctactt aacctctatt attgtaatgc caagtcaagt ccttatctag
1017

ctagtacatg agtttctgtt ttacttggtt aagccat
1054

<210> 106 <211> 234 <212> PRT <213> Arabidopsis thaliana <400>
106

Met Leu Ser Ser Ala Lys His Asn Lys Ile Asn Asn His Ser Ala Phe
1 5 10 15

Ser Ile Ser Ser Ser Ser Ser Ser Leu Ser Thr Ser Ser Ser Leu Gly
20 25 30

His Asn Lys Ser Gln Val Thr Met Glu Glu Val Trp Lys Glu Ile Asn
35 40 45

Leu Gly Ser Leu His Tyr His Arg Gln Leu Asn Ile Gly His Glu Pro
50 55 60

Met Leu Lys Asn Gln Asn Pro Asn Asn Ser Ile Phe Gln Asp Phe Leu
65 70 75 80

Asn Met Pro Leu Asn Gln Pro Pro Pro Pro Pro Pro Pro Ser Ser
85 90 95

Ser Thr Ile Val Thr Ala Leu Tyr Gly Ser Leu Pro Leu Pro Pro Pro
100 105 110

Ala Thr Val Leu Ser Leu Asn Ser Gly Val Gly Phe Glu Phe Leu Asp
115 120 125

Thr Thr Glu Asn Leu Leu Ala Ser Asn Pro Arg Ser Phe Glu Glu Ser
130 135 140

Ala Lys Phe Gly Cys Leu Gly Lys Lys Arg Gly Gln Asp Ser Asp Asp
145 150 155 160

Thr Arg Gly Asp Arg Arg Tyr Lys Arg Met Ile Lys Asn Arg Glu Ser
 165 170 175

Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Asn Glu Leu Glu
 180 185 190

Leu Glu Ile Ala His Leu Gln Thr Glu Asn Ala Arg Leu Lys Ile Gln
 195 200 205

Gln Glu Gln Leu Lys Ile Ala Glu Ala Thr Gln Asn Gln Val Lys Lys
 210 215 220

Thr Leu Gln Arg Ser Ser Thr Ala Pro Phe
 225 230

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aatgttttag cttaaactgc tttttttttg ttgttggtgt a atg ata tca cag aga
 116

Met Ile Ser Gln Arg
 1 5

gaa gaa aga gaa gag aag aag cag aga gtg atg gga gat aag aaa ttg
 164
 Glu Glu Arg Glu Glu Lys Lys Gln Arg Val Met Gly Asp Lys Lys Leu
 10 15 20

att tca tct tct tct tct tcc tcg gtt tac gat act cgt atc aat cat
 212
 Ile Ser Ser Ser Ser Ser Ser Ser Val Tyr Asp Thr Arg Ile Asn His
 25 30 35

cat ctt cat cat cct ccg tct tct tcc gac gaa atc tct cag ttt ctc
 260
 His Leu His His Pro Pro Ser Ser Ser Asp Glu Ile Ser Gln Phe Leu
 40 45 50

cgg cat att ttc gac cgt tct tct cct tta cct tct tac tac tcc ccg
 308
 Arg His Ile Phe Asp Arg Ser Ser Pro Leu Pro Ser Tyr Tyr Ser Pro
 55 60 65

gcg acg act aca acg acg gcg tct ttg att ggt gtg cac ggg agc ggt
 356
 Ala Thr Thr Thr Thr Thr Ala Ser Leu Ile Gly Val His Gly Ser Gly
 70 75 80 85

gac cca cat gca gat aac tcg aga agt ctc gtt tct cat cat cca ccg
 404
 Asp Pro His Ala Asp Asn Ser Arg Ser Leu Val Ser His His Pro Pro
 90 95 100

tca gat tct gtg ctt atg tcg aaa cgt gtc gga gat ttc tct gag gtt
 452
 Ser Asp Ser Val Leu Met Ser Lys Arg Val Gly Asp Phe Ser Glu Val
 105 110 115

tta atc ggc gga gga tca ggc tca gcc gcc gcg tgt ttt ggt ttc tcc
 500
 Leu Ile Gly Gly Gly Ser Gly Ser Ala Ala Ala Cys Phe Gly Phe Ser
 120 125 130

ggt ggt ggt aat aat aac aac gtt caa gga aat agc tct ggg act cga
 548
 Gly Gly Gly Asn Asn Asn Asn Val Gln Gly Asn Ser Ser Gly Thr Arg
 135 140 145

gta tcg tct tct tcc gtt gga gct agt ggc aac gag aca gat gag tat
 596
 Val Ser Ser Ser Ser Val Gly Ala Ser Gly Asn Glu Thr Asp Glu Tyr
 150 155 160 165

gac tgt gaa agc gag gaa gga gga gaa gct gta gtt gat gaa gct ccc
 644
 Asp Cys Glu Ser Glu Glu Gly Gly Glu Ala Val Val Asp Glu Ala Pro
 170 175 180

tct tcc aag tca ggt cct tct tct cgt agt tca tct aaa aga tgc aga
 692
 Ser Ser Lys Ser Gly Pro Ser Ser Arg Ser Ser Ser Lys Arg Cys Arg
 185 190 195

gct gct gaa gtt cat aat ctc tct gag aag agg agg aga agt aga att
 740
 Ala Ala Glu Val His Asn Leu Ser Glu Lys Arg Arg Arg Ser Arg Ile
 200 205 210

aat gaa aaa atg aaa gct tta caa agt ctc atc cct aat tca aat aag
 788
 Asn Glu Lys Met Lys Ala Leu Gln Ser Leu Ile Pro Asn Ser Asn Lys
 215 220 225

acg gat aag gct tca atg ctt gat gaa gcc att gag tat ctg aaa cag
 836
 Thr Asp Lys Ala Ser Met Leu Asp Glu Ala Ile Glu Tyr Leu Lys Gln
 230 235 240 245

ctt cag ctc caa gtt cag atg ttg act atg aga aat gga ata aac ttg
 884
 Leu Gln Leu Gln Val Gln Met Leu Thr Met Arg Asn Gly Ile Asn Leu
 250 255 260

cat cct ttg tgt tta cct gga act aca tta cac cca ttg caa ctc tct
 932
 His Pro Leu Cys Leu Pro Gly Thr Thr Leu His Pro Leu Gln Leu Ser
 265 270 275

cag att cga ccc cct gaa gca acc aat gat cct ctg ctt aat cat acc
 980
 Gln Ile Arg Pro Pro Glu Ala Thr Asn Asp Pro Leu Leu Asn His Thr
 280 285 290

aat cag ttt gct tcg act tct aat gca ccg gaa atg atc aat act gtg
1028

Asn Gln Phe Ala Ser Thr Ser Asn Ala Pro Glu Met Ile Asn Thr Val
295 300 305

gct tct tca tac gct ttg gaa cct tct att cgc agt cac ttt gga cct
1076

Ala Ser Ser Tyr Ala Leu Glu Pro Ser Ile Arg Ser His Phe Gly Pro
310 315 320 325

ttc cct ctc ctt act tca ccc gtg gag atg agt cgg gaa ggt ggg tta
1124

Phe Pro Leu Leu Thr Ser Pro Val Glu Met Ser Arg Glu Gly Gly Leu
330 335 340

act cat cca agg ttg aac att ggt cat tcc aac gca aac ata acc ggg
1172

Thr His Pro Arg Leu Asn Ile Gly His Ser Asn Ala Asn Ile Thr Gly
345 350 355

gaa caa gct ctg ttt gat gga caa cct gac cta aaa gat cga att act
1220

Glu Gln Ala Leu Phe Asp Gly Gln Pro Asp Leu Lys Asp Arg Ile Thr
360 365 370

tga acagtgtccc aacttcggga tctctatgtg ttcttgtttc ttagaacgca
1273

agccataaag ctgtctgac
1292

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108

Met Ile Ser Gln Arg Glu Glu Arg Glu Glu Lys Lys Gln Arg Val Met
1 5 10 15

Gly Asp Lys Lys Leu Ile Ser Ser Ser Ser Ser Ser Ser Val Tyr Asp
20 25 30

Thr Arg Ile Asn His His Leu His His Pro Pro Ser Ser Ser Asp Glu
35 40 45

Ile Ser Gln Phe Leu Arg His Ile Phe Asp Arg Ser Ser Pro Leu Pro
50 55 60

Ser Tyr Tyr Ser Pro Ala Thr Thr Thr Thr Thr Ala Ser Leu Ile Gly
65 70 75 80

Val His Gly Ser Gly Asp Pro His Ala Asp Asn Ser Arg Ser Leu Val
85 90 95

Ser His His Pro Pro Ser Asp Ser Val Leu Met Ser Lys Arg Val Gly
100 105 110

Asp Phe Ser Glu Val Leu Ile Gly Gly Gly Ser Gly Ser Ala Ala Ala
 115 120 125

Cys Phe Gly Phe Ser Gly Gly Gly Asn Asn Asn Asn Val Gln Gly Asn
 130 135 140

Ser Ser Gly Thr Arg Val Ser Ser Ser Ser Val Gly Ala Ser Gly Asn
 145 150 155 160

Glu Thr Asp Glu Tyr Asp Cys Glu Ser Glu Glu Gly Gly Glu Ala Val
 165 170 175

Val Asp Glu Ala Pro Ser Ser Lys Ser Gly Pro Ser Ser Arg Ser Ser
 180 185 190

Ser Lys Arg Cys Arg Ala Ala Glu Val His Asn Leu Ser Glu Lys Arg
 195 200 205

Arg Arg Ser Arg Ile Asn Glu Lys Met Lys Ala Leu Gln Ser Leu Ile
 210 215 220

Pro Asn Ser Asn Lys Thr Asp Lys Ala Ser Met Leu Asp Glu Ala Ile
 225 230 235 240

Glu Tyr Leu Lys Gln Leu Gln Leu Gln Val Gln Met Leu Thr Met Arg
 245 250 255

Asn Gly Ile Asn Leu His Pro Leu Cys Leu Pro Gly Thr Thr Leu His
 260 265 270

Pro Leu Gln Leu Ser Gln Ile Arg Pro Pro Glu Ala Thr Asn Asp Pro
 275 280 285

Leu Leu Asn His Thr Asn Gln Phe Ala Ser Thr Ser Asn Ala Pro Glu
 290 295 300

Met Ile Asn Thr Val Ala Ser Ser Tyr Ala Leu Glu Pro Ser Ile Arg
 305 310 315 320

Ser His Phe Gly Pro Phe Pro Leu Leu Thr Ser Pro Val Glu Met Ser
 325 330 335

Arg Glu Gly Gly Leu Thr His Pro Arg Leu Asn Ile Gly His Ser Asn
 340 345 350

Ala Asn Ile Thr Gly Glu Gln Ala Leu Phe Asp Gly Gln Pro Asp Leu
 355 360 365

Lys Asp Arg Ile Thr
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 57

Met Asp Leu Ser
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gta ctt gat agg ctt aag tgg ctg caa cag caa caa atg gtt tca cct
 105
 Val Leu Asp Arg Leu Lys Trp Leu Gln Gln Gln Gln Met Val Ser Pro
 5 10 15 20

gag ttt ctt cag ata ctt ggc tca gat ggg aga gaa gag ctc aaa aga
 153
 Glu Phe Leu Gln Ile Leu Gly Ser Asp Gly Arg Glu Glu Leu Lys Arg
 25 30 35

gtt gag agt tac ttg gga aac aac aat gat gag ctg cag agt ttc aga
 201
 Val Glu Ser Tyr Leu Gly Asn Asn Asn Asp Glu Leu Gln Ser Phe Arg
 40 45 50

cat ttt ccc gaa ttc gga ccg gat tat gat act act gat ggc tgc att
 249
 His Phe Pro Glu Phe Gly Pro Asp Tyr Asp Thr Thr Asp Gly Cys Ile
 55 60 65

tct agg aca agt agc ttc cat atg gag cca gtg aag aat aat gga cac
 297
 Ser Arg Thr Ser Ser Phe His Met Glu Pro Val Lys Asn Asn Gly His
 70 75 80

agc aga gcc att acc ttg cag aac aag aga aaa cca gag ggt aag aca
 345
 Ser Arg Ala Ile Thr Leu Gln Asn Lys Arg Lys Pro Glu Gly Lys Thr
 85 90 95 100

gaa aag aga gag aag aag aag atc aaa gca gag gat gaa aca gag cca
 393
 Glu Lys Arg Glu Lys Lys Lys Ile Lys Ala Glu Asp Glu Thr Glu Pro
 105 110 115

agc atg aaa ggg aaa tca aac atg agt aac aca gag aca tct tca gaa
 441
 Ser Met Lys Gly Lys Ser Asn Met Ser Asn Thr Glu Thr Ser Ser Glu
 120 125 130

att cag aaa cca gat tac att cat gtt agg gct aga cga ggt gaa gcc
 489
 Ile Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg Arg Gly Glu Ala

135 140 145
 acc gac aga cat agc tta gca gag agg gca aga aga gaa aag ata agc
 537
 Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser
 150 155 160
 aag aag atg aaa tgt cta caa gat att gtt cct gga tgc aac aaa gtt
 585
 Lys Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val
 165 170 175 180
 act gga aaa gct ggt atg ctt gat gag atc atc aac tat gtc caa tct
 633
 Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser
 185 190 195
 ctg caa caa caa gtc gag ttc ttg tcg atg aaa ctc tct gtc ata aat
 681
 Leu Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu Ser Val Ile Asn
 200 205 210
 cca gaa ctt gag tgt cat atc gat gat tta tcc gca aaa cag ttt cag
 729
 Pro Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala Lys Gln Phe Gln
 215 220 225
 gct tac ttc aca ggt cct cca gaa ggt gac tcg aag cag tca atc atg
 777
 Ala Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys Gln Ser Ile Met
 230 235 240
 gcg gat ttt cgg tct ttt cca tta cat cag caa gga tct tta gat tac
 825
 Ala Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly Ser Leu Asp Tyr
 245 250 255 260
 tca gtc ata aac tca gac cac acc aca tct ctc ggc gct aaa gat cat
 873
 Ser Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly Ala Lys Asp His
 265 270 275
 aca tca tca agc tgg gaa act cac tca cag tgt ctt tac aac agc ttg
 921
 Thr Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu Tyr Asn Ser Leu
 280 285 290
 aga acc gat tct gtt tcc aat ttc ttc agc ctc aag taa aaaaattagg
 970
 Arg Thr Asp Ser Val Ser Asn Phe Phe Ser Leu Lys
 295 300
 gatagcctca ttaaaaaaat cgcggttttt tgttggtgtc ttatccattt atctatctta
 1030
 tctgaaattt gaaccagaaa gacagaggaa accaatccaa agatctttct caatctatta
 1090
 tcttcataca aatatagtga tttacatata ttccagggga tatgtatatg tgtagaagaa
 1150

agagaaaaaa ctcttggtggt catagcaatt cctttttttg tacattgtag aatcaaactc
1210

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1270

ccttttggcc ctgggatcaa ca
1292

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Met Asp Leu Ser Val Leu Asp Arg Leu Lys Trp Leu Gln Gln Gln Gln
1 5 10 15

Met Val Ser Pro Glu Phe Leu Gln Ile Leu Gly Ser Asp Gly Arg Glu
20 25 30

Glu Leu Lys Arg Val Glu Ser Tyr Leu Gly Asn Asn Asn Asp Glu Leu
35 40 45

Gln Ser Phe Arg His Phe Pro Glu Phe Gly Pro Asp Tyr Asp Thr Thr
50 55 60

Asp Gly Cys Ile Ser Arg Thr Ser Ser Phe His Met Glu Pro Val Lys
65 70 75 80

Asn Asn Gly His Ser Arg Ala Ile Thr Leu Gln Asn Lys Arg Lys Pro
85 90 95

Glu Gly Lys Thr Glu Lys Arg Glu Lys Lys Lys Ile Lys Ala Glu Asp
100 105 110

Glu Thr Glu Pro Ser Met Lys Gly Lys Ser Asn Met Ser Asn Thr Glu
115 120 125

Thr Ser Ser Glu Ile Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg
130 135 140

Arg Gly Glu Ala Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg
145 150 155 160

Glu Lys Ile Ser Lys Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly
165 170 175

Cys Asn Lys Val Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn
180 185 190

Tyr Val Gln Ser Leu Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu
 195 200 205

Ser Val Ile Asn Pro Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala
 210 215 220

Lys Gln Phe Gln Ala Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys
 225 230 235 240

Gln Ser Ile Met Ala Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly
 245 250 255

Ser Leu Asp Tyr Ser Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly
 260 265 270

Ala Lys Asp His Thr Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu
 275 280 285

Tyr Asn Ser Leu Arg Thr Asp Ser Val Ser Asn Phe Phe Ser Leu Lys
 290 295 300

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ttcacttcca tcaaaactct ctctctatat ctctctctct atatatctct ctctatatct
 120

ctctctctct tcactctctc tttctttcaa a atg gaa aaa ctc atg gtt ccg
 172

Met Glu Lys Leu Met Val Pro
 1 5

aca tgg aga ccc gac ccg gtt tac cgt cca ccg gaa aca cca ctc gaa
 220

Thr Trp Arg Pro Asp Pro Val Tyr Arg Pro Pro Glu Thr Pro Leu Glu
 10 15 20

ccg atg gag ttt tta gct cgt tca tgg agc gtc tct gct ctc gaa gtc
 268

Pro Met Glu Phe Leu Ala Arg Ser Trp Ser Val Ser Ala Leu Glu Val
 25 30 35

tcc aag gct cta aca cca ccc aac cct cag att ctc ctc tcc aaa acc
 316

Ser Lys Ala Leu Thr Pro Pro Asn Pro Gln Ile Leu Leu Ser Lys Thr
 40 45 50 55

gaa gaa gaa gaa gaa gaa gaa ccc atc tcc tct gtc gta gac ggc gac
 364

Glu Glu Glu Glu Glu Glu Glu Pro Ile Ser Ser Val Val Asp Gly Asp

	60		65		70
ggc gac acg gaa gac acc gga ctt gtc acc gga aac cca ttc tcc ttc					
412					
Gly Asp Thr Glu Asp Thr Gly Leu Val Thr Gly Asn Pro Phe Ser Phe					
	75		80		85
gct tgt tca gaa act tct caa atg gtc atg gat cgt atc ttg tct cac					
460					
Ala Cys Ser Glu Thr Ser Gln Met Val Met Asp Arg Ile Leu Ser His					
	90		95		100
tct caa gaa gta tca cca aga aca tct ggt cgg cta tct cac agt agt					
508					
Ser Gln Glu Val Ser Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser					
	105		110		115
ggt cca ctt aat ggt tct ttg acc gac agt cct cct gtg tct cct ccc					
556					
Gly Pro Leu Asn Gly Ser Leu Thr Asp Ser Pro Pro Val Ser Pro Pro					
	120		125		130
gaa tcc gac gac att aag caa ttt tgc aga gcg aac aaa aat tca ttg					
604					
Glu Ser Asp Asp Ile Lys Gln Phe Cys Arg Ala Asn Lys Asn Ser Leu					
	140		145		150
aac agt gta aat tct cag ttc cgt tca acg gcg gca act ccg gga cct					
652					
Asn Ser Val Asn Ser Gln Phe Arg Ser Thr Ala Ala Thr Pro Gly Pro					
	155		160		165
ata acc gct aca gct aca cag tcc aag acg gtg gga cgg tgg ctt aag					
700					
Ile Thr Ala Thr Ala Thr Gln Ser Lys Thr Val Gly Arg Trp Leu Lys					
	170		175		180
gac cgg aga gag aaa aag aaa gag gag act cgg gct cat aac gct cag					
748					
Asp Arg Arg Glu Lys Lys Lys Glu Glu Thr Arg Ala His Asn Ala Gln					
	185		190		195
att cac gct gct gtc tct gtc gcc ggc gtt gct gca gct gtt gct gct					
796					
Ile His Ala Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala					
	200		205		210
att gca gca gcc acc gct gcg tct tct agc tgt ggt aag gat gag cag					
844					
Ile Ala Ala Ala Thr Ala Ala Ser Ser Ser Cys Gly Lys Asp Glu Gln					
	220		225		230
atg gct aaa act gac atg gcc gtt gct tct gct gcg acc ctt gtg gct					
892					
Met Ala Lys Thr Asp Met Ala Val Ala Ser Ala Ala Thr Leu Val Ala					
	235		240		245
gct cag tgt gtg gaa gct gct gaa gtt atg gga gct gag aga gag tat					
940					
Ala Gln Cys Val Glu Ala Ala Glu Val Met Gly Ala Glu Arg Glu Tyr					
	250		255		260

ttg gct tct gtt gtt agc tcc gcc gtc aat gtt cgt tct gcc gga gat
 988
 Leu Ala Ser Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp
 265 270 275

att atg act ctc acc gcc gga gca gct aca gct tta aga gga gtg caa
 1036
 Ile Met Thr Leu Thr Ala Gly Ala Ala Thr Ala Leu Arg Gly Val Gln
 280 285 290 295

aca ttg aag gca agg gca atg aag gaa gtg tgg aac ata gca tca gtg
 1084
 Thr Leu Lys Ala Arg Ala Met Lys Glu Val Trp Asn Ile Ala Ser Val
 300 305 310

ata cca atg gat aaa gga ctc act tct aca gga gga agc agc aat aat
 1132
 Ile Pro Met Asp Lys Gly Leu Thr Ser Thr Gly Gly Ser Ser Asn Asn
 315 320 325

gtt aat ggt agc aat gga agc tca agc agt agt cac agt ggt gaa ctt
 1180
 Val Asn Gly Ser Asn Gly Ser Ser Ser Ser Ser His Ser Gly Glu Leu
 330 335 340

gta caa cag gag aat ttc ttg gga act tgt agt aga gaa tgg ctc gct
 1228
 Val Gln Gln Glu Asn Phe Leu Gly Thr Cys Ser Arg Glu Trp Leu Ala
 345 350 355

aga ggt tgt gaa ctc ctc aaa cgc act cgc aaa ggt gat ctc cac tgg
 1276
 Arg Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His Trp
 360 365 370 375

aag ata gta tct gtt tac atc aac aaa atg aat cag gtt atg ttg aag
 1324
 Lys Ile Val Ser Val Tyr Ile Asn Lys Met Asn Gln Val Met Leu Lys
 380 385 390

atg aag agc agg cat gtt gga gga acc ttc acc aag aag aaa aag aac
 1372
 Met Lys Ser Arg His Val Gly Gly Thr Phe Thr Lys Lys Lys Lys Asn
 395 400 405

att gtg ctt gat gtg atc aag aat gtc ccg gcc tgg cct gga cga cat
 1420
 Ile Val Leu Asp Val Ile Lys Asn Val Pro Ala Trp Pro Gly Arg His
 410 415 420

ttg cta gag gga gga gat gat cta aga tac ttc ggt ttg aag acg gtt
 1468
 Leu Leu Glu Gly Gly Asp Asp Leu Arg Tyr Phe Gly Leu Lys Thr Val
 425 430 435

atg cga ggt gat gtt gaa ttc gag gtc aag agc caa agg gaa tat gaa
 1516
 Met Arg Gly Asp Val Glu Phe Glu Val Lys Ser Gln Arg Glu Tyr Glu
 440 445 450 455

atg tgg aca caa ggt gtc tca agg ctt ctt gtt ctt gct gct gag agg
1564

Met Trp Thr Gln Gly Val Ser Arg Leu Leu Val Leu Ala Ala Glu Arg
460 465 470

aag ttt agg atg tga ataaacgttc aatggctgct tggtttaagt gtgagttttt
1619

Lys Phe Arg Met
475

ttttaactta tgtgggtcaaa tttcattagt aggggttctt ttaaggtaat ggtttttttg
1679

gttgggtata ggataaaatg gacctaccag tcaagggtgag gaagcatttg ggtaaacaaa
1739

acttagtggg ggtgatctgt aatatctatg ttcttagttt ttttttggtt gttgggtggtc
1799

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1857

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112

Met Glu Lys Leu Met Val Pro Thr Trp Arg Pro Asp Pro Val Tyr Arg
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Pro Pro Glu Thr Pro Leu Glu Pro Met Glu Phe Leu Ala Arg Ser Trp
20 25 30

Ser Val Ser Ala Leu Glu Val Ser Lys Ala Leu Thr Pro Pro Asn Pro
35 40 45

Gln Ile Leu Leu Ser Lys Thr Glu Glu Glu Glu Glu Glu Glu Pro Ile
50 55 60

Ser Ser Val Val Asp Gly Asp Gly Asp Thr Glu Asp Thr Gly Leu Val
65 70 75 80

Thr Gly Asn Pro Phe Ser Phe Ala Cys Ser Glu Thr Ser Gln Met Val
85 90 95

Met Asp Arg Ile Leu Ser His Ser Gln Glu Val Ser Pro Arg Thr Ser
100 105 110

Gly Arg Leu Ser His Ser Ser Gly Pro Leu Asn Gly Ser Leu Thr Asp
115 120 125

Ser Pro Pro Val Ser Pro Pro Glu Ser Asp Asp Ile Lys Gln Phe Cys
130 135 140

Arg Ala Asn Lys Asn Ser Leu Asn Ser Val Asn Ser Gln Phe Arg Ser
 145 150 155 160
 Thr Ala Ala Thr Pro Gly Pro Ile Thr Ala Thr Ala Thr Gln Ser Lys
 165 170 175
 Thr Val Gly Arg Trp Leu Lys Asp Arg Arg Glu Lys Lys Lys Glu Glu
 180 185 190
 Thr Arg Ala His Asn Ala Gln Ile His Ala Ala Val Ser Val Ala Gly
 195 200 205
 Val Ala Ala Ala Val Ala Ala Ile Ala Ala Ala Thr Ala Ala Ser Ser
 210 215 220
 Ser Cys Gly Lys Asp Glu Gln Met Ala Lys Thr Asp Met Ala Val Ala
 225 230 235 240
 Ser Ala Ala Thr Leu Val Ala Ala Gln Cys Val Glu Ala Ala Glu Val
 245 250 255
 Met Gly Ala Glu Arg Glu Tyr Leu Ala Ser Val Val Ser Ser Ala Val
 260 265 270
 Asn Val Arg Ser Ala Gly Asp Ile Met Thr Leu Thr Ala Gly Ala Ala
 275 280 285
 Thr Ala Leu Arg Gly Val Gln Thr Leu Lys Ala Arg Ala Met Lys Glu
 290 295 300
 Val Trp Asn Ile Ala Ser Val Ile Pro Met Asp Lys Gly Leu Thr Ser
 305 310 315 320
 Thr Gly Gly Ser Ser Asn Asn Val Asn Gly Ser Asn Gly Ser Ser Ser
 325 330 335
 Ser Ser His Ser Gly Glu Leu Val Gln Gln Glu Asn Phe Leu Gly Thr
 340 345 350
 Cys Ser Arg Glu Trp Leu Ala Arg Gly Cys Glu Leu Leu Lys Arg Thr
 355 360 365
 Arg Lys Gly Asp Leu His Trp Lys Ile Val Ser Val Tyr Ile Asn Lys
 370 375 380

Met Asn Gln Val Met Leu Lys Met Lys Ser Arg His Val Gly Gly Thr
385 390 395 400

Phe Thr Lys Lys Lys Lys Asn Ile Val Leu Asp Val Ile Lys Asn Val
405 410 415

Pro Ala Trp Pro Gly Arg His Leu Leu Glu Gly Gly Asp Asp Leu Arg
420 425 430

Tyr Phe Gly Leu Lys Thr Val Met Arg Gly Asp Val Glu Phe Glu Val
435 440 445

Lys Ser Gln Arg Glu Tyr Glu Met Trp Thr Gln Gly Val Ser Arg Leu
450 455 460

Leu Val Leu Ala Ala Glu Arg Lys Phe Arg Met
465 470 475

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Met Glu Ile Met Arg Pro Gly Val Ser Glu Asn Thr Leu Lys Gly Lys
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ata aga atc aca acg cgg tgc atg tgg ctt gac aaa gga aga ctt tta
96
Ile Arg Ile Thr Thr Arg Cys Met Trp Leu Asp Lys Gly Arg Leu Leu
20 25 30
gat gca ctt cac aaa gca gct cat gct gct cta tca agt tgt cct gtg
144
Asp Ala Leu His Lys Ala Ala His Ala Ala Leu Ser Ser Cys Pro Val
35 40 45
aca tgt ccc ttg tct cac atg gaa aga aca gtc tcc gaa gtc ctg agg
192
Thr Cys Pro Leu Ser His Met Glu Arg Thr Val Ser Glu Val Leu Arg
50 55 60
aag att gta agg aag tac agt ggt aaa agg cct gaa gtc atc gct ata
240
Lys Ile Val Arg Lys Tyr Ser Gly Lys Arg Pro Glu Val Ile Ala Ile
65 70 75 80
gcc act gag aat cca atg gct gtc cga gct gat gag gtc agt gcg aga
288
Ala Thr Glu Asn Pro Met Ala Val Arg Ala Asp Glu Val Ser Ala Arg
85 90 95
ctg tct ggt gat cca agt gtt ggt tct gga gtt gca gct tta agg aaa
336
Leu Ser Gly Asp Pro Ser Val Gly Ser Gly Val Ala Ala Leu Arg Lys

100	105	110
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Val Val Glu Gly Asn Asp Lys Arg Ser Arg Ala Lys Lys Ala Pro Ser 115 120 125		
caa gaa gct tcc ccc aaa gaa gta gat cgc act ttg gaa gat gat atc 432		
Gln Glu Ala Ser Pro Lys Glu Val Asp Arg Thr Leu Glu Asp Asp Ile 130 135 140		
att gat agt gca aga cta ctg gct gaa gaa gaa act gcg gca tca aca 480		
Ile Asp Ser Ala Arg Leu Leu Ala Glu Glu Glu Thr Ala Ala Ser Thr 145 150 155 160		
tac acg gaa gaa gtt gat acg ccc gtt ggg agt tct tca gaa gag tca 528		
Tyr Thr Glu Glu Val Asp Thr Pro Val Gly Ser Ser Ser Glu Glu Ser 165 170 175		
gac gat ttt tgg aaa tca ttc atc aat cca tca tcg tca cct tca ccg 576		
Asp Asp Phe Trp Lys Ser Phe Ile Asn Pro Ser Ser Ser Pro Ser Pro 180 185 190		
agt gaa aca gaa aat atg aat aag gta gct gat acg gag cct aaa gca 624		
Ser Glu Thr Glu Asn Met Asn Lys Val Ala Asp Thr Glu Pro Lys Ala 195 200 205		
gag ggt aag gaa aac agc aga gac gac gat gaa tta gct gat gct tca 672		
Glu Gly Lys Glu Asn Ser Arg Asp Asp Asp Glu Leu Ala Asp Ala Ser 210 215 220		
gat tct gaa acc aag tca tca cca aaa cgt gtg agg aag aac aaa tgg 720		
Asp Ser Glu Thr Lys Ser Ser Pro Lys Arg Val Arg Lys Asn Lys Trp 225 230 235 240		
aaa ccg gag gag ata aag aag gta atc aga atg cga gga gag ctg cac 768		
Lys Pro Glu Glu Ile Lys Lys Val Ile Arg Met Arg Gly Glu Leu His 245 250 255		
agt aga ttt caa gtg gtg aaa ggt aga atg gca ttg tgg gaa gag atc 816		
Ser Arg Phe Gln Val Val Lys Gly Arg Met Ala Leu Trp Glu Glu Ile 260 265 270		
tct tca aat cta tca gct gaa gga atc aat cga agc ccg gga caa tgc 864		
Ser Ser Asn Leu Ser Ala Glu Gly Ile Asn Arg Ser Pro Gly Gln Cys 275 280 285		
aaa tct ctc tgg gca tca ctt att cag aaa tac gag gag agc aag gct 912		
Lys Ser Leu Trp Ala Ser Leu Ile Gln Lys Tyr Glu Glu Ser Lys Ala 290 295 300		

gat gag aga agc aag acg agt tgg cca cat ttt gag gat atg aac aac
960

Asp Glu Arg Ser Lys Thr Ser Trp Pro His Phe Glu Asp Met Asn Asn
305 310 315 320

att ttg tca gag cta ggc aca cct gcg tct taa

993

Ile Leu Ser Glu Leu Gly Thr Pro Ala Ser
325 330

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114

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20 25 30

Asp Ala Leu His Lys Ala Ala His Ala Ala Leu Ser Ser Cys Pro Val
35 40 45

Thr Cys Pro Leu Ser His Met Glu Arg Thr Val Ser Glu Val Leu Arg
50 55 60

Lys Ile Val Arg Lys Tyr Ser Gly Lys Arg Pro Glu Val Ile Ala Ile
65 70 75 80

Ala Thr Glu Asn Pro Met Ala Val Arg Ala Asp Glu Val Ser Ala Arg
85 90 95

Leu Ser Gly Asp Pro Ser Val Gly Ser Gly Val Ala Ala Leu Arg Lys
100 105 110

Val Val Glu Gly Asn Asp Lys Arg Ser Arg Ala Lys Lys Ala Pro Ser
115 120 125

Gln Glu Ala Ser Pro Lys Glu Val Asp Arg Thr Leu Glu Asp Asp Ile
130 135 140

Ile Asp Ser Ala Arg Leu Leu Ala Glu Glu Glu Thr Ala Ala Ser Thr
145 150 155 160

Tyr Thr Glu Glu Val Asp Thr Pro Val Gly Ser Ser Ser Glu Glu Ser
165 170 175

Asp Asp Phe Trp Lys Ser Phe Ile Asn Pro Ser Ser Ser Pro Ser Pro
180 185 190

Ser Glu Thr Glu Asn Met Asn Lys Val Ala Asp Thr Glu Pro Lys Ala
 195 200 205

Glu Gly Lys Glu Asn Ser Arg Asp Asp Asp Glu Leu Ala Asp Ala Ser
 210 215 220

Asp Ser Glu Thr Lys Ser Ser Pro Lys Arg Val Arg Lys Asn Lys Trp
 225 230 235 240

Lys Pro Glu Glu Ile Lys Lys Val Ile Arg Met Arg Gly Glu Leu His
 245 250 255

Ser Arg Phe Gln Val Val Lys Gly Arg Met Ala Leu Trp Glu Glu Ile
 260 265 270

Ser Ser Asn Leu Ser Ala Glu Gly Ile Asn Arg Ser Pro Gly Gln Cys
 275 280 285

Lys Ser Leu Trp Ala Ser Leu Ile Gln Lys Tyr Glu Glu Ser Lys Ala
 290 295 300

Asp Glu Arg Ser Lys Thr Ser Trp Pro His Phe Glu Asp Met Asn Asn
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Ile Leu Ser Glu Leu Gly Thr Pro Ala Ser
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ttcggctgaa tataaatctg aaaaa atg gat caa gat cag cat cct cag tac
 112

Met Asp Gln Asp Gln His Pro Gln Tyr
 1 5

ggt ata ccg gag ctc cgg cag ctc atg aaa ggc gga gga agg acg act
 160

Gly Ile Pro Glu Leu Arg Gln Leu Met Lys Gly Gly Gly Arg Thr Thr
 10 15 20 25

act aca aca ccg tct act tct tct cat ttt ccc tct gat ttc ttc ggt
 208

Thr Thr Thr Pro Ser Thr Ser Ser His Phe Pro Ser Asp Phe Phe Gly
 30 35 40

ttt aac ctt gct ccg gtg cag cca ccg cca cac cgt ctt cat cag ttc
 256
 Phe Asn Leu Ala Pro Val Gln Pro Pro Pro His Arg Leu His Gln Phe
 45 50 55

act act gat caa gat atg ggt ttc ttg cca cgt ggc ata cat gga ttg
 304
 Thr Thr Asp Gln Asp Met Gly Phe Leu Pro Arg Gly Ile His Gly Leu
 60 65 70

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 352
 Gly Gly Gly Ser Ser Thr Ala Gly Asn Asn Ser Asn Leu Asn Ala Ser
 75 80 85

act agt ggt gga gga gtt ggg ttt agt ggg ttt ctt gac ggt ggt ggt
 400
 Thr Ser Gly Gly Gly Val Gly Phe Ser Gly Phe Leu Asp Gly Gly Gly
 90 95 100 105

ttc ggc agc gga gta gga gga gac ggt gga gga act gga agg tgg ccg
 448
 Phe Gly Ser Gly Val Gly Gly Asp Gly Gly Gly Thr Gly Arg Trp Pro
 110 115 120

aga caa gaa acc cta act ctg ttg gaa att aga tct cgt ctt gat cat
 496
 Arg Gln Glu Thr Leu Thr Leu Leu Glu Ile Arg Ser Arg Leu Asp His
 125 130 135

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 544
 Lys Phe Lys Glu Ala Asn His Lys Gly Pro Leu Trp Asp Glu Val Ser
 140 145 150

agg att atg tcc gag gaa cat gga tac caa agg agt ggg aag aaa tgc
 592
 Arg Ile Met Ser Glu Glu His Gly Tyr Gln Arg Ser Gly Lys Lys Cys
 155 160 165

aga gag aag ttt gag aat ctg tac aaa tac tat agt aag act aaa gaa
 640
 Arg Glu Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr Ser Lys Thr Lys Glu
 170 175 180 185

ggc gaa gcc gga aga caa gac gga aaa cat cac aga ttt ttc cgc cag
 688
 Gly Glu Ala Gly Arg Gln Asp Gly Lys His His Arg Phe Phe Arg Gln
 190 195 200

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 736
 Leu Gln Ala Leu Tyr Gly Asp Ser Asn Asn Leu Val Ser Cys Pro Asn
 205 210 215

cat aac acg cag ttc atg agc agt gct ctt cat ggt ttc cat act caa
 784
 His Asn Thr Gln Phe Met Ser Ser Ala Leu His Gly Phe His Thr Gln
 220 225 230

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 Asn Pro Met Asn Val Ala Thr Thr Thr Ser Asn Ile His Asn Val Asp
 235 240 245
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 880
 Ser Val His Gly Phe His Gln Ser Leu Ser Leu Ser Asn Asn Tyr Asn
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 Ser Ser Glu Leu Glu Leu Met Thr Ser Ser Ser Glu Gly Asn Asp Ser
 270 275 280
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 976
 Ser Ser Arg Arg Lys Lys Arg Ser Trp Lys Ala Lys Ile Lys Glu Phe
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 1024
 Ile Asp Thr Asn Met Lys Arg Leu Ile Glu Arg Gln Asp Val Trp Leu
 300 305 310
 gag aag ttg aca aag gtt att gaa gac aaa gag gaa caa cgg atg atg
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 1120
 Lys Glu Glu Glu Trp Arg Lys Ile Glu Ala Ala Arg Ile Asp Lys Glu
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 1168
 His Leu Phe Trp Ala Lys Glu Arg Ala Arg Met Glu Ala Arg Asp Val
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 1216
 Ala Val Ile Glu Ala Leu Gln Tyr Leu Thr Gly Lys Pro Leu Ile Lys
 365 370 375
 ccg ctg tgt tca tcc ccg gaa gag agg aca aat ggt aat aat gag atc
 1264
 Pro Leu Cys Ser Ser Pro Glu Glu Arg Thr Asn Gly Asn Asn Glu Ile
 380 385 390
 cga aac aat agt gag aca cag aat gag aat gga agc gat caa acg atg
 1312
 Arg Asn Asn Ser Glu Thr Gln Asn Glu Asn Gly Ser Asp Gln Thr Met
 395 400 405
 act aac aat gtt tgt gtt aaa gga agt agt agc tgc tgg ggt gag caa
 1360
 Thr Asn Asn Val Cys Val Lys Gly Ser Ser Ser Cys Trp Gly Glu Gln
 410 415 420 425

gag att tta aag ctt atg gag ata aga acg agc atg gac tcg acc ttt
1408

Glu Ile Leu Lys Leu Met Glu Ile Arg Thr Ser Met Asp Ser Thr Phe
430 435 440

caa gag ata tta gga ggg tgc tcg gat gag ttt cta tgg gag gaa atc
1456

Gln Glu Ile Leu Gly Gly Cys Ser Asp Glu Phe Leu Trp Glu Glu Ile
445 450 455

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1504

Ala Ala Lys Leu Ile Gln Leu Gly Phe Asp Gln Arg Ser Ala Leu Leu
460 465 470

tgc aag gaa aag tgg gaa tgg ata agc aat gga atg agg aaa gaa aag
1552

Cys Lys Glu Lys Trp Glu Trp Ile Ser Asn Gly Met Arg Lys Glu Lys
475 480 485

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1600

Lys Gln Ile Asn Lys Lys Arg Lys Asp Asn Ser Ser Ser Cys Gly Val
490 495 500 505

tac tac ccg aga aac gaa gaa aat cca atc tac aat aat cga gaa agt
1648

Tyr Tyr Pro Arg Asn Glu Glu Asn Pro Ile Tyr Asn Asn Arg Glu Ser
510 515 520

gga tat aat gat aat gat ccg cat caa atc aac gaa caa ggc aat gta
1696

Gly Tyr Asn Asp Asn Asp Pro His Gln Ile Asn Glu Gln Gly Asn Val
525 530 535

ggt tct tca aca tca aac gca aac gca aac gta acc act gga
1744

Gly Ser Ser Thr Ser Asn Ala Asn Ala Asn Ala Asn Val Thr Thr Gly
540 545 550

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1792

Asn Pro Ser Gly Ala Met Ala Ala Ser Thr Asn Cys Phe Pro Phe Phe
555 560 565

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1840

Met Gly Asp Gly Asp Gln Asn Leu Trp Glu Ser Tyr Gly Leu Arg Leu
570 575 580 585

agt aaa gaa gag aat cag taa gtaatttctc ttaatgaaga agaagaaggt
1891

Ser Lys Glu Glu Asn Gln
590

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1951

tattatatgt cacatgctgc ttagaattaa gaaatatttg ttggggctta acgaattata
2011

tatcagcata tataagatga gagtctaaga attatatcaa attaggcttt aaccaacgta
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2131

ctaaa
2136

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Ser His Phe Pro Ser Asp Phe Phe Gly Phe Asn Leu Ala Pro Val Gln
35 40 45

Pro Pro Pro His Arg Leu His Gln Phe Thr Thr Asp Gln Asp Met Gly
50 55 60

Phe Leu Pro Arg Gly Ile His Gly Leu Gly Gly Gly Ser Ser Thr Ala
65 70 75 80

Gly Asn Asn Ser Asn Leu Asn Ala Ser Thr Ser Gly Gly Gly Val Gly
85 90 95

Phe Ser Gly Phe Leu Asp Gly Gly Gly Phe Gly Ser Gly Val Gly Gly
100 105 110

Asp Gly Gly Gly Thr Gly Arg Trp Pro Arg Gln Glu Thr Leu Thr Leu
115 120 125

Leu Glu Ile Arg Ser Arg Leu Asp His Lys Phe Lys Glu Ala Asn His
130 135 140

Lys Gly Pro Leu Trp Asp Glu Val Ser Arg Ile Met Ser Glu Glu His
145 150 155 160

Gly Tyr Gln Arg Ser Gly Lys Lys Cys Arg Glu Lys Phe Glu Asn Leu
165 170 175

Tyr Lys Tyr Tyr Ser Lys Thr Lys Glu Gly Glu Ala Gly Arg Gln Asp
180 185 190

Gly Lys His His Arg Phe Phe Arg Gln Leu Gln Ala Leu Tyr Gly Asp
 195 200 205
 Ser Asn Asn Leu Val Ser Cys Pro Asn His Asn Thr Gln Phe Met Ser
 210 215 220
 Ser Ala Leu His Gly Phe His Thr Gln Asn Pro Met Asn Val Ala Thr
 225 230 235 240
 Thr Thr Ser Asn Ile His Asn Val Asp Ser Val His Gly Phe His Gln
 245 250 255
 Ser Leu Ser Leu Ser Asn Asn Tyr Asn Ser Ser Glu Leu Glu Leu Met
 260 265 270
 Thr Ser Ser Ser Glu Gly Asn Asp Ser Ser Ser Arg Arg Lys Lys Arg
 275 280 285
 Ser Trp Lys Ala Lys Ile Lys Glu Phe Ile Asp Thr Asn Met Lys Arg
 290 295 300
 Leu Ile Glu Arg Gln Asp Val Trp Leu Glu Lys Leu Thr Lys Val Ile
 305 310 315 320
 Glu Asp Lys Glu Glu Gln Arg Met Met Lys Glu Glu Glu Trp Arg Lys
 325 330 335
 Ile Glu Ala Ala Arg Ile Asp Lys Glu His Leu Phe Trp Ala Lys Glu
 340 345 350
 Arg Ala Arg Met Glu Ala Arg Asp Val Ala Val Ile Glu Ala Leu Gln
 355 360 365
 Tyr Leu Thr Gly Lys Pro Leu Ile Lys Pro Leu Cys Ser Ser Pro Glu
 370 375 380
 Glu Arg Thr Asn Gly Asn Asn Glu Ile Arg Asn Asn Ser Glu Thr Gln
 385 390 395 400
 Asn Glu Asn Gly Ser Asp Gln Thr Met Thr Asn Asn Val Cys Val Lys
 405 410 415
 Gly Ser Ser Ser Cys Trp Gly Glu Gln Glu Ile Leu Lys Leu Met Glu
 420 425 430
 Ile Arg Thr Ser Met Asp Ser Thr Phe Gln Glu Ile Leu Gly Gly Cys

435 440 445
 Ser Asp Glu Phe Leu Trp Glu Glu Ile Ala Ala Lys Leu Ile Gln Leu
 450 455 460
 Gly Phe Asp Gln Arg Ser Ala Leu Leu Cys Lys Glu Lys Trp Glu Trp
 465 470 475 480
 Ile Ser Asn Gly Met Arg Lys Glu Lys Lys Gln Ile Asn Lys Lys Arg
 485 490 495
 Lys Asp Asn Ser Ser Ser Cys Gly Val Tyr Tyr Pro Arg Asn Glu Glu
 500 505 510
 Asn Pro Ile Tyr Asn Asn Arg Glu Ser Gly Tyr Asn Asp Asn Asp Pro
 515 520 525
 His Gln Ile Asn Glu Gln Gly Asn Val Gly Ser Ser Thr Ser Asn Ala
 530 535 540
 Asn Ala Asn Ala Asn Val Thr Thr Gly Asn Pro Ser Gly Ala Met Ala
 545 550 555 560
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 Met Val Arg Thr Pro Cys Cys Lys Ala Glu Leu Gly Leu Lys Lys Gly
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gct tgg act ccc gag gaa gat cag aag ctt ctc tct tac ctt aac cgc
 156
 Ala Trp Thr Pro Glu Glu Asp Gln Lys Leu Leu Ser Tyr Leu Asn Arg
 20 25 30

cac ggt gaa ggt gga tgg cga act ctc ccc gaa aaa gct gga ctc aag
 204
 His Gly Glu Gly Gly Trp Arg Thr Leu Pro Glu Lys Ala Gly Leu Lys
 35 40 45

aga tgc ggc aaa agc tgc aga ctg aga tgg gcc aat tat ctt aga cct
 252
 Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ala Asn Tyr Leu Arg Pro
 50 55 60

gac atc aaa aga gga gag ttc act gaa gac gaa gaa cgt tca atc atc
 300
 Asp Ile Lys Arg Gly Glu Phe Thr Glu Asp Glu Glu Arg Ser Ile Ile
 65 70 75 80

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 348
 Ser Leu His Ala Leu His Gly Asn Lys Trp Ser Ala Ile Ala Arg Gly
 85 90 95

cta cca gga aga acc gat aac gag atc aag aac tac tgg aac act cat
 396
 Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
 100 105 110

atc aaa aaa cgt ttg atc aag aaa ggt att gat cca gtt aca cac aag
 444
 Ile Lys Lys Arg Leu Ile Lys Lys Gly Ile Asp Pro Val Thr His Lys
 115 120 125

ggc ata acc tcc ggt acc gac aaa tca gaa aac ctc ccg gag aaa caa
 492
 Gly Ile Thr Ser Gly Thr Asp Lys Ser Glu Asn Leu Pro Glu Lys Gln
 130 135 140

aat gtt aat ctg aca act agt gac cat gat ctt gat aat gac aag gcg
 540
 Asn Val Asn Leu Thr Thr Ser Asp His Asp Leu Asp Asn Asp Lys Ala
 145 150 155 160

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 Lys Lys Asn Asn Lys Asn Phe Gly Leu Ser Ser Ala Ser Phe Leu Asn
 165 170 175

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 636
 Lys Val Ala Asn Arg Phe Gly Lys Arg Ile Asn Gln Ser Val Leu Ser
 180 185 190

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 684
 Glu Ile Ile Gly Ser Gly Gly Pro Leu Ala Ser Thr Ser His Thr Thr
 195 200 205

aat act aca act aca agt gtt tcc gtt gac tct gaa tca gtt aag tca
 732
 Asn Thr Thr Thr Thr Ser Val Ser Val Asp Ser Glu Ser Val Lys Ser
 210 215 220

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 780
 Thr Ser Ser Ser Phe Ala Pro Thr Ser Asn Leu Leu Cys His Gly Thr
 225 230 235 240

ggt gca aca aca cca gtt tca tgc aac ttt gac gtt gat ggt aac gtt
828

Val Ala Thr Thr Pro Val Ser Ser Asn Phe Asp Val Asp Gly Asn Val
245 250 255

aat ctg acg tgt tct tgc tcc acg ttc tct gat tcc tcc gtt aac aat
876

Asn Leu Thr Cys Ser Ser Ser Thr Phe Ser Asp Ser Ser Val Asn Asn
260 265 270

cct cta atg tac tgc gat aat ttc gtt ggt aat aac aac gtt gat gat
924

Pro Leu Met Tyr Cys Asp Asn Phe Val Gly Asn Asn Asn Val Asp Asp
275 280 285

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972

Glu Asp Thr Ile Gly Phe Ser Thr Phe Leu Asn Asp Glu Asp Phe Met
290 295 300

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1020

Met Leu Glu Glu Ser Cys Val Glu Asn Thr Ala Phe Met Lys Glu Leu
305 310 315 320

acg agg ttt ctt cac gag gat gaa aac gac gtc gtt gat gtg acg ccg
1068

Thr Arg Phe Leu His Glu Asp Glu Asn Asp Val Val Asp Val Thr Pro
325 330 335

gtc tat gaa cgt caa gac ttg ttt gac gaa att gat aac tat ttt gga
1116

Val Tyr Glu Arg Gln Asp Leu Phe Asp Glu Ile Asp Asn Tyr Phe Gly
340 345 350

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1169

atggatatgt taccttgatg atgttgatgg taataataat aaataataga tggatgatgat
1229

gaccatgcat gaatcatgaa tgtagttcgt gttgtcacat atgcttgtgt ttttgtgttt
1289

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1384

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 35 40 45
 Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ala Asn Tyr Leu Arg Pro
 50 55 60
 Asp Ile Lys Arg Gly Glu Phe Thr Glu Asp Glu Glu Arg Ser Ile Ile
 65 70 75 80
 Ser Leu His Ala Leu His Gly Asn Lys Trp Ser Ala Ile Ala Arg Gly
 85 90 95
 Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
 100 105 110
 Ile Lys Lys Arg Leu Ile Lys Lys Gly Ile Asp Pro Val Thr His Lys
 115 120 125
 Gly Ile Thr Ser Gly Thr Asp Lys Ser Glu Asn Leu Pro Glu Lys Gln
 130 135 140
 Asn Val Asn Leu Thr Thr Ser Asp His Asp Leu Asp Asn Asp Lys Ala
 145 150 155 160
 Lys Lys Asn Asn Lys Asn Phe Gly Leu Ser Ser Ala Ser Phe Leu Asn
 165 170 175
 Lys Val Ala Asn Arg Phe Gly Lys Arg Ile Asn Gln Ser Val Leu Ser
 180 185 190
 Glu Ile Ile Gly Ser Gly Gly Pro Leu Ala Ser Thr Ser His Thr Thr
 195 200 205
 Asn Thr Thr Thr Thr Ser Val Ser Val Asp Ser Glu Ser Val Lys Ser
 210 215 220
 Thr Ser Ser Ser Phe Ala Pro Thr Ser Asn Leu Leu Cys His Gly Thr
 225 230 235 240
 Val Ala Thr Thr Pro Val Ser Ser Asn Phe Asp Val Asp Gly Asn Val
 245 250 255
 Asn Leu Thr Cys Ser Ser Ser Thr Phe Ser Asp Ser Ser Val Asn Asn
 260 265 270

Pro Leu Met Tyr Cys Asp Asn Phe Val Gly Asn Asn Asn Val Asp Asp
 275 280 285

Glu Asp Thr Ile Gly Phe Ser Thr Phe Leu Asn Asp Glu Asp Phe Met
 290 295 300

Met Leu Glu Glu Ser Cys Val Glu Asn Thr Ala Phe Met Lys Glu Leu
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Thr Arg Phe Leu His Glu Asp Glu Asn Asp Val Val Asp Val Thr Pro
 325 330 335

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 340 345 350

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 240

aaactttcat gtttggggag atcaaagatg gtttcttttt tatactttac ttgtagaga
 300

ggatttgaag cagcgaatag ctgcaaccgg tcctggtt atg gat act aat aca tct
 355

Met Asp Thr Asn Thr Ser
 1 5

gga gaa gaa tta tta gct aag gca aga aag cca tat aca ata aca aag
 403

Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys Pro Tyr Thr Ile Thr Lys
 10 15 20

cag cga gag cga tgg act gag gat gag cat gag agg ttt cta gaa gcc
 451

Gln Arg Glu Arg Trp Thr Glu Asp Glu His Glu Arg Phe Leu Glu Ala
 25 30 35

ttg agg ctt tat gga aga gct tgg caa cga att gaa gaa cat att ggg
 499

Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg Ile Glu Glu His Ile Gly
 40 45 50

aca aag act gct gtt cag atc aga agt cat gca caa aag ttc ttc aca
 547

Thr Lys Thr Ala Val Gln Ile Arg Ser His Ala Gln Lys Phe Phe Thr
 55 60 65 70
 aag ttg gag aaa gag gct gaa gtt aaa ggc atc cct gtt tgc caa gct
 595
 Lys Leu Glu Lys Glu Ala Glu Val Lys Gly Ile Pro Val Cys Gln Ala
 75 80 85
 ttg gac ata gaa att ccg cct cct cgt cct aaa cga aaa ccc aat act
 643
 Leu Asp Ile Glu Ile Pro Pro Pro Arg Pro Lys Arg Lys Pro Asn Thr
 90 95 100
 cct tat cct cga aaa cct ggg aac aac ggt aca tct tcc tct caa gta
 691
 Pro Tyr Pro Arg Lys Pro Gly Asn Asn Gly Thr Ser Ser Ser Gln Val
 105 110 115
 tca tca gca aaa gat gca aaa ctt gtt tca tgc gcc tct tct tca cag
 739
 Ser Ser Ala Lys Asp Ala Lys Leu Val Ser Ser Ala Ser Ser Ser Gln
 120 125 130
 ttg aat cag gcg ttc ttg gat ttg gaa aaa atg ccg ttc tct gag aaa
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 135 140 145 150
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 155 160 165
 act gtg aac aag tat ccc tta cca acg aaa cag gta agt ggc gac att
 883
 Thr Val Asn Lys Tyr Pro Leu Pro Thr Lys Gln Val Ser Gly Asp Ile
 170 175 180
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 931
 Glu Thr Ser Lys Thr Ser Thr Val Asp Asn Ala Val Gln Asp Val Pro
 185 190 195
 aag aag aac aaa gac aaa gat ggt aac gat ggt act act gtg cac agc
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 Lys Lys Asn Lys Asp Lys Asp Gly Asn Asp Gly Thr Thr Val His Ser
 200 205 210
 atg caa aac tac cct tgg cat ttc cac gca gat att gtg aac ggg aat
 1027
 Met Gln Asn Tyr Pro Trp His Phe His Ala Asp Ile Val Asn Gly Asn
 215 220 225 230
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 1075
 Ile Ala Lys Cys Pro Gln Asn His Pro Ser Gly Met Val Ser Gln Asp
 235 240 245
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 Phe Met Phe His Pro Met Arg Glu Glu Thr His Gly His Ala Asn Leu

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265	270	275
cca gct tgt cat tca cag gat gat tac cgt tcg ttt ctc cag ata tca		
1219		
Pro Ala Cys His Ser Gln Asp Asp Tyr Arg Ser Phe Leu Gln Ile Ser		
280	285	290
tct act ttc tcc aat ctt att atg tca act ctc cta cag aat cct gca		
1267		
Ser Thr Phe Ser Asn Leu Ile Met Ser Thr Leu Leu Gln Asn Pro Ala		
295	300	305 310
gct cat gct gca gct aca ttc gct gct tcg gtc tgg cct tat gcg agt		
1315		
Ala His Ala Ala Ala Thr Phe Ala Ala Ser Val Trp Pro Tyr Ala Ser		
315	320	325
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1363		
Val Gly Asn Ser Gly Asp Ser Ser Thr Pro Met Ser Ser Ser Pro Pro		
330	335	340
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1411		
Ser Ile Thr Ala Ile Ala Ala Ala Thr Val Ala Ala Ala Thr Ala Trp		
345	350	355
tgg gct tct cat gga ctt ctt cct gta tgc gct cca gct cca ata aca		
1459		
Trp Ala Ser His Gly Leu Leu Pro Val Cys Ala Pro Ala Pro Ile Thr		
360	365	370
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1507		
Cys Val Pro Phe Ser Thr Val Ala Val Pro Thr Pro Ala Met Thr Glu		
375	380	385 390
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395	400	405
ctg caa gat caa acc ttg gct tcg aaa tct cca gct tca tca tct gat		
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1651		
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425	430	435
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1699		
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440	445	450

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 455 460 465 470

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 1795
 Ser Asn Thr Pro Ser Gly Ser Asp Ala Glu Thr Asp Ala Leu Asp Lys
 475 480 485

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 1843
 Met Glu Lys Asp Lys Glu Asp Val Lys Glu Thr Asp Glu Asn Gln Pro
 490 495 500

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 1891
 Asp Val Ile Glu Leu Asn Asn Arg Lys Ile Lys Met Arg Asp Asn Asn
 505 510 515

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 1939
 Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp Lys Glu Val Ser Glu Glu
 520 525 530

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 Gly Arg Ile Ala Phe Gln Ala Leu Phe Ala Arg Glu Arg Leu Pro Gln
 535 540 545 550

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 2035
 Ser Phe Ser Pro Pro Gln Val Ala Glu Asn Val Asn Arg Lys Gln Ser
 555 560 565

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 2083
 Asp Thr Ser Met Pro Leu Ala Pro Asn Phe Lys Ser Gln Asp Ser Cys
 570 575 580

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 2131
 Ala Ala Asp Gln Glu Gly Val Val Met Ile Gly Val Gly Thr Cys Lys
 585 590 595

agt ctt aaa acg aga cag aca gga ttt aag cca tac aag aga tgt tca
 2179
 Ser Leu Lys Thr Arg Gln Thr Gly Phe Lys Pro Tyr Lys Arg Cys Ser
 600 605 610

atg gaa gtg aaa gag agc caa gtt ggg aac ata aac aat caa agt gat
 2227
 Met Glu Val Lys Glu Ser Gln Val Gly Asn Ile Asn Asn Gln Ser Asp
 615 620 625 630

gaa aaa gtc tgc aaa agg ctt cga ttg gaa gga gaa gct tct aca tga
 2275
 Glu Lys Val Cys Lys Arg Leu Arg Leu Glu Gly Glu Ala Ser Thr
 635 640 645

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2335

agtagtttgc ttctccaatc tttatgaaag agacttttaa ttttccttcc gaacatttct
2395

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2455

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2526

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35 40 45

Ile Glu Glu His Ile Gly Thr Lys Thr Ala Val Gln Ile Arg Ser His
50 55 60

Ala Gln Lys Phe Phe Thr Lys Leu Glu Lys Glu Ala Glu Val Lys Gly
65 70 75 80

Ile Pro Val Cys Gln Ala Leu Asp Ile Glu Ile Pro Pro Pro Arg Pro
85 90 95

Lys Arg Lys Pro Asn Thr Pro Tyr Pro Arg Lys Pro Gly Asn Asn Gly
100 105 110

Thr Ser Ser Ser Gln Val Ser Ser Ala Lys Asp Ala Lys Leu Val Ser
115 120 125

Ser Ala Ser Ser Ser Gln Leu Asn Gln Ala Phe Leu Asp Leu Glu Lys
130 135 140

Met Pro Phe Ser Glu Lys Thr Ser Thr Gly Lys Glu Asn Gln Asp Glu
145 150 155 160

Asn Cys Ser Gly Val Ser Thr Val Asn Lys Tyr Pro Leu Pro Thr Lys
165 170 175

Gln Val Ser Gly Asp Ile Glu Thr Ser Lys Thr Ser Thr Val Asp Asn
 180 185 190

Ala Val Gln Asp Val Pro Lys Lys Asn Lys Asp Lys Asp Gly Asn Asp
 195 200 205

Gly Thr Thr Val His Ser Met Gln Asn Tyr Pro Trp His Phe His Ala
 210 215 220

Asp Ile Val Asn Gly Asn Ile Ala Lys Cys Pro Gln Asn His Pro Ser
 225 230 235 240

Gly Met Val Ser Gln Asp Phe Met Phe His Pro Met Arg Glu Glu Thr
 245 250 255

His Gly His Ala Asn Leu Gln Ala Thr Thr Ala Ser Ala Thr Thr Thr
 260 265 - 270

Ala Ser His Gln Ala Phe Pro Ala Cys His Ser Gln Asp Asp Tyr Arg
 275 280 285

Ser Phe Leu Gln Ile Ser Ser Thr Phe Ser Asn Leu Ile Met Ser Thr
 290 295 300

Leu Leu Gln Asn Pro Ala Ala His Ala Ala Ala Thr Phe Ala Ala Ser
 305 310 315 320

Val Trp Pro Tyr Ala Ser Val Gly Asn Ser Gly Asp Ser Ser Thr Pro
 325 330 335

Met Ser Ser Ser Pro Pro Ser Ile Thr Ala Ile Ala Ala Ala Thr Val
 340 345 350

Ala Ala Ala Thr Ala Trp Trp Ala Ser His Gly Leu Leu Pro Val Cys
 355 360 365

Ala Pro Ala Pro Ile Thr Cys Val Pro Phe Ser Thr Val Ala Val Pro
 370 375 380

Thr Pro Ala Met Thr Glu Met Asp Thr Val Glu Asn Thr Gln Pro Phe
 385 390 395 400

Glu Lys Gln Asn Thr Ala Leu Gln Asp Gln Thr Leu Ala Ser Lys Ser
 405 410 415

Pro Ala Ser Ser Ser Asp Asp Ser Asp Glu Thr Gly Val Thr Lys Leu
 420 425 430

Asn Ala Asp Ser Lys Thr Asn Asp Asp Lys Ile Glu Glu Val Val Val
 435 440 445

Thr Ala Ala Val His Asp Ser Asn Thr Ala Gln Lys Lys Asn Leu Val
 450 455 460

Asp Arg Ser Ser Cys Gly Ser Asn Thr Pro Ser Gly Ser Asp Ala Glu
 465 470 475 480

Thr Asp Ala Leu Asp Lys Met Glu Lys Asp Lys Glu Asp Val Lys Glu
 485 490 495

Thr Asp Glu Asn Gln Pro Asp Val Ile Glu Leu Asn Asn Arg Lys Ile
 500 505 510

Lys Met Arg Asp Asn Asn Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp
 515 520 525

Lys Glu Val Ser Glu Glu Gly Arg Ile Ala Phe Gln Ala Leu Phe Ala
 530 535 540

Arg Glu Arg Leu Pro Gln Ser Phe Ser Pro Pro Gln Val Ala Glu Asn
 545 550 555 560

Val Asn Arg Lys Gln Ser Asp Thr Ser Met Pro Leu Ala Pro Asn Phe
 565 570 575

Lys Ser Gln Asp Ser Cys Ala Ala Asp Gln Glu Gly Val Val Met Ile
 580 585 590

Gly Val Gly Thr Cys Lys Ser Leu Lys Thr Arg Gln Thr Gly Phe Lys
 595 600 605

Pro Tyr Lys Arg Cys Ser Met Glu Val Lys Glu Ser Gln Val Gly Asn
 610 615 620

Ile Asn Asn Gln Ser Asp Glu Lys Val Cys Lys Arg Leu Arg Leu Glu
 625 630 635 640

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 180
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 240
 ttcttctcca gttctcatct gggttcttca atg gcg agt gtt gaa ggt gat gat
 294
 Met Ala Ser Val Glu Gly Asp Asp
 1 5
 gat ttc gga agt tct tcg tca agg tct tat caa gat caa cta tac aca
 342
 Asp Phe Gly Ser Ser Ser Ser Arg Ser Tyr Gln Asp Gln Leu Tyr Thr
 10 15 20
 gag cta tgg aaa gtt tgt gca ggt cca tta gtg gaa gtt cct cgt gct
 390
 Glu Leu Trp Lys Val Cys Ala Gly Pro Leu Val Glu Val Pro Arg Ala
 25 30 35 40
 caa gag aga gtt ttc tac ttc cct cag ggt cac atg gaa caa ctt gtg
 438
 Gln Glu Arg Val Phe Tyr Phe Pro Gln Gly His Met Glu Gln Leu Val
 45 50 55
 gcg tca act aat caa gga atc aat tca gaa gaa ata cct gtt ttt gat
 486
 Ala Ser Thr Asn Gln Gly Ile Asn Ser Glu Glu Ile Pro Val Phe Asp
 60 65 70
 ctt cct cca aag ata ctt tgt cga gtt ctt gat gtc act tta aag gcg
 534
 Leu Pro Pro Lys Ile Leu Cys Arg Val Leu Asp Val Thr Leu Lys Ala
 75 80 85
 gag cat gaa aca gat gag gtt tac gct cag atc aca tta caa cca gag
 582
 Glu His Glu Thr Asp Glu Val Tyr Ala Gln Ile Thr Leu Gln Pro Glu
 90 95 100
 gaa gat caa agt gaa cca aca agt ctt gat cca cct att gtt gga cca
 630
 Glu Asp Gln Ser Glu Pro Thr Ser Leu Asp Pro Pro Ile Val Gly Pro
 105 110 115 120
 act aag caa gag ttt cat tcg ttt gtt aag att tta acg gct tca gat
 678
 Thr Lys Gln Glu Phe His Ser Phe Val Lys Ile Leu Thr Ala Ser Asp
 125 130 135

aca agc act cat ggt gga ttc tct gtt ctt cgt aaa cac gcc act gaa
 726
 Thr Ser Thr His Gly Gly Phe Ser Val Leu Arg Lys His Ala Thr Glu
 140 145 150
 tgc ttg cct tct ttg gat atg aca caa gct act cct act caa gaa ctt
 774
 Cys Leu Pro Ser Leu Asp Met Thr Gln Ala Thr Pro Thr Gln Glu Leu
 155 160 165
 gtg act aga gat ctt cat ggc ttt gaa tgg agg ttt aag cat ata ttc
 822
 Val Thr Arg Asp Leu His Gly Phe Glu Trp Arg Phe Lys His Ile Phe
 170 175 180
 aga gga caa cca cgg agg cat ttg ctt act acg ggt tgg agt aca ttt
 870
 Arg Gly Gln Pro Arg Arg His Leu Leu Thr Thr Gly Trp Ser Thr Phe
 185 190 195 200
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 918
 Val Ser Ser Lys Arg Leu Val Ala Gly Asp Ala Phe Val Phe Leu Arg
 205 210 215
 ggt gag aat ggg gat tta cgg gtt gga gtg aga cga tta gct cgg cat
 966
 Gly Glu Asn Gly Asp Leu Arg Val Gly Val Arg Arg Leu Ala Arg His
 220 225 230
 caa agc aca atg cct act tcg gtt att tca agt cag agc atg cat ttg
 1014
 Gln Ser Thr Met Pro Thr Ser Val Ile Ser Ser Gln Ser Met His Leu
 235 240 245
 gga gtt ctt gct aca gct tct cat gct gtg cgt aca aca aca atc ttt
 1062
 Gly Val Leu Ala Thr Ala Ser His Ala Val Arg Thr Thr Thr Ile Phe
 250 255 260
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 1110
 Val Val Phe Tyr Lys Pro Arg Ile Ser Gln Phe Ile Val Gly Val Asn
 265 270 275 280
 aag tat atg gaa gct ata aag cat gga ttt tct ctc ggt acc cga ttc
 1158
 Lys Tyr Met Glu Ala Ile Lys His Gly Phe Ser Leu Gly Thr Arg Phe
 285 290 295
 aga atg agg ttt gaa gga gaa gag tct cct gag aga ata ttt act ggt
 1206
 Arg Met Arg Phe Glu Gly Glu Glu Ser Pro Glu Arg Ile Phe Thr Gly
 300 305 310
 acg att gtg gga agt gga gat cta tct tca caa tgg cca gct tct aaa
 1254
 Thr Ile Val Gly Ser Gly Asp Leu Ser Ser Gln Trp Pro Ala Ser Lys
 315 320 325

tgg agg tca ttg cag gta caa tgg gat gag cca aca aca gtt cag aga
 1302
 Trp Arg Ser Leu Gln Val Gln Trp Asp Glu Pro Thr Thr Val Gln Arg
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cca gat aaa gtc tca cca tgg gag ata gag cct ttc ttg gca act tcc
 1350
 Pro Asp Lys Val Ser Pro Trp Glu Ile Glu Pro Phe Leu Ala Thr Ser
 345 350 355 360

cca att tca act cct gct caa caa cca caa tcg aaa tgc aag cgg tca
 1398
 Pro Ile Ser Thr Pro Ala Gln Gln Pro Gln Ser Lys Cys Lys Arg Ser
 365 370 375

aga ccc atc gag cca tca gtt aaa aca cca gcc cca cct agt ttc ttg
 1446
 Arg Pro Ile Glu Pro Ser Val Lys Thr Pro Ala Pro Pro Ser Phe Leu
 380 385 390

tac agc ctc cct cag agc caa gat tcc att aat gca tcc ctt aaa ctg
 1494
 Tyr Ser Leu Pro Gln Ser Gln Asp Ser Ile Asn Ala Ser Leu Lys Leu
 395 400 405

ttt caa gat cca tca ctt gag aga att tca ggt gga tac tcc tca aac
 1542
 Phe Gln Asp Pro Ser Leu Glu Arg Ile Ser Gly Gly Tyr Ser Ser Asn
 410 415 420

aac agc ttc aaa ccc gag act cct cct cct cca acg aat tgt agc tat
 1590
 Asn Ser Phe Lys Pro Glu Thr Pro Pro Pro Pro Thr Asn Cys Ser Tyr
 425 430 435 440

agg ttg ttt gga ttt gat ctc aca agc aat tct cct gct cca atc cct
 1638
 Arg Leu Phe Gly Phe Asp Leu Thr Ser Asn Ser Pro Ala Pro Ile Pro
 445 450 455

caa gac aag caa ccg atg gat act tgt gga gct gcc aag tgt caa gaa
 1686
 Gln Asp Lys Gln Pro Met Asp Thr Cys Gly Ala Ala Lys Cys Gln Glu
 460 465 470

ccc atc act cca acc tca atg agt gag cag aag aag caa caa aca tca
 1734
 Pro Ile Thr Pro Thr Ser Met Ser Glu Gln Lys Lys Gln Gln Thr Ser
 475 480 485

aga agt cga act aaa gtg caa atg caa ggc att gcg gtt ggt cgt gcg
 1782
 Arg Ser Arg Thr Lys Val Gln Met Gln Gly Ile Ala Val Gly Arg Ala
 490 495 500

gtt gat tta aca ctg ttg aaa tct tac gat gaa ctg att gat gag ctt
 1830
 Val Asp Leu Thr Leu Leu Lys Ser Tyr Asp Glu Leu Ile Asp Glu Leu
 505 510 515 520

gag gag atg ttt gag att caa gga cag ctt ctt gcc cga gac aaa tgg
1878

Glu Glu Met Phe Glu Ile Gln Gly Gln Leu Leu Ala Arg Asp Lys Trp
525 530 535

atc gtt gtc ttc act gat gat gaa gga gat atg atg ctt gct ggt gat
1926

Ile Val Val Phe Thr Asp Asp Glu Gly Asp Met Met Leu Ala Gly Asp
540 545 550

gat ccg tgg aat gag ttt tgc aag atg gca aag aag ata ttt ata tat
1974

Asp Pro Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Ile Phe Ile Tyr
555 560 565

tcg agc gat gag gtt aag aaa atg aca acg aaa ctg aag att tct tcg
2022

Ser Ser Asp Glu Val Lys Lys Met Thr Thr Lys Leu Lys Ile Ser Ser
570 575 580

tcg tta gag aat gag gaa tat ggt aat gaa tca ttc gaa aat cgt agt
2070

Ser Leu Glu Asn Glu Glu Tyr Gly Asn Glu Ser Phe Glu Asn Arg Ser
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2119

Arg Gly

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2179

ttttcatgt caatttttca agttggcgat ttaatatattc ggttttggga cagtgggtga
2239

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2299

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20 25 30

Pro Leu Val Glu Val Pro Arg Ala Gln Glu Arg Val Phe Tyr Phe Pro
35 40 45

Gln Gly His Met Glu Gln Leu Val Ala Ser Thr Asn Gln Gly Ile Asn
50 55 60

Ser Glu Glu Ile Pro Val Phe Asp Leu Pro Pro Lys Ile Leu Cys Arg
65 70 75 80

Val Leu Asp Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val Tyr
 85 90 95

Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr Ser
 100 105 110

Leu Asp Pro Pro Ile Val Gly Pro Thr Lys Gln Glu Phe His Ser Phe
 115 120 125

Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe Ser
 130 135 140

Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met Thr
 145 150 155 160

Gln Ala Thr Pro Thr Gln Glu Leu Val Thr Arg Asp Leu His Gly Phe
 165 170 175

Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His Leu
 180 185 190

Leu Thr Thr Gly Trp Ser Thr Phe Val Ser Ser Lys Arg Leu Val Ala
 195 200 205

Gly Asp Ala Phe Val Phe Leu Arg Gly Glu Asn Gly Asp Leu Arg Val
 210 215 220

Gly Val Arg Arg Leu Ala Arg His Gln Ser Thr Met Pro Thr Ser Val
 225 230 235 240

Ile Ser Ser Gln Ser Met His Leu Gly Val Leu Ala Thr Ala Ser His
 245 250 255

Ala Val Arg Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg Ile
 260 265 270

Ser Gln Phe Ile Val Gly Val Asn Lys Tyr Met Glu Ala Ile Lys His
 275 280 285

Gly Phe Ser Leu Gly Thr Arg Phe Arg Met Arg Phe Glu Gly Glu Glu
 290 295 300

Ser Pro Glu Arg Ile Phe Thr Gly Thr Ile Val Gly Ser Gly Asp Leu
 305 310 315 320

Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Val Gln Trp
 325 330 335
 Asp Glu Pro Thr Thr Val Gln Arg Pro Asp Lys Val Ser Pro Trp Glu
 340 345 350
 Ile Glu Pro Phe Leu Ala Thr Ser Pro Ile Ser Thr Pro Ala Gln Gln
 355 360 365
 Pro Gln Ser Lys Cys Lys Arg Ser Arg Pro Ile Glu Pro Ser Val Lys
 370 375 380
 Thr Pro Ala Pro Pro Ser Phe Leu Tyr Ser Leu Pro Gln Ser Gln Asp
 385 390 395 400
 Ser Ile Asn Ala Ser Leu Lys Leu Phe Gln Asp Pro Ser Leu Glu Arg
 405 410 415
 Ile Ser Gly Gly Tyr Ser Ser Asn Asn Ser Phe Lys Pro Glu Thr Pro
 420 425 430
 Pro Pro Pro Thr Asn Cys Ser Tyr Arg Leu Phe Gly Phe Asp Leu Thr
 435 440 445
 Ser Asn Ser Pro Ala Pro Ile Pro Gln Asp Lys Gln Pro Met Asp Thr
 450 455 460
 Cys Gly Ala Ala Lys Cys Gln Glu Pro Ile Thr Pro Thr Ser Met Ser
 465 470 475 480
 Glu Gln Lys Lys Gln Gln Thr Ser Arg Ser Arg Thr Lys Val Gln Met
 485 490 495
 Gln Gly Ile Ala Val Gly Arg Ala Val Asp Leu Thr Leu Leu Lys Ser
 500 505 510
 Tyr Asp Glu Leu Ile Asp Glu Leu Glu Glu Met Phe Glu Ile Gln Gly
 515 520 525
 Gln Leu Leu Ala Arg Asp Lys Trp Ile Val Val Phe Thr Asp Asp Glu
 530 535 540
 Gly Asp Met Met Leu Ala Gly Asp Asp Pro Trp Asn Glu Phe Cys Lys
 545 550 555 560

Met Ala Lys Lys Ile Phe Ile Tyr Ser Ser Asp Glu Val Lys Lys Met
565 570 575

Thr Thr Lys Leu Lys Ile Ser Ser Ser Leu Glu Asn Glu Glu Tyr Gly
580 585 590

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gca ttt aac act cga aca ata aaa aat gaa gaa gag aca cac ccg ccg
96
Ala Phe Asn Thr Arg Thr Ile Lys Asn Glu Glu Glu Thr His Pro Pro
20 25 30
gag caa gaa gcc aca ata gcc gtt aga tca tca toa tca tcg gat ctg
144
Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu
35 40 45
acg gcc gag aag cgt ccg gat aag atc ata gca tgt cca aga tgc aag
192
Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys
50 55 60
agc atg gag aca aag ttc tgt tac ttc aac aac tac aac ggt aat cag
240
Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Gly Asn Gln
65 70 75 80
cct cga cac ttt tgt aaa ggc tgc cac cgt tac tgg acc gcc ggt ggt
288
Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly
85 90 95
gca ctc cgg aac gtt ccc gtc ggc gcc ggt cgt cgg aag tcc aaa cca
336
Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro
100 105 110
cct ggt cgt gtc gtg gtt ggt atg ctt gga gat gga aat ggt gtt cgc
384
Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg
115 120 125
caa gtc gag ctt ata aat ggc ttg ctc gtt gag gag tgg cag cat gcc
432
Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala
130 135 140

gca gcc gca gct cac ggt agt ttc cgg cat gat ttt ccc atg aag cgg
480

Ala Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg
145 150 155 160

ctc cgg tgt tac tcc gac ggt caa tcg tgc tga
513

Leu Arg Cys Tyr Ser Asp Gly Gln Ser Cys
165 170

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Glu Gln Glu Ala Thr Ile Ala Val Arg Ser Ser Ser Ser Ser Asp Leu
35 40 45

Thr Ala Glu Lys Arg Pro Asp Lys Ile Ile Ala Cys Pro Arg Cys Lys
50 55 60

Ser Met Glu Thr Lys Phe Cys Tyr Phe Asn Asn Tyr Asn Gly Asn Gln
65 70 75 80

Pro Arg His Phe Cys Lys Gly Cys His Arg Tyr Trp Thr Ala Gly Gly
85 90 95

Ala Leu Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Ser Lys Pro
100 105 110

Pro Gly Arg Val Val Val Gly Met Leu Gly Asp Gly Asn Gly Val Arg
115 120 125

Gln Val Glu Leu Ile Asn Gly Leu Leu Val Glu Glu Trp Gln His Ala
130 135 140

Ala Ala Ala Ala His Gly Ser Phe Arg His Asp Phe Pro Met Lys Arg
145 150 155 160

Leu Arg Cys Tyr Ser Asp Gly Gln Ser Cys
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60

catagagaga agaagacgga acagaggctc caaaaaa atg atg atg gag act aga
115

Met Met Met Glu Thr Arg
1 5

gat cca gct att aag ctt ttc ggt atg aaa atc cct ttt ccg tcg gtt
163

Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile Pro Phe Pro Ser Val
10 15 20

ttt gaa tcg gca gtt acg gtg gag gat gac gaa gaa gat gac tgg agc
211

Phe Glu Ser Ala Val Thr Val Glu Asp Asp Glu Glu Asp Asp Trp Ser
25 30 35

ggc gga gat gac aaa tca cca gag aag gta act cca gag tta tca gat
259

Gly Gly Asp Asp Lys Ser Pro Glu Lys Val Thr Pro Glu Leu Ser Asp
40 45 50

aag aac aac aac aac tgt aac gac aac agt ttt aac aat tcg aaa ccc
307

Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser Phe Asn Asn Ser Lys Pro
55 60 65 70

gaa acc ttg gac aaa gag gaa gcg aca tca act gat cag ata gag agt
355

Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser Thr Asp Gln Ile Glu Ser
75 80 85

agt gac acg cct gag gat aat cag cag acg aca cct gat ggt aaa acc
403

Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr Thr Pro Asp Gly Lys Thr
90 95 100

cta aag aaa ccg act aag att cta ccg tgt ccg aga tgc aaa agc atg
451

Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Lys Ser Met
105 110 115

gag acc aag ttc tgt tat tac aac aac tac aac ata aac cag cct cgt
499

Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Ile Asn Gln Pro Arg
120 125 130

cat ttc tgc aag gct tgt cag aga tat tgg act gct gga ggg act atg
547

His Phe Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ala Gly Gly Thr Met
135 140 145 150

agg aat gtt cct gtg ggg gca gga cgt cgt aag aac aaa agc tca tct
595

Arg Asn Val Pro Val Gly Ala Gly Arg Arg Lys Asn Lys Ser Ser Ser
155 160 165

tct cat tac cgt cac atc act att tcc gag gct ctt gag gct gcg agg
643

Ser His Tyr Arg His Ile Thr Ile Ser Glu Ala Leu Glu Ala Ala Arg
 170 175 180
 ctt gac ccg ggc tta cag gca aac aca agg gtc ttg agt ttt ggt ctc
 691
 Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg Val Leu Ser Phe Gly Leu
 185 190 195
 gaa gct cag cag cag cac gtt gct gct ccc atg aca cct gtt atg aag
 739
 Glu Ala Gln Gln Gln His Val Ala Ala Pro Met Thr Pro Val Met Lys
 200 205 210
 cta caa gaa gat caa aag gtc tca aac ggt gct agg aac agg ttt cac
 787
 Leu Gln Glu Asp Gln Lys Val Ser Asn Gly Ala Arg Asn Arg Phe His
 215 220 225 230
 ggg tta gcg gat caa cgg ctt gta gct cgg gta gag aat gga gat gat
 835
 Gly Leu Ala Asp Gln Arg Leu Val Ala Arg Val Glu Asn Gly Asp Asp
 235 240 245
 tgc tca agc gga tcc tct gtg acc acc tct aac aat cac tca gtg gat
 883
 Cys Ser Ser Gly Ser Ser Val Thr Thr Ser Asn Asn His Ser Val Asp
 250 255 260
 gaa tca aga gca caa agc ggc agt gtt gtt gaa gca caa atg aac aac
 931
 Glu Ser Arg Ala Gln Ser Gly Ser Val Val Glu Ala Gln Met Asn Asn
 265 270 275
 aac aac aac aat aac atg aat ggt tat gct tgc atc cca ggt gtt cca
 979
 Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala Cys Ile Pro Gly Val Pro
 280 285 290
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 1027
 Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro Pro Pro Gly Phe Tyr Pro
 295 300 305 310
 cct cca ggg tat cca atg ccg ttt tac cct tac tgg acc atc cca atg
 1075
 Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro Tyr Trp Thr Ile Pro Met
 315 320 325
 cta cca ccg cat caa tcc tca tcg cct ata agc caa aag tgt tca aat
 1123
 Leu Pro Pro His Gln Ser Ser Ser Pro Ile Ser Gln Lys Cys Ser Asn
 330 335 340
 aca aac tct ccg act ctc gga aag cat ccg aga gat gaa gga tca tcg
 1171
 Thr Asn Ser Pro Thr Leu Gly Lys His Pro Arg Asp Glu Gly Ser Ser
 345 350 355
 aaa aag gac aat gag aca gag cga aaa cag aag gcc ggg tgc gtt ctg
 1219
 Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln Lys Ala Gly Cys Val Leu

360 365 370
 gtc ccg aaa acg ttg aga ata gat gat cct aac gaa gca gca aag agc
 1267
 Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu Ala Ala Lys Ser
 375 380 385 390
 tcg ata tgg aca aca ttg gga atc aag aac gag gcg atg tgc aaa gcc
 1315
 Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Ala Met Cys Lys Ala
 395 400 405
 ggt ggt atg ttc aaa ggg ttt gat cat aag aca aag atg tat aac aac
 1363
 Gly Gly Met Phe Lys Gly Phe Asp His Lys Thr Lys Met Tyr Asn Asn
 410 415 420
 gac aaa gct gag aac tcc cct gtt ctt tct gct aac cct gct gct cta
 1411
 Asp Lys Ala Glu Asn Ser Pro Val Leu Ser Ala Asn Pro Ala Ala Leu
 425 430 435
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 1464
 Ser Arg Ser His Asn Phe His Glu Gln Ile
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 1524
 aactcttttc ttctttctag tgattgcctt tattccttta catgttttgg ttctctgtac
 1584
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 35 40 45
 Thr Pro Glu Leu Ser Asp Lys Asn Asn Asn Asn Cys Asn Asp Asn Ser
 50 55 60

Phe Asn Asn Ser Lys Pro Glu Thr Leu Asp Lys Glu Glu Ala Thr Ser
 65 70 75 80
 Thr Asp Gln Ile Glu Ser Ser Asp Thr Pro Glu Asp Asn Gln Gln Thr
 85 90 95
 Thr Pro Asp Gly Lys Thr Leu Lys Lys Pro Thr Lys Ile Leu Pro Cys
 100 105 110
 Pro Arg Cys Lys Ser Met Glu Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr
 115 120 125
 Asn Ile Asn Gln Pro Arg His Phe Cys Lys Ala Cys Gln Arg Tyr Trp
 130 135 140
 Thr Ala Gly Gly Thr Met Arg Asn Val Pro Val Gly Ala Gly Arg Arg
 145 150 155 160
 Lys Asn Lys Ser Ser Ser Ser His Tyr Arg His Ile Thr Ile Ser Glu
 165 170 175
 Ala Leu Glu Ala Ala Arg Leu Asp Pro Gly Leu Gln Ala Asn Thr Arg
 180 185 190
 Val Leu Ser Phe Gly Leu Glu Ala Gln Gln Gln His Val Ala Ala Pro
 195 200 205
 Met Thr Pro Val Met Lys Leu Gln Glu Asp Gln Lys Val Ser Asn Gly
 210 215 220
 Ala Arg Asn Arg Phe His Gly Leu Ala Asp Gln Arg Leu Val Ala Arg
 225 230 235 240
 Val Glu Asn Gly Asp Asp Cys Ser Ser Gly Ser Ser Val Thr Thr Ser
 245 250 255
 Asn Asn His Ser Val Asp Glu Ser Arg Ala Gln Ser Gly Ser Val Val
 260 265 270
 Glu Ala Gln Met Asn Asn Asn Asn Asn Asn Met Asn Gly Tyr Ala
 275 280 285
 Cys Ile Pro Gly Val Pro Trp Pro Tyr Thr Trp Asn Pro Ala Met Pro
 290 295 300

Pro Pro Gly Phe Tyr Pro Pro Pro Gly Tyr Pro Met Pro Phe Tyr Pro
305 310 315 320

Tyr Trp Thr Ile Pro Met Leu Pro Pro His Gln Ser Ser Ser Pro Ile
325 330 335

Ser Gln Lys Cys Ser Asn Thr Asn Ser Pro Thr Leu Gly Lys His Pro
340 345 350

Arg Asp Glu Gly Ser Ser Lys Lys Asp Asn Glu Thr Glu Arg Lys Gln
355 360 365

Lys Ala Gly Cys Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro
370 375 380

Asn Glu Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn
385 390 395 400

Glu Ala Met Cys Lys Ala Gly Gly Met Phe Lys Gly Phe Asp His Lys
405 410 415

Thr Lys Met Tyr Asn Asn Asp Lys Ala Glu Asn Ser Pro Val Leu Ser
420 425 430

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118

Met Lys Met
1

gaa aat ggt atg tat aaa aag aaa gga gtg tgc gac tct tgt gtc tcg
166
Glu Asn Gly Met Tyr Lys Lys Lys Gly Val Cys Asp Ser Cys Val Ser
5 10 15

tcc aaa agc aga tcc aac cac agc ccc aaa aga agc atg atg gag cct
214
Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met Glu Pro
20 25 30 35

cag cct cac cat ctc ctc atg gat tgg aac aaa gct aat gat ctt ctc
262
Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu Leu

40 45 50
 aca caa gaa cac gca gct ttt ctc aat gat cct cac cat ctc atg tta
 310
 Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met Leu
 55 60 65
 gat cca cct ccc gaa acc cta att cac ttg gac gaa gac gaa gag tac
 358
 Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu Tyr
 70 75 80
 gat gaa gac atg gat gcg atg aag gag atg cag tac atg atc gcc gtc
 406
 Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala Val
 85 90 95
 atg cag ccc gta gac atc gac cct gcc acg gtc cct aag ccg aac cgc
 454
 Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn Arg
 100 105 110 115
 cgt aac gta agg ata agc gac gat cct cag acg gtg gtt gct cgt cgg
 502
 Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg
 120 125 130
 cgt cgg gaa agg atc agc gag aag atc cga att ctc aag agg atc gtg
 550
 Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile Val
 135 140 145
 cct ggt ggt gcg aag atg gac aca gct tcc atg ctc gac gaa gcc ata
 598
 Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile
 150 155 160
 cgt tac acc aag ttc ttg aaa cgg cag gtg agg att ctt cag cct cac
 646
 Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro His
 165 170 175
 tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt tat tac
 694
 Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr Tyr
 180 185 190 195
 cac aac tcc caa ccc tga tgaactacac agaagctcgc tagctagaca
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 His Asn Ser Gln Pro
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Cys Val Ser Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met
 20 25 30

 Met Glu Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn
 35 40 45

 Asp Leu Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His
 50 55 60

 Leu Met Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp
 65 70 75 80

 Glu Glu Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met
 85 90 95

 Ile Ala Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys
 100 105 110

 Pro Asn Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val
 115 120 125

 Ala Arg Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys
 130 135 140

 Arg Ile Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp
 145 150 155 160

 Glu Ala Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu
 165 170 175

 Gln Pro His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu
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 Cys Tyr Tyr His Asn Ser Gln Pro
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 120

cgagaaggtt ttggagatag aatcttttgt tcttcttttg tccctccttg ctgcattttt
180

gttacgtgtg aagcaataaa aaaaaactga tatagctaaa tcttccatcc attcagaggc
240

ttctaaatct gatctgac atg gaa caa gtg ttt gct gat tgg aat ttt gaa
291

Met Glu Gln Val Phe Ala Asp Trp Asn Phe Glu
1 5 10

gat aat ttt cac atg tcc act aat aaa aga tca atc aga cca gaa gat
339

Asp Asn Phe His Met Ser Thr Asn Lys Arg Ser Ile Arg Pro Glu Asp
15 20 25

gaa tta gtg gag cta ttg tgg aga gat ggt caa gtg gtt tta caa agc
387

Glu Leu Val Glu Leu Leu Trp Arg Asp Gly Gln Val Val Leu Gln Ser
30 35 40

caa gct cgt aga gaa ccg tca gtc caa gtc caa acc cac aaa caa gaa
435

Gln Ala Arg Arg Glu Pro Ser Val Gln Val Gln Thr His Lys Gln Glu
45 50 55

acc cta aga aaa ccc aac aat att ttt ctt gac aac caa gaa aca gta
483

Thr Leu Arg Lys Pro Asn Asn Ile Phe Leu Asp Asn Gln Glu Thr Val
60 65 70 75

caa aag cct aac tac gct gct cta gat gat caa gaa acc gtc tcc tgg
531

Gln Lys Pro Asn Tyr Ala Ala Leu Asp Asp Gln Glu Thr Val Ser Trp
80 85 90

ata caa tac cct ccg gat gac gtc atc gac cct ttc gaa tcc gag ttc
579

Ile Gln Tyr Pro Pro Asp Asp Val Ile Asp Pro Phe Glu Ser Glu Phe
95 100 105

tcc tct cat ttc ttc tct tcg atc gat cac ctc gga ggt cct gag aag
627

Ser Ser His Phe Phe Ser Ser Ile Asp His Leu Gly Gly Pro Glu Lys
110 115 120

cca cga acg atc gaa gag aca gtt aag cat gag gct caa gcc atg gct
675

Pro Arg Thr Ile Glu Glu Thr Val Lys His Glu Ala Gln Ala Met Ala
125 130 135

cct cct aag ttt aga tcc tcg gtt ata aca gtc gga ccg agt cat tgc
723

Pro Pro Lys Phe Arg Ser Ser Val Ile Thr Val Gly Pro Ser His Cys
140 145 150 155

ggc agc aac cag tca aca aat att cat cag gcc act aca ctt ccg gtt
771

Gly Ser Asn Gln Ser Thr Asn Ile His Gln Ala Thr Thr Leu Pro Val
160 165 170

tct atg agt gat aga agc aag aac gtc gaa gaa aga ctt gac act tcg
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 Ser Met Ser Asp Arg Ser Lys Asn Val Glu Glu Arg Leu Asp Thr Ser
 175 180 185

tca ggt ggc tcc tcc ggt tgc agc tat gga agg aac aac aaa gaa acc
 867
 Ser Gly Gly Ser Ser Gly Cys Ser Tyr Gly Arg Asn Asn Lys Glu Thr
 190 195 200

gtt agt gga aca agt gta acc att gac cgt aaa aga aaa cat gtt atg
 915
 Val Ser Gly Thr Ser Val Thr Ile Asp Arg Lys Arg Lys His Val Met
 205 210 215

gat gct gat caa gaa tct gtg tct caa tca gat ata ggt ttg acc tca
 963
 Asp Ala Asp Gln Glu Ser Val Ser Gln Ser Asp Ile Gly Leu Thr Ser
 220 225 230 235

acc gat gat caa acc atg ggt aac aaa tcg agc caa cgg tca gga tct
 1011
 Thr Asp Asp Gln Thr Met Gly Asn Lys Ser Ser Gln Arg Ser Gly Ser
 240 245 250

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 1059
 Thr Arg Arg Ser Arg Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg
 255 260 265

agg aga gat cgg atc aat gaa aga atg aaa gct ctt caa gaa ctc ata
 1107
 Arg Arg Asp Arg Ile Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile
 270 275 280

cct cac tgc agc aga aca gat aaa gct tcg ata ttg gat gaa gca att
 1155
 Pro His Cys Ser Arg Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile
 285 290 295

gat tac tta aaa tca ctt caa atg caa ctc caa gtg atg tgg atg gga
 1203
 Asp Tyr Leu Lys Ser Leu Gln Met Gln Leu Gln Val Met Trp Met Gly
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 1251
 Ser Gly Met Ala Ala Ala Ala Ala Ala Ala Ser Pro Met Met Phe
 320 325 330

ccc ggg gta caa tca tct cca tac att aat cag atg gct atg caa agt
 1299
 Pro Gly Val Gln Ser Ser Pro Tyr Ile Asn Gln Met Ala Met Gln Ser
 335 340 345

cag atg caa ttg tct caa ttc ccg gtt atg aac ccg tcc gct ccg cag
 1347
 Gln Met Gln Leu Ser Gln Phe Pro Val Met Asn Arg Ser Ala Pro Gln
 350 355 360

aac cat ccc ggt tta gta tgt caa aac ccg gta cag ttg cag ctc caa
1395

Asn His Pro Gly Leu Val Cys Gln Asn Pro Val Gln Leu Gln Leu Gln
365 370 375

gca cag aac caa atc tta tcg gag cag ctc gct agg tac atg ggc ggg
1443

Ala Gln Asn Gln Ile Leu Ser Glu Gln Leu Ala Arg Tyr Met Gly Gly
380 385 390 395

att ccc cag atg ccg ccg gcg gga aat cag atg cag acc gtg caa caa
1491

Ile Pro Gln Met Pro Pro Ala Gly Asn Gln Met Gln Thr Val Gln Gln
400 405 410

caa cca gcg gac atg ttg gga ttt gga tct ccg gcg gga ccg caa agt
1539

Gln Pro Ala Asp Met Leu Gly Phe Gly Ser Pro Ala Gly Pro Gln Ser
415 420 425

caa ctg tcg gca ccg gcg acc acc gac agt ctt cat atg ggt aaa ata
1587

Gln Leu Ser Ala Pro Ala Thr Thr Asp Ser Leu His Met Gly Lys Ile
430 435 440

ggc tga cttggcatat agttttcctc cgaaattatt cttcttacag ttggtgattg
1643

Gly

ttatttattt ttggtcgcct aagcaagcat aaaagctaag tcaaattgat tatagagatc
1703

taataagtta gtctcactat tataacttat ttttaaacag ttgaattata gtatcaatca
1763

agtgttggga acctaaagat catacatgtg tcaatacttt tatatttggt ctcaagggtc
1823

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1913

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20 25 30

Leu Trp Arg Asp Gly Gln Val Val Leu Gln Ser Gln Ala Arg Arg Glu
35 40 45

Pro Ser Val Gln Val Gln Thr His Lys Gln Glu Thr Leu Arg Lys Pro
 50 55 60

Asn Asn Ile Phe Leu Asp Asn Gln Glu Thr Val Gln Lys Pro Asn Tyr
 65 70 75 80

Ala Ala Leu Asp Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro
 85 90 95

Asp Asp Val Ile Asp Pro Phe Glu Ser Glu Phe Ser Ser His Phe Phe
 100 105 110

Ser Ser Ile Asp His Leu Gly Gly Pro Glu Lys Pro Arg Thr Ile Glu
 115 120 125

Glu Thr Val Lys His Glu Ala Gln Ala Met Ala Pro Pro Lys Phe Arg
 130 135 140

Ser Ser Val Ile Thr Val Gly Pro Ser His Cys Gly Ser Asn Gln Ser
 145 150 155 160

Thr Asn Ile His Gln Ala Thr Thr Leu Pro Val Ser Met Ser Asp Arg
 165 170 175

Ser Lys Asn Val Glu Glu Arg Leu Asp Thr Ser Ser Gly Gly Ser Ser
 180 185 190

Gly Cys Ser Tyr Gly Arg Asn Asn Lys Glu Thr Val Ser Gly Thr Ser
 195 200 205

Val Thr Ile Asp Arg Lys Arg Lys His Val Met Asp Ala Asp Gln Glu
 210 215 220

Ser Val Ser Gln Ser Asp Ile Gly Leu Thr Ser Thr Asp Asp Gln Thr
 225 230 235 240

Met Gly Asn Lys Ser Ser Gln Arg Ser Gly Ser Thr Arg Arg Ser Arg
 245 250 255

Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg Ile
 260 265 270

Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser Arg
 275 280 285

Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys Ser
 230

290 295 300
 Leu Gln Met Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala Ala
 305 310 315 320
 Ala Ala Ala Ala Ala Ala Ser Pro Met Met Phe Pro Gly Val Gln Ser
 325 330 335
 Ser Pro Tyr Ile Asn Gln Met Ala Met Gln Ser Gln Met Gln Leu Ser
 340 345 350
 Gln Phe Pro Val Met Asn Arg Ser Ala Pro Gln Asn His Pro Gly Leu
 355 360 365
 Val Cys Gln Asn Pro Val Gln Leu Gln Leu Gln Ala Gln Asn Gln Ile
 370 375 380
 Leu Ser Glu Gln Leu Ala Arg Tyr Met Gly Gly Ile Pro Gln Met Pro
 385 390 395 400
 Pro Ala Gly Asn Gln Met Gln Thr Val Gln Gln Gln Pro Ala Asp Met
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 120
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 178
 Met Val
 1
 tca ccc gaa aac gct aat tgg att tgt gac ttg atc gat gct gat tac
 226
 Ser Pro Glu Asn Ala Asn Trp Ile Cys Asp Leu Ile Asp Ala Asp Tyr
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 274

Gly Ser Phe Thr Ile Gln Gly Pro Gly Phe Ser Trp Pro Val Gln Gln
 20 25 30
 cct att ggt gtt tct tct aac tcc agt gct gga gtt gat ggc tcg gct
 322
 Pro Ile Gly Val Ser Ser Asn Ser Ser Ala Gly Val Asp Gly Ser Ala
 35 40 45 50
 gga aac tca gaa gct agc aaa gaa cct gga tcc aaa aag agg ggg aga
 370
 Gly Asn Ser Glu Ala Ser Lys Glu Pro Gly Ser Lys Lys Arg Gly Arg
 55 60 65
 tgt gaa tca tcc tct gcc act agc tcg aaa gca tgt aga gag aag cag
 418
 Cys Glu Ser Ser Ser Ala Thr Ser Ser Lys Ala Cys Arg Glu Lys Gln
 70 75 80
 cga cgg gac agg ttg aat gac aag ttt atg gaa ttg ggt gca att ttg
 466
 Arg Arg Asp Arg Leu Asn Asp Lys Phe Met Glu Leu Gly Ala Ile Leu
 85 90 95
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 514
 Glu Pro Gly Asn Pro Pro Lys Thr Asp Lys Ala Ala Ile Leu Val Asp
 100 105 110
 gct gtc cgc atg gtg aca cag cta cgg ggc gag gcc cag aag ctg aag
 562
 Ala Val Arg Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys Leu Lys
 115 120 125 130
 gac tcc aat tca agt ctt cag gac aaa atc aaa gag tta aag act gag
 610
 Asp Ser Asn Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys Thr Glu
 135 140 145
 aaa aac gag ctg cga gat gag aaa cag agg ctg aag aca gag aaa gaa
 658
 Lys Asn Glu Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu Lys Glu
 150 155 160
 aag ctg gag cag cag ctg aaa gcc atg aat gct cct caa cca agt ttt
 706
 Lys Leu Glu Gln Gln Leu Lys Ala Met Asn Ala Pro Gln Pro Ser Phe
 165 170 175
 ttc cca gcc cca cct atg atg cct act gct ttt gct tca gcg caa ggc
 754
 Phe Pro Ala Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala Gln Gly
 180 185 190
 caa gct cct gga aac aag atg gtg cca atc atc agt tac cca gga gtt
 802
 Gln Ala Pro Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro Gly Val
 195 200 205 210
 gcc atg tgg cag ttc atg cct cct gct tca gtc gat act tct cag gat
 850
 Ala Met Trp Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser Gln Asp

215 220 225
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 897
 His Val Leu Arg Pro Pro Val Ala
 230
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 957
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 50 55 60
 Gly Arg Cys Glu Ser Ser Ser Ala Thr Ser Ser Lys Ala Cys Arg Glu
 65 70 75 80
 Lys Gln Arg Arg Asp Arg Leu Asn Asp Lys Phe Met Glu Leu Gly Ala
 85 90 95
 Ile Leu Glu Pro Gly Asn Pro Pro Lys Thr Asp Lys Ala Ala Ile Leu
 100 105 110
 Val Asp Ala Val Arg Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys
 115 120 125
 Leu Lys Asp Ser Asn Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys
 130 135 140
 Thr Glu Lys Asn Glu Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu
 145 150 155 160

Lys Glu Lys Leu Glu Gln Gln Leu Lys Ala Met Asn Ala Pro Gln Pro
 165 170 175

Ser Phe Phe Pro Ala Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala
 180 185 190

Gln Gly Gln Ala Pro Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro
 195 200 205

Gly Val Ala Met Trp Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser
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Gln Asp His Val Leu Arg Pro Pro Val Ala
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aac ggc atc ata gtc gag cag acg tca aac aaa gga cct ctt aac gcc
 101

Asn Gly Ile Ile Val Glu Gln Thr Ser Asn Lys Gly Pro Leu Asn Ala
 10 15 20 25

gtt aag aaa cca ccg tct aaa gat cga cac agc aaa gtt gac gga aga
 149

Val Lys Lys Pro Pro Ser Lys Asp Arg His Ser Lys Val Asp Gly Arg
 30 35 40

gga aga agg att cgt atg cca atc att tgc gca gct cga gtt ttt caa
 197

Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe Gln
 45 50 55

ttg acc aga gag tta ggt cac aag tcc gat ggt caa acc ata gag tgg
 245

Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu Trp
 60 65 70

ctt ctc cgt caa gct gag cct tct atc ata gcc gcc act gga act ggc
 293

Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly
 75 80 85

act act ccg gcg agt ttc tcc act gct tct ctc tcc act tct tct ccg
 341

Thr Thr Pro Ala Ser Phe Ser Thr Ala Ser Leu Ser Thr Ser Ser Pro
 90 95 100 105

ttt act'ctc ggg aaa cgt gtc gtc aga gcg gag gaa gga gaa tcc ggc
389

Phe Thr Leu Gly Lys Arg Val Val Arg Ala Glu Glu Gly Glu Ser Gly
110 115 120

ggc gga gga gga gga ggg tta aca gtg gga cac aca atg ggg act tcg
437

Gly Gly Gly Gly Gly Gly Leu Thr Val Gly His Thr Met Gly Thr Ser
125 130 135

tta atg ggt ggt ggt ggt tct ggt ggg ttt tgg gct gtt ccg gcg agg
485

Leu Met Gly Gly Gly Gly Ser Gly Gly Phe Trp Ala Val Pro Ala Arg
140 145 150

ccg gat ttc gga caa gtc tgg agc ttt gca acc gga gct cca ccg gaa
533

Pro Asp Phe Gly Gln Val Trp Ser Phe Ala Thr Gly Ala Pro Pro Glu
155 160 165

atg gtt ttt gcg cag cag cag caa cca gct aca ctc ttc gtc cgc cac
581

Met Val Phe Ala Gln Gln Gln Gln Pro Ala Thr Leu Phe Val Arg His
170 175 180 185

cag cag caa cag caa gct tcc gcc gcc gca gca gct gca atg ggt gag
629

Gln Gln Gln Gln Gln Ala Ser Ala Ala Ala Ala Ala Ala Met Gly Glu
190 195 200

gct tca gca gct aga gtt ggg aat tat ctt ccg ggt cat cat ctc aat
677

Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His His Leu Asn
205 210 215

ttg ctt gct tct ttg tct ggt gga gct aac ggg tcg ggt cgg agg gaa
725

Leu Leu Ala Ser Leu Ser Gly Gly Ala Asn Gly Ser Gly Arg Arg Glu
220 225 230

gac gac cac gaa cca cgt tga gaaatggtat tgtctttttg gtaatgtata
776

Asp Asp His Glu Pro Arg
235

gaaaaattcc tatgttttat gtcacgaaa gtgttttagaa agtacctcta atttgcggtt
836

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956

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1009

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 Thr Ser Asn Lys Gly Pro Leu Asn Ala Val Lys Lys Pro Pro Ser Lys
 20 25 30
 Asp Arg His Ser Lys Val Asp Gly Arg Gly Arg Arg Ile Arg Met Pro
 35 40 45
 Ile Ile Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu Gly His
 50 55 60
 Lys Ser Asp Gly Gln Thr Ile Glu Trp Leu Leu Arg Gln Ala Glu Pro
 65 70 75 80
 Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Thr Pro Ala Ser Phe Ser
 85 90 95
 Thr Ala Ser Leu Ser Thr Ser Ser Pro Phe Thr Leu Gly Lys Arg Val
 100 105 110
 Val Arg Ala Glu Glu Gly Glu Ser Gly Gly Gly Gly Gly Gly Gly Leu
 115 120 125
 Thr Val Gly His Thr Met Gly Thr Ser Leu Met Gly Gly Gly Gly Ser
 130 135 140
 Gly Gly Phe Trp Ala Val Pro Ala Arg Pro Asp Phe Gly Gln Val Trp
 145 150 155 160
 Ser Phe Ala Thr Gly Ala Pro Pro Glu Met Val Phe Ala Gln Gln Gln
 165 170 175
 Gln Pro Ala Thr Leu Phe Val Arg His Gln Gln Gln Gln Gln Ala Ser
 180 185 190
 Ala Ala Ala Ala Ala Ala Met Gly Glu Ala Ser Ala Ala Arg Val Gly
 195 200 205
 Asn Tyr Leu Pro Gly His His Leu Asn Leu Leu Ala Ser Leu Ser Gly
 210 215 220
 Gly Ala Asn Gly Ser Gly Arg Arg Glu Asp Asp His Glu Pro Arg
 225 230 235

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 116

Met
 1

gag tcc cac aac aac aac cag agc aac aac aac acc act ggt tcg gcc
 164

Glu Ser His Asn Asn Asn Gln Ser Asn Asn Asn Thr Thr Gly Ser Ala
 5 10 15

cat ctg gtc cca tcc atg gga cca atc tcc ggt tca gtc tca tta acc
 212

His Leu Val Pro Ser Met Gly Pro Ile Ser Gly Ser Val Ser Leu Thr
 20 25 30

acc act gct cca aac tcc act acc acc acc gtc acc gcc gct aaa aca
 260

Thr Thr Ala Pro Asn Ser Thr Thr Thr Thr Val Thr Ala Ala Lys Thr
 35 40 45

ccc gca aaa cga ccg tcc aag gac cgt cac atc aaa gta gac gga cgt
 308

Pro Ala Lys Arg Pro Ser Lys Asp Arg His Ile Lys Val Asp Gly Arg
 50 55 60 65

ggc cgg agg ata cgt atg ccg gct atc tgc gca gca cgt gtc ttc caa
 356

Gly Arg Arg Ile Arg Met Pro Ala Ile Cys Ala Ala Arg Val Phe Gln
 70 75 80

cta aca cgt gag tta caa cac aaa tcg gac ggc gag act ata gag tgg
 404

Leu Thr Arg Glu Leu Gln His Lys Ser Asp Gly Glu Thr Ile Glu Trp
 85 90 95

ctg ctc caa caa gcg gag cca gct atc atc gca gcc acc gga act gga
 452

Leu Leu Gln Gln Ala Glu Pro Ala Ile Ile Ala Ala Thr Gly Thr Gly
 100 105 110

acc ata ccg gcg aat atc tct act ttg aac atc tct ctt cga agc agt
 500

Thr Ile Pro Ala Asn Ile Ser Thr Leu Asn Ile Ser Leu Arg Ser Ser
 115 120 125

ggc tct act ctt tca gct cca ctg tct aaa tct ttc cac atg gga aga
 548

Gly Ser Thr Leu Ser Ala Pro Leu Ser Lys Ser Phe His Met Gly Arg
 130 135 140 145

gcg gct caa aac gct gcc gtt ttt ggg ttc cag caa cag ctt tat cat
 596

Ala Ala Gln Asn Ala Ala Val Phe Gly Phe Gln Gln Gln Leu Tyr His
 150 155 160

cct cat cat atc acg aca gat tct tct tct tct tct ctt ccc aaa aca
 644
 Pro His His Ile Thr Thr Asp Ser Ser Ser Ser Ser Leu Pro Lys Thr
 165 170 175

ttc cgt gaa gaa gat ctt ttt aaa gat cct aat ttt cta gat caa gaa
 692
 Phe Arg Glu Glu Asp Leu Phe Lys Asp Pro Asn Phe Leu Asp Gln Glu
 180 185 190

ccc ggt tca aga tca cct aaa ccg gga tcc gaa gct cct gat caa gat
 740
 Pro Gly Ser Arg Ser Pro Lys Pro Gly Ser Glu Ala Pro Asp Gln Asp
 195 200 205

ccg ggt tcg acc ccg tca aga aca caa aat atg ata ccg ccg atg tgg
 788
 Pro Gly Ser Thr Arg Ser Arg Thr Gln Asn Met Ile Pro Pro Met Trp
 210 215 220 225

gca cta gcg cca acg cca gcc tcc aca aac gga ggt agt gct ttt tgg
 836
 Ala Leu Ala Pro Thr Pro Ala Ser Thr Asn Gly Gly Ser Ala Phe Trp
 230 235 240

atg tta cca gtc gga gga gga gga ggt ccg gct aac gtt cag gat cca
 884
 Met Leu Pro Val Gly Gly Gly Gly Gly Pro Ala Asn Val Gln Asp Pro
 245 250 255

tca cag cac atg tgg gcg ttt aat ccg ggt cat tac ccg ggt cga atc
 932
 Ser Gln His Met Trp Ala Phe Asn Pro Gly His Tyr Pro Gly Arg Ile
 260 265 270

ggg tcg gtt cag cta ggg tct atg tta gtg gga ggt caa cag tta ggg
 980
 Gly Ser Val Gln Leu Gly Ser Met Leu Val Gly Gly Gln Gln Leu Gly
 275 280 285

tta ggt gtt gca gaa aat aac aat ttg ggg cta ttt tcc ggc gga gga
 1028
 Leu Gly Val Ala Glu Asn Asn Asn Leu Gly Leu Phe Ser Gly Gly Gly
 290 295 300 305

gga gac ggt ggt ccg gtt ggt ctc gga atg agt ctt gag caa aag cct
 1076
 Gly Asp Gly Gly Arg Val Gly Leu Gly Met Ser Leu Glu Gln Lys Pro
 310 315 320

caa cat caa gtg agt gat cat gct act aga gac caa aat cct act ata
 1124
 Gln His Gln Val Ser Asp His Ala Thr Arg Asp Gln Asn Pro Thr Ile
 325 330 335

gat ggt tct cct tga aagacttcat gattttctttg gtttttaaaa agtgtgaatg
 1179
 Asp Gly Ser Pro
 340

tgtgatttat tgcaactttt gttgaggact ccaatgtaa tatgggtttt agggttggct
1239

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1263

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Ala His Leu Val Pro Ser Met Gly Pro Ile Ser Gly Ser Val Ser Leu
20 25 30

Thr Thr Thr Ala Pro Asn Ser Thr Thr Thr Val Thr Ala Ala Lys
35 40 45

Thr Pro Ala Lys Arg Pro Ser Lys Asp Arg His Ile Lys Val Asp Gly
50 55 60

Arg Gly Arg Arg Ile Arg Met Pro Ala Ile Cys Ala Ala Arg Val Phe
65 70 75 80

Gln Leu Thr Arg Glu Leu Gln His Lys Ser Asp Gly Glu Thr Ile Glu
85 90 95

Trp Leu Leu Gln Gln Ala Glu Pro Ala Ile Ile Ala Ala Thr Gly Thr
100 105 110

Gly Thr Ile Pro Ala Asn Ile Ser Thr Leu Asn Ile Ser Leu Arg Ser
115 120 125

Ser Gly Ser Thr Leu Ser Ala Pro Leu Ser Lys Ser Phe His Met Gly
130 135 140

Arg Ala Ala Gln Asn Ala Ala Val Phe Gly Phe Gln Gln Gln Leu Tyr
145 150 155 160

His Pro His His Ile Thr Thr Asp Ser Ser Ser Ser Ser Leu Pro Lys
165 170 175

Thr Phe Arg Glu Glu Asp Leu Phe Lys Asp Pro Asn Phe Leu Asp Gln
180 185 190

Glu Pro Gly Ser Arg Ser Pro Lys Pro Gly Ser Glu Ala Pro Asp Gln
195 200 205

Asp Pro Gly Ser Thr Arg Ser Arg Thr Gln Asn Met Ile Pro Pro Met
 210 215 220

Trp Ala Leu Ala Pro Thr Pro Ala Ser Thr Asn Gly Gly Ser Ala Phe
 225 230 235 240

Trp Met Leu Pro Val Gly Gly Gly Gly Gly Pro Ala Asn Val Gln Asp
 245 250 255

Pro Ser Gln His Met Trp Ala Phe Asn Pro Gly His Tyr Pro Gly Arg
 260 265 270

Ile Gly Ser Val Gln Leu Gly Ser Met Leu Val Gly Gly Gln Gln Leu
 275 280 285

Gly Leu Gly Val Ala Glu Asn Asn Asn Leu Gly Leu Phe Ser Gly Gly
 290 295 300

Gly Gly Asp Gly Gly Arg Val Gly Leu Gly Met Ser Leu Glu Gln Lys
 305 310 315 320

Pro Gln His Gln Val Ser Asp His Ala Thr Arg Asp Gln Asn Pro Thr
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Ile Asp Gly Ser Pro
 340

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ccacttcccc ccaccaaag cttcgatcat catcatcatc atcatc atg gat ccg
 115

Met Asp Pro
 1

gat ccg gat cat aac cat cga ccc aac ttc cct ctc cag ctt ctt gat
 163

Asp Pro Asp His Asn His Arg Pro Asn Phe Pro Leu Gln Leu Leu Asp
 5 10 15

tct tct acc tcc tcc tct tcc act tcc tta gcc atc atc tct act act
 211

Ser Ser Thr Ser Ser Ser Ser Thr Ser Leu Ala Ile Ile Ser Thr Thr
 20 25 30 35

tcc gaa cct aac tcc gaa cct aag aag cct cct cct aaa cga acc tct
 259

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Ser Glu Pro Asn Ser Glu Pro Lys Lys Pro Pro Pro Lys Arg Thr Ser
      40      45      50
act aaa gac cga cac acc aaa gtc gaa ggc cga ggc cgt cgg atc cgt
307
Thr Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile Arg
      55      60      65
atg cct gcc atg tgt gct gca cgt gtc ttt cag ctc aca cgt gag ctt
355
Met Pro Ala Met Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu
      70      75      80
ggg cac aaa tcc gac ggt gaa act att gag tgg cta ctc caa caa gca
403
Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala
      85      90      95
gaa cca gcg gtt ata gcc gct aca ggg act gga acc att ccg gct aac
451
Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn
100      105      110      115
ttc act tct tta aac atc tca ctt cgt agc tca aga tct tct ctc tct
499
Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Arg Ser Ser Leu Ser
      120      125      130
gct gct cat ctt cgt aca act cct agt agc tat tac ttt cat tca cca
547
Ala Ala His Leu Arg Thr Thr Pro Ser Ser Tyr Tyr Phe His Ser Pro
      135      140      145
cat cag tcc atg act cat cat ctt caa cat cag cat cag gtt cgt ccc
595
His Gln Ser Met Thr His His Leu Gln His Gln His Gln Val Arg Pro
      150      155      160
aag aac gag tca cat tct tcg tct tct tct tct tca cag ctt tta gat
643
Lys Asn Glu Ser His Ser Ser Ser Ser Ser Ser Ser Gln Leu Leu Asp
      165      170      175
cac aac caa atg ggt aac tat cta gta caa tca act gct gga tct tta
691
His Asn Gln Met Gly Asn Tyr Leu Val Gln Ser Thr Ala Gly Ser Leu
180      185      190      195
cct acg agt cag agt cct gca acg gca ccg ttt tgg agt agt ggt gac
739
Pro Thr Ser Gln Ser Pro Ala Thr Ala Pro Phe Trp Ser Ser Gly Asp
      200      205      210
aac aca cag aat ctt tgg gct ttt aat att aat cct cat cat tcc ggt
787
Asn Thr Gln Asn Leu Trp Ala Phe Asn Ile Asn Pro His His Ser Gly
      215      220      225
gtt gtc gcc gga gat gtt tac aac ccc aac agt ggt ggt agt ggc ggc
835
Val Val Ala Gly Asp Val Tyr Asn Pro Asn Ser Gly Gly Ser Gly Gly

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230 235 240
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 883
 Gly Ser Gly Val His Leu Met Asn Phe Ala Ala Pro Ile Ala Leu Phe
 245 250 255
 tct gga cag cct ttg gct tct ggt tat gga gga gga gga ggt ggc ggt
 931
 Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly Gly Gly Gly
 260 265 270 275
 gga gaa cat agc cat tat gga gtt tta gcg gcg ttg aat gct gct tac
 979
 Gly Glu His Ser His Tyr Gly Val Leu Ala Ala Leu Asn Ala Ala Tyr
 280 285 290
 cga ccg gtg gcg gag acg ggg aac cat aac aac aac cag caa aac cgt
 1027
 Arg Pro Val Ala Glu Thr Gly Asn His Asn Asn Asn Gln Gln Asn Arg
 295 300 305
 gac gga gat cat cat cac aac cat caa gaa gat gga agc acc agt cat
 1075
 Asp Gly Asp His His His Asn His Gln Glu Asp Gly Ser Thr Ser His
 310 315 320
 cat tcc tag gcaaacatac acaaacaaat atattctgtg agatttattt
 1124
 His Ser
 325
 ttcttttttt gtcttttctg ttgtttgttt gttcttaaca agcgtgtttt ttttgcattg
 1184
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 1231
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 Ser Thr Thr Ser Glu Pro Asn Ser Glu Pro Lys Lys Pro Pro Pro Lys
 35 40 45
 Arg Thr Ser Thr Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg
 50 55 60
 Arg Ile Arg Met Pro Ala Met Cys Ala Ala Arg Val Phe Gln Leu Thr
 65 70 75 80

Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu
85 90 95

Gln Gln Ala Glu Pro Ala Val Ile Ala Ala Thr Gly Thr Gly Thr Ile
100 105 110

Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Arg Ser
115 120 125

Ser Leu Ser Ala Ala His Leu Arg Thr Thr Pro Ser Ser Tyr Tyr Phe
130 135 140

His Ser Pro His Gln Ser Met Thr His His Leu Gln His Gln His Gln
145 150 155 160

Val Arg Pro Lys Asn Glu Ser His Ser Ser Ser Ser Ser Ser Ser Gln
165 170 175

Leu Leu Asp His Asn Gln Met Gly Asn Tyr Leu Val Gln Ser Thr Ala
180 185 190

Gly Ser Leu Pro Thr Ser Gln Ser Pro Ala Thr Ala Pro Phe Trp Ser
195 200 205

Ser Gly Asp Asn Thr Gln Asn Leu Trp Ala Phe Asn Ile Asn Pro His
210 215 220

His Ser Gly Val Val Ala Gly Asp Val Tyr Asn Pro Asn Ser Gly Gly
225 230 235 240

Ser Gly Gly Gly Ser Gly Val His Leu Met Asn Phe Ala Ala Pro Ile
245 250 255

Ala Leu Phe Ser Gly Gln Pro Leu Ala Ser Gly Tyr Gly Gly Gly Gly
260 265 270

Gly Gly Gly Gly Glu His Ser His Tyr Gly Val Leu Ala Ala Leu Asn
275 280 285

Ala Ala Tyr Arg Pro Val Ala Glu Thr Gly Asn His Asn Asn Asn Gln
290 295 300

Gln Asn Arg Asp Gly Asp His His His Asn His Gln Glu Asp Gly Ser
305 310 315 320

Thr Ser His His Ser
325

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cagg atg atg aac ccg ttt ctc ccg gaa ggc tgc gat cca cca cca cca
109

Met Met Asn Pro Phe Leu Pro Glu Gly Cys Asp Pro Pro Pro Pro
1 5 10 15

cca caa cca atg gag ggt tta cac gaa aat gct cca cct cca ttt ctg
157

Pro Gln Pro Met Glu Gly Leu His Glu Asn Ala Pro Pro Pro Phe Leu
20 25 30

acc aag aca ttt gag atg gtg gat gat cca aac act gac cac atc gta
205

Thr Lys Thr Phe Glu Met Val Asp Asp Pro Asn Thr Asp His Ile Val
35 40 45

tct tgg aac aga gga gga aca agt ttt gtc gtc tgg gat ttg cat tct
253

Ser Trp Asn Arg Gly Gly Thr Ser Phe Val Val Trp Asp Leu His Ser
50 55 60

ttc tcc acg att cto ctt cct cgt cat ttc aaa cac agc aat ttc tca
301

Phe Ser Thr Ile Leu Leu Pro Arg His Phe Lys His Ser Asn Phe Ser
65 70 75

agt ttc atc aga caa ctc aat act tat ggt ttc aga aag ata gaa gca
349

Ser Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala
80 85 90 95

gag aga tgg gaa ttt gca aac gaa gag ttt ttg tta gga caa aga cag
397

Glu Arg Trp Glu Phe Ala Asn Glu Glu Phe Leu Leu Gly Gln Arg Gln
100 105 110

ttg ttg aag aac atc aag agg aga aac cct ttt act cca tca tct tca
445

Leu Leu Lys Asn Ile Lys Arg Arg Asn Pro Phe Thr Pro Ser Ser Ser
115 120 125

cca agc cat gac gct tgc aac gag ctt cgc aga gag aag caa gtg cta
493

Pro Ser His Asp Ala Cys Asn Glu Leu Arg Arg Glu Lys Gln Val Leu
130 135 140

atg atg gag ata gtg agt cta aga cag cag caa caa aca acg aaa agc
541

Met Met Glu Ile Val Ser Leu Arg Gln Gln Gln Gln Thr Thr Lys Ser
145 150 155

tac atc aaa gct atg gaa cag agg ata gaa gga aca gag agg aaa cag
589
Tyr Ile Lys Ala Met Glu Gln Arg Ile Glu Gly Thr Glu Arg Lys Gln
160 165 170 175

aga caa atg atg tcg ttt ctg gct aga gca atg cag agt cct tcg ttt
637
Arg Gln Met Met Ser Phe Leu Ala Arg Ala Met Gln Ser Pro Ser Phe
180 185 190

ttg cat cag ttg ttg aaa caa aga gat aaa aaa att aag gag ctt gag
685
Leu His Gln Leu Leu Lys Gln Arg Asp Lys Lys Ile Lys Glu Leu Glu
195 200 205

gat aat gag tca gca aag agg aaa aga ggt tct tct tcg atg tcg gaa
733
Asp Asn Glu Ser Ala Lys Arg Lys Arg Gly Ser Ser Ser Met Ser Glu
210 215 220

ttg gaa gtt ttg gct ttg gag atg caa ggg cat gga aaa cag agg aat
781
Leu Glu Val Leu Ala Leu Glu Met Gln Gly His Gly Lys Gln Arg Asn
225 230 235

atg ttg gaa gaa gag gat cat caa ctg gtg gta gag aga gag ttg gat
829
Met Leu Glu Glu Glu Asp His Gln Leu Val Val Glu Arg Glu Leu Asp
240 245 250 255

gat ggt ttc tgg gaa gag ttg ctt agt gat gag agt ttg gct tcc acc
877
Asp Gly Phe Trp Glu Glu Leu Leu Ser Asp Glu Ser Leu Ala Ser Thr
260 265 270

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933
Ser

tcatttttctt ctgtcacao
952

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140

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Gln Pro Met Glu Gly Leu His Glu Asn Ala Pro Pro Pro Phe Leu Thr
20 25 30

Lys Thr Phe Glu Met Val Asp Asp Pro Asn Thr Asp His Ile Val Ser
35 40 45

Trp Asn Arg Gly Gly Thr Ser Phe Val Val Trp Asp Leu His Ser Phe
50 55 60

Ser Thr Ile Leu Leu Pro Arg His Phe Lys His Ser Asn Phe Ser Ser
65 70 75 80

Phe Ile Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu
85 90 95

Arg Trp Glu Phe Ala Asn Glu Glu Phe Leu Leu Gly Gln Arg Gln Leu
100 105 110

Leu Lys Asn Ile Lys Arg Arg Asn Pro Phe Thr Pro Ser Ser Ser Pro
115 120 125

Ser His Asp Ala Cys Asn Glu Leu Arg Arg Glu Lys Gln Val Leu Met
130 135 140

Met Glu Ile Val Ser Leu Arg Gln Gln Gln Gln Thr Thr Lys Ser Tyr
145 150 - 155 160

Ile Lys Ala Met Glu Gln Arg Ile Glu Gly Thr Glu Arg Lys Gln Arg
165 170 175

Gln Met Met Ser Phe Leu Ala Arg Ala Met Gln Ser Pro Ser Phe Leu
180 185 190

His Gln Leu Leu Lys Gln Arg Asp Lys Lys Ile Lys Glu Leu Glu Asp
195 200 205

Asn Glu Ser Ala Lys Arg Lys Arg Gly Ser Ser Ser Met Ser Glu Leu
210 215 220

Glu Val Leu Ala Leu Glu Met Gln Gly His Gly Lys Gln Arg Asn Met
225 230 235 240

Leu Glu Glu Glu Asp His Gln Leu Val Val Glu Arg Glu Leu Asp Asp
245 250 255

Gly Phe Trp Glu Glu Leu Leu Ser Asp Glu Ser Leu Ala Ser Thr Ser
260 265 270

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120

ggaatttggg ttttaagata gcgtgatctg taataataag tggttcgcga tcgtgatcaa
180

gaaactgggt gctgatagtg atatgcatat ttgagag atg gtg ttc aag aga aag
235

Met Val Phe Lys Arg Lys
1 5

tta gat tgc ctt tcc gtg gga ttt gat ttt ccc aac att ccc aga gct
283

Leu Asp Cys Leu Ser Val Gly Phe Asp Phe Pro Asn Ile Pro Arg Ala
10 15 20

cct cgt tca tgc agg agg aag gtt cta aac aag agg att gat cat gat
331

Pro Arg Ser Cys Arg Arg Lys Val Leu Asn Lys Arg Ile Asp His Asp
25 30 35

gat gat aac act cag atc tgt gca att gac tta cta gct ttg gct gga
379

Asp Asp Asn Thr Gln Ile Cys Ala Ile Asp Leu Leu Ala Leu Ala Gly
40 45 50

aag att cta cag gaa agc gag agt tcc tct gcg tct tct aat gca ttt
427

Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser Ala Ser Ser Asn Ala Phe
55 60 65 70

gaa gaa att aag caa gag aaa gta gaa aat tgc aag act att aaa tct
475

Glu Glu Ile Lys Gln Glu Lys Val Glu Asn Cys Lys Thr Ile Lys Ser
75 80 85

gag tct tct gac caa gga aac tct gtg tca aag cct act tat gat atc
523

Glu Ser Ser Asp Gln Gly Asn Ser Val Ser Lys Pro Thr Tyr Asp Ile
90 95 100

tct act gag aag tgt gtg gtg aac agt tgt ttt tca ttt ccg gat agt
571

Ser Thr Glu Lys Cys Val Val Asn Ser Cys Phe Ser Phe Pro Asp Ser
105 110 115

gac ggc gtt ttg gag cgg act ccg atg tct gat tac aag aag att cat
619

Asp Gly Val Leu Glu Arg Thr Pro Met Ser Asp Tyr Lys Lys Ile His
120 125 130

ggt ttg atg gat gta ggg tgt gaa aac aag aat gta aat aat ggg ttc
667

Gly Leu Met Asp Val Gly Cys Glu Asn Lys Asn Val Asn Asn Gly Phe
135 140 145 150

gag caa gga gaa gca acc gat cgc gtg ggt gat gga ggc tta gtc act
715

Glu Gln Gly Glu Ala Thr Asp Arg Val Gly Asp Gly Gly Leu Val Thr
155 160 165

gat act tgc aac tta gag gat gca act gcg tta ggt ctg cag ttt ccg
 763
 Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala Leu Gly Leu Gln Phe Pro
 170 175 180

aaa tca gtc tgt gtg ggt ggt gat tta aaa tca cca tcc acc ttg gat
 811
 Lys Ser Val Cys Val Gly Gly Asp Leu Lys Ser Pro Ser Thr Leu Asp
 185 190 195

atg acc cct aat ggt tcc tat gct aga cat ggg aac cat act aac cta
 859
 Met Thr Pro Asn Gly Ser Tyr Ala Arg His Gly Asn His Thr Asn Leu
 200 205 210

ggt aga aaa gat gat gat gaa aaa ttc tat agt tac cat aaa ctt agc
 907
 Gly Arg Lys Asp Asp Asp Glu Lys Phe Tyr Ser Tyr His Lys Leu Ser
 215 220 225 230

aat aaa ttt aag tcg tat agg tct cca aca att cga aga ata aga aag
 955
 Asn Lys Phe Lys Ser Tyr Arg Ser Pro Thr Ile Arg Arg Ile Arg Lys
 235 240 245

tcc atg tcg tcc aaa tac tgg aaa caa gtt cca aaa gat ttt gga tac
 1003
 Ser Met Ser Ser Lys Tyr Trp Lys Gln Val Pro Lys Asp Phe Gly Tyr
 250 255 260

agt aga gct gat gtg ggt gtg aag act ctt tat cgc aaa aga aaa tca
 1051
 Ser Arg Ala Asp Val Gly Val Lys Thr Leu Tyr Arg Lys Arg Lys Ser
 265 270 275

tgt tat ggt tac aac gca tgg cag cgt gag atc att tat aag aga aga
 1099
 Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu Ile Ile Tyr Lys Arg Arg
 280 285 290

aga tca cct gac aga agc tcg gtc gta act tct gat gga gga ctc agt
 1147
 Arg Ser Pro Asp Arg Ser Ser Val Val Thr Ser Asp Gly Gly Leu Ser
 295 300 305 310

agt gga agt gtt tcc aag tta ccc aag aag gga gat aca gta aag cta
 1195
 Ser Gly Ser Val Ser Lys Leu Pro Lys Lys Gly Asp Thr Val Lys Leu
 315 320 325

agc att aag tcc ttt agg att cca gag ctt ttt att gaa gtt cca gaa
 1243
 Ser Ile Lys Ser Phe Arg Ile Pro Glu Leu Phe Ile Glu Val Pro Glu
 330 335 340

act gca aca gta gga tca cta aag agg act gtg atg gag gct gtc agt
 1291
 Thr Ala Thr Val Gly Ser Leu Lys Arg Thr Val Met Glu Ala Val Ser
 345 350 355

gtt tta ctc agc gga gga ata cgt gtt ggg gtg tta atg cat ggg aag
 1339
 Val Leu Leu Ser Gly Gly Ile Arg Val Gly Val Leu Met His Gly Lys
 360 365 370
 aag gtt aga gat gaa agg aaa act ctg tcc cag act ggg atc tca tgt
 1387
 Lys Val Arg Asp Glu Arg Lys Thr Leu Ser Gln Thr Gly Ile Ser Cys
 375 380 385 390
 gat gaa aat cta gac aac ctt ggg ttc acc ttg gag cct agt ccc agc
 1435
 Asp Glu Asn Leu Asp Asn Leu Gly Phe Thr Leu Glu Pro Ser Pro Ser
 395 400 405
 aaa gtt ccc cta cct ttg tgt tct gaa gat cct gct gtg cca acc gac
 1483
 Lys Val Pro Leu Pro Leu Cys Ser Glu Asp Pro Ala Val Pro Thr Asp
 410 415 420
 cct aca agt ttg tct gaa cgg tct gcg gcg tct cct atg cta gat tct
 1531
 Pro Thr Ser Leu Ser Glu Arg Ser Ala Ala Ser Pro Met Leu Asp Ser
 425 430 435
 gga att cca cat gca gat gac gtg att gat tca aga aat att gtg gac
 1579
 Gly Ile Pro His Ala Asp Asp Val Ile Asp Ser Arg Asn Ile Val Asp
 440 445 450
 agt aac ctc gaa tta gtt cca tat cag ggt gac ata tct gtt gat gaa
 1627
 Ser Asn Leu Glu Leu Val Pro Tyr Gln Gly Asp Ile Ser Val Asp Glu
 455 460 465 470
 cct tca tca gat tca aaa gag ctt gtc cca ctt cca gag ttg gaa gtc
 1675
 Pro Ser Ser Asp Ser Lys Glu Leu Val Pro Leu Pro Glu Leu Glu Val
 475 480 485
 aag gcg ctt gcc ata gtt ccg ttg aac cag aaa cct aag cgt act gag
 1723
 Lys Ala Leu Ala Ile Val Pro Leu Asn Gln Lys Pro Lys Arg Thr Glu
 490 495 500
 cta gcc cag agg aga act agg aga ccc ttc tct gtg aca gag gta gaa
 1771
 Leu Ala Gln Arg Arg Thr Arg Arg Pro Phe Ser Val Thr Glu Val Glu
 505 510 515
 gct ctt gta caa gca gtt gag gaa ctc ggg act gga aga tgg cgt gat
 1819
 Ala Leu Val Gln Ala Val Glu Glu Leu Gly Thr Gly Arg Trp Arg Asp
 520 525 530
 gta aaa ttg cgt gct ttc gag gat gca gat cat cgg act tac gtg gac
 1867
 Val Lys Leu Arg Ala Phe Glu Asp Ala Asp His Arg Thr Tyr Val Asp
 535 540 545 550

ttg aag gac aaa tgg aag acg cta gtt cac aca gca agt ata tcc cca
1915

Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr Ala Ser Ile Ser Pro
555 560 565

cag caa cga aga gga gag ccg gtg cca caa gaa ctg cta gac aga gtc
1963

Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu Leu Leu Asp Arg Val
570 575 580

ttg agg gca tac ggg tat tgg tcg cag cac caa gga aaa cat cag gcg
2011

Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His Gln Gly Lys His Gln Ala
585 590 595

aga gga gcg tcc aaa gat cca gac atg aac aga ggt gga gct ttt gaa
2059

Arg Gly Ala Ser Lys Asp Pro Asp Met Asn Arg Gly Gly Ala Phe Glu
600 605 610

tca ggt gtt tca gtg taa aaaaggaggt acgcattggt ggggtgggtgt
2107

Ser Gly Val Ser Val
615

acagaagcaa acaacacaat aaatggacaa ctcaatttct gcaaagtta attgtcttta
2167

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2214

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20 25 30

Lys Arg Ile Asp His Asp Asp Asp Asn Thr Gln Ile Cys Ala Ile Asp
35 40 45

Leu Leu Ala Leu Ala Gly Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser
50 55 60

Ala Ser Ser Asn Ala Phe Glu Glu Ile Lys Gln Glu Lys Val Glu Asn
65 70 75 80

Cys Lys Thr Ile Lys Ser Glu Ser Ser Asp Gln Gly Asn Ser Val Ser
85 90 95

Lys Pro Thr Tyr Asp Ile Ser Thr Glu Lys Cys Val Val Asn Ser Cys
100 105 110

250

Phe Ser Phe Pro Asp Ser Asp Gly Val Leu Glu Arg Thr Pro Met Ser
 115 120 125

Asp Tyr Lys Lys Ile His Gly Leu Met Asp Val Gly Cys Glu Asn Lys
 130 135 140

Asn Val Asn Asn Gly Phe Glu Gln Gly Glu Ala Thr Asp Arg Val Gly
 145 150 155 160

Asp Gly Gly Leu Val Thr Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala
 165 170 175

Leu Gly Leu Gln Phe Pro Lys Ser Val Cys Val Gly Gly Asp Leu Lys
 180 185 190

Ser Pro Ser Thr Leu Asp Met Thr Pro Asn Gly Ser Tyr Ala Arg His
 195 200 205

Gly Asn His Thr Asn Leu Gly Arg Lys Asp Asp Asp Glu Lys Phe Tyr
 210 215 220

Ser Tyr His Lys Leu Ser Asn Lys Phe Lys Ser Tyr Arg Ser Pro Thr
 225 230 235 240

Ile Arg Arg Ile Arg Lys Ser Met Ser Ser Lys Tyr Trp Lys Gln Val
 245 250 255

Pro Lys Asp Phe Gly Tyr Ser Arg Ala Asp Val Gly Val Lys Thr Leu
 260 265 270

Tyr Arg Lys Arg Lys Ser Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu
 275 280 285

Ile Ile Tyr Lys Arg Arg Arg Ser Pro Asp Arg Ser Ser Val Val Thr
 290 295 300

Ser Asp Gly Gly Leu Ser Ser Gly Ser Val Ser Lys Leu Pro Lys Lys
 305 310 315 320

Gly Asp Thr Val Lys Leu Ser Ile Lys Ser Phe Arg Ile Pro Glu Leu
 325 330 335

Phe Ile Glu Val Pro Glu Thr Ala Thr Val Gly Ser Leu Lys Arg Thr
 340 345 350

Val Met Glu Ala Val Ser Val Leu Leu Ser Gly Gly Ile Arg Val Gly
 355 360 365

Val Leu Met His Gly Lys Lys Val Arg Asp Glu Arg Lys Thr Leu Ser
 370 375 380

Gln Thr Gly Ile Ser Cys Asp Glu Asn Leu Asp Asn Leu Gly Phe Thr
 385 390 395 400

Leu Glu Pro Ser Pro Ser Lys Val Pro Leu Pro Leu Cys Ser Glu Asp
 405 410 415

Pro Ala Val Pro Thr Asp Pro Thr Ser Leu Ser Glu Arg Ser Ala Ala
 420 425 430

Ser Pro Met Leu Asp Ser Gly Ile Pro His Ala Asp Asp Val Ile Asp
 435 440 445

Ser Arg Asn Ile Val Asp Ser Asn Leu Glu Leu Val Pro Tyr Gln Gly
 450 455 460

Asp Ile Ser Val Asp Glu Pro Ser Ser Asp Ser Lys Glu Leu Val Pro
 465 470 475 480

Leu Pro Glu Leu Glu Val Lys Ala Leu Ala Ile Val Pro Leu Asn Gln
 485 490 495

Lys Pro Lys Arg Thr Glu Leu Ala Gln Arg Arg Thr Arg Arg Pro Phe
 500 505 510

Ser Val Thr Glu Val Glu Ala Leu Val Gln Ala Val Glu Glu Leu Gly
 515 520 525

Thr Gly Arg Trp Arg Asp Val Lys Leu Arg Ala Phe Glu Asp Ala Asp
 530 535 540

His Arg Thr Tyr Val Asp Leu Lys Asp Lys Trp Lys Thr Leu Val His
 545 550 555 560

Thr Ala Ser Ile Ser Pro Gln Gln Arg Arg Gly Glu Pro Val Pro Gln
 565 570 575

Glu Leu Leu Asp Arg Val Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His
 580 585 590

Gln Gly Lys His Gln Ala Arg Gly Ala Ser Lys Asp Pro Asp Met Asn
 595 600 605

Arg Gly Gly Ala Phe Glu Ser Gly Val Ser Val
 610 615

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acaacaaaaa acacattgta acattagttt aagcattaag cttcttt atg tcg aat
 116

Met Ser Asn
 1

aat aat aat tct ccg acc acc gtg aat caa gaa acg acg acg tct cgt
 164

Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr Thr Ser Arg
 5 10 15

gaa gtc tca atc aca ttg cct act gat caa tct cct caa acc tca cca
 212

Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln Thr Ser Pro
 20 25 30 35

gga tca tct tct tct cct tca ccg aga cct tcc ggt gga tca ccg gcg
 260

Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly Ser Pro Ala
 40 45 50

aga aga acg gcg act gga tta tcc ggc aag cac tct att ttc agg ggg
 308

Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile Phe Arg Gly
 55 60 65

att cga cta cgt aac gga aaa tgg gta tcg gag att aga gag cca cgt
 356

Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg
 70 75 80

aaa acg aca aga att tgg ctc ggg act tat ccg gta ccg gag atg gct
 404

Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro Glu Met Ala
 85 90 95

gcc gcc gct tac gac gtg gct gcg tta gct tta aaa gga ccc gac gcc
 452

Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Pro Asp Ala
 100 105 110 115

gtt ttg aat ttt cct ggt tta gct ttg act tac gtg gct ccg gtt tca
 500

Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala Pro Val Ser
 120 125 130

aac tct gct gcg gat ata aga gcg gct gct agt aga gca gcg gag atg
548

Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala Ala Glu Met
135 140 145

aag caa ccg gat cag ggt ggg gat gag aag gta ttg gaa ccg gtt caa
596

Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu Pro Val Gln
150 155 160

ccc ggc aaa gag gaa gaa tta gaa gaa gtg tcg tgt aac tcg tgt tcg
644

Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn Ser Cys Ser
165 170 175

ttg gag ttt atg gat gag gaa gcg atg ttg aat atg ccg act ttg ttg
692

Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro Thr Leu Leu
180 185 190 195

acg gag atg gct gaa ggg atg ttg atg agt cca ccg aga atg atg ata
740

Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg Met Met Ile
200 205 210

cat ccg acg atg gaa gat gat tcg ccg gag aat cat gaa gga gat aat
788

His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu Gly Asp Asn
215 220 225

ctt tgg agt tat aaa tga atccattgaa gctgctctct tttttattgt
836

Leu Trp Ser Tyr Lys
230

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890

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144

Met Ser Asn Asn Asn Asn Ser Pro Thr Thr Val Asn Gln Glu Thr Thr
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Thr Ser Arg Glu Val Ser Ile Thr Leu Pro Thr Asp Gln Ser Pro Gln
20 25 30

Thr Ser Pro Gly Ser Ser Ser Ser Pro Ser Pro Arg Pro Ser Gly Gly
35 40 45

Ser Pro Ala Arg Arg Thr Ala Thr Gly Leu Ser Gly Lys His Ser Ile
50 55 60

Phe Arg Gly Ile Arg Leu Arg Asn Gly Lys Trp Val Ser Glu Ile Arg
65 70 75 80

Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Val Pro
85 90 95

Glu Met Ala¹ Ala Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly
100 105 110

Pro Asp Ala Val Leu Asn Phe Pro Gly Leu Ala Leu Thr Tyr Val Ala
115 120 125

Pro Val Ser Asn Ser Ala Ala Asp Ile Arg Ala Ala Ala Ser Arg Ala
130 135 140

Ala Glu Met Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu
145 150 155 160

Pro Val Gln Pro Gly Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn
165 170 175

Ser Cys Ser Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro
180 185 190

Thr Leu Leu Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg
195 200 205

Met Met Ile His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu
210 215 220

Gly Asp Asn Leu Trp Ser Tyr Lys
225 230

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60

cacacatata catccacaag aacccatata gaagattcat cctacatata ttac atg
118

Met
1

gat cag tac tca tcc tct ttg gtc gat act tca tta gat ctc act att
166

Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr Ile
5 10 15

ggc gtt act cgt atg cga gtt gaa gaa gat cca ccg aca agt gct ttg
214

Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala Leu

20 25 30
 gtg gaa gaa tta aac cga gtt agt gct gag aac aag aag ctc tcg gag
 262
 Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser Glu
 35 40 45
 atg cta act ttg atg tgt gac aac tac aac gtc ttg agg aag caa ctt
 310
 Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln Leu
 50 55 60 65
 atg gaa tat gtt aac aag agc aac ata acc gag agg gat caa atc agc
 358
 Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile Ser
 70 75 80
 cct ccc aag aaa cgc aaa tcc ccg gcg aga gag gac gca ttc agc tgc
 406
 Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser Cys
 85 90 95
 gcg gtt att ggc gga gtg tcg gag agt agc tca acg gat caa gat gag
 454
 Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp Glu
 100 105 110
 tat ttg tgt aag aag cag aga gaa gag act gtc gtg aag gag aaa gtc
 502
 Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys Val
 115 120 125
 tca agg gtc tat tac aag acc gaa gct tct gac act acc ctc gtt gtg
 550
 Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val Val
 130 135 140 145
 aaa gat ggg tat caa tgg agg aaa tat gga cag aaa gtg act aga gac
 598
 Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp
 150 155 160
 aat cca tct cca aga gct tac ttc aaa tgt gct tgt gct cca agc tgt
 646
 Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser Cys
 165 170 175
 tct gtc aaa aag aag gtt cag aga agt gtg gag gat cag tcc gtg tta
 694
 Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val Leu
 180 185 190
 gtt gca act tat gag ggt gaa cac aac cat cca atg cca tcg cag atc
 742
 Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln Ile
 195 200 205
 gat tca aac aat ggc tta aac cgc cac atc tct cat ggt ggt tca gct
 790
 Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser Ala
 210 215 220 225

tca aca ccc gtt gca gca aac aga aga agt agc ttg act gtg ccg gtg
838

Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro Val
230 235 240

act acc gta gat atg att gaa tcg aag aaa gtg acg agc cca acg tca
886

Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr Ser
245 250 255

aga atc gat ttt ccc caa gtt cag aaa ctt ttg gtg gag caa atg gct
934

Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met Ala
260 265 270

tct tcc tta acc aaa gat cct aac ttt aca gca gct tta gca gca gct
982

Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Ala
275 280 285

gtt acc gga aaa ttg tat caa cag aat cat acc gag aaa tag
1024

Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
290 295 300

tttagcttca aattccgtta gagtttttag atttgaattt gtcattgagta agagaaagag
1084

agtagattat aatccattgt gatactgaaa aaaaaaaaaa aaaaaa
1130

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146

Met Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr
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Ile Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala
20 25 30

Leu Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser
35 40 45

Glu Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln
50 55 60

Leu Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile
65 70 75 80

Ser Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser
85 90 95

Cys Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp

100 105 110
 Glu Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys
 115 120 125
 Val Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val
 130 135 140
 Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg
 145 150 155 160
 Asp Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser
 165 170 175
 Cys Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val
 180 185 190
 Leu Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln
 195 200 205
 Ile Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser
 210 215 220
 Ala Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro
 225 230 235 240
 Val Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr
 245 250 255
 Ser Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met
 260 265 270
 Ala Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala
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 Ala Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
 290 295 300
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gtt tgt agc tcg gcg cct cca ttt aca gag gga cat atg tgt tct gat
 98
 Val Cys Ser Ser Ala Pro Pro Phe Thr Glu Gly His Met Cys Ser Asp
 15 20 25 30
 tcg cat acg gct ttg tgc gat gat ctg agt agt gat gag gaa atg gaa
 146
 Ser His Thr Ala Leu Cys Asp Asp Leu Ser Ser Asp Glu Glu Met Glu
 35 40 45
 ata gag gag ctt gag aag aag atc tgg aga gac aag cag cgt tta aag
 194
 Ile Glu Glu Leu Glu Lys Lys Ile Trp Arg Asp Lys Gln Arg Leu Lys
 50 55 60
 cgg ctc aag gaa atg gcg aag aac ggt cta gga aca aga ttg ttg ttg
 242
 Arg Leu Lys Glu Met Ala Lys Asn Gly Leu Gly Thr Arg Leu Leu Leu
 65 70 75
 aag cag caa cat gat gat ttt cca gag cac tct agt aag aga acc atg
 290
 Lys Gln Gln His Asp Asp Phe Pro Glu His Ser Ser Lys Arg Thr Met
 80 85 90
 tac aag gca caa gat ggg atc ttg aag tac atg tcg aag aca atg gag
 338
 Tyr Lys Ala Gln Asp Gly Ile Leu Lys Tyr Met Ser Lys Thr Met Glu
 95 100 105 110
 cga tat aaa gct caa ggt ttt gtt tat ggg att gtg tta gag aat ggg
 386
 Arg Tyr Lys Ala Gln Gly Phe Val Tyr Gly Ile Val Leu Glu Asn Gly
 115 120 125
 aaa acg gta gcg gga tct tct gat aat ctc cgt gaa tgg tgg aaa gac
 434
 Lys Thr Val Ala Gly Ser Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp
 130 135 140
 aaa gtg agg ttt gat agg aac ggc cca gct gct ata atc aag cac caa
 482
 Lys Val Arg Phe Asp Arg Asn Gly Pro Ala Ala Ile Ile Lys His Gln
 145 150 155
 agg gat atc aat ctt tct gat gga agt gat tca ggg tct gag gtt ggg
 530
 Arg Asp Ile Asn Leu Ser Asp Gly Ser Asp Ser Gly Ser Glu Val Gly
 160 165 170
 gat tct acc gca cag aag ttg ctt gag ctt caa gat act act ctt gga
 578
 Asp Ser Thr Ala Gln Lys Leu Leu Glu Leu Gln Asp Thr Thr Leu Gly
 175 180 185 190
 gct ctg tta tcg gct ctg ttt cct cac tgc aac cct cct cag agg cgg
 626
 Ala Leu Leu Ser Ala Leu Phe Pro His Cys Asn Pro Pro Gln Arg Arg
 195 200 205

ttt ccg ttg gag aaa ggc gtg aca ccg cca tgg tgg cca acg ggg aaa
 674
 Phe Pro Leu Glu Lys Gly Val Thr Pro Pro Trp Trp Pro Thr Gly Lys
 210 215 220

gaa gat tgg tgg gat caa ctg tct tta ccc gtt gat ttt cga ggt gtt
 722
 Glu Asp Trp Trp Asp Gln Leu Ser Leu Pro Val Asp Phe Arg Gly Val
 225 230 235

ccg cca cct tac aag aag cct cat gat ctc aag aag ctg tgg aaa att
 770
 Pro Pro Pro Tyr Lys Lys Pro His Asp Leu Lys Lys Leu Trp Lys Ile
 240 245 250

ggt gtt ttg att ggt gta atc aga cat atg gct tct gac att agc aac
 818
 Gly Val Leu Ile Gly Val Ile Arg His Met Ala Ser Asp Ile Ser Asn
 255 260 265 270

ata ccc aat ctc gtg aga cgg tct aga agt ttg cag gag aaa atg acg
 866
 Ile Pro Asn Leu Val Arg Arg Ser Arg Ser Leu Gln Glu Lys Met Thr
 275 280 285

tca aga gaa ggc gct tta tgg ctc gct gct ctt tac cga gaa aag gct
 914
 Ser Arg Glu Gly Ala Leu Trp Leu Ala Ala Leu Tyr Arg Glu Lys Ala
 290 295 300

att gtt gat caa ata gcc atg tct aga gaa aac aac aac act tct aac
 962
 Ile Val Asp Gln Ile Ala Met Ser Arg Glu Asn Asn Asn Thr Ser Asn
 305 310 315

ttt ctt gtt cct gca acc ggt gga gac cca gat gtt ttg ttt cct gaa
 1010
 Phe Leu Val Pro Ala Thr Gly Gly Asp Pro Asp Val Leu Phe Pro Glu
 320 325 330

tct aca gac tat gat gtt gaa ctg att ggt ggc act cat cgg acc aat
 1058
 Ser Thr Asp Tyr Asp Val Glu Leu Ile Gly Gly Thr His Arg Thr Asn
 335 340 345 350

cag cag tat cct gaa ttt gaa aac aac tac aac tgt gtt tac aag aga
 1106
 Gln Gln Tyr Pro Glu Phe Glu Asn Asn Tyr Asn Cys Val Tyr Lys Arg
 355 360 365

aag ttt gaa gaa gat ttt ggg atg cca atg cat cca aca ctc cta aca
 1154
 Lys Phe Glu Glu Asp Phe Gly Met Pro Met His Pro Thr Leu Leu Thr
 370 375 380

tgt gag aac agt ctc tgt cct tat agc caa cca cat atg gga ttt ctt
 1202
 Cys Glu Asn Ser Leu Cys Pro Tyr Ser Gln Pro His Met Gly Phe Leu
 385 390 395

gac agg aac tta aga gag aat cac caa atg act tgt cct tat aaa gtc
1250

Asp Arg Asn Leu Arg Glu Asn His Gln Met Thr Cys Pro Tyr Lys Val
400 405 410

act tcc ttc tac caa cca act aaa ccc tat ggt atg acg ggt tta atg
1298

Thr Ser Phe Tyr Gln Pro Thr Lys Pro Tyr Gly Met Thr Gly Leu Met
415 420 425 430

gtt cct tgt ccg gat tat aac ggg atg cag cag cag gtt cag agc ttt
1346

Val Pro Cys Pro Asp Tyr Asn Gly Met Gln Gln Gln Val Gln Ser Phe
435 440 445

caa gac cag ttt aat cat ccc aac gat ctc tac aga cca aaa gct cca
1394

Gln Asp Gln Phe Asn His Pro Asn Asp Leu Tyr Arg Pro Lys Ala Pro
450 455 460

caa aga ggc aac gat gac ttg gtt gag gat ttg aat cct tct cct tcg
1442

Gln Arg Gly Asn Asp Asp Leu Val Glu Asp Leu Asn Pro Ser Pro Ser
465 470 475

acg ctg aat cag aat ctt ggt tta gtc tta cct act gac ttc aat gga
1490

Thr Leu Asn Gln Asn Leu Gly Leu Val Leu Pro Thr Asp Phe Asn Gly
480 485 490

ggt gag gaa aca gta gga aca gag aac aat ctg cat aat caa ggg caa
1538

Gly Glu Glu Thr Val Gly Thr Glu Asn Asn Leu His Asn Gln Gly Gln
495 500 505 510

gag ttg ccc aca tct tgg att cag taa agaaagcttc agagttttct
1585

Glu Leu Pro Thr Ser Trp Ile Gln
515

ttttatgttt tctagtcttt atagctttgt ctcttgctta ttctctcatt aaacacagtt
1645

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1705

taataaccaa attcaaa
1722

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20 25 30

Thr Ala Leu Cys Asp Asp Leu Ser Ser Asp Glu Glu Met Glu Ile Glu
 35 40 45

Glu Leu Glu Lys Lys Ile Trp Arg Asp Lys Gln Arg Leu Lys Arg Leu
 50 55 60

Lys Glu Met Ala Lys Asn Gly Leu Gly Thr Arg Leu Leu Leu Lys Gln
 65 70 75 80

Gln His Asp Asp Phe Pro Glu His Ser Ser Lys Arg Thr Met Tyr Lys
 85 90 95

Ala Gln Asp Gly Ile Leu Lys Tyr Met Ser Lys Thr Met Glu Arg Tyr
 100 105 110

Lys Ala Gln Gly Phe Val Tyr Gly Ile Val Leu Glu Asn Gly Lys Thr
 115 120 125

Val Ala Gly Ser Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val
 130 135 140

Arg Phe Asp Arg Asn Gly Pro Ala Ala Ile Ile Lys His Gln Arg Asp
 145 150 155 160

Ile Asn Leu Ser Asp Gly Ser Asp Ser Gly Ser Glu Val Gly Asp Ser
 165 170 175

Thr Ala Gln Lys Leu Leu Glu Leu Gln Asp Thr Thr Leu Gly Ala Leu
 180 185 190

Leu Ser Ala Leu Phe Pro His Cys Asn Pro Pro Gln Arg Arg Phe Pro
 195 200 205

Leu Glu Lys Gly Val Thr Pro Pro Trp Trp Pro Thr Gly Lys Glu Asp
 210 215 220

Trp Trp Asp Gln Leu Ser Leu Pro Val Asp Phe Arg Gly Val Pro Pro
 225 230 235 240

Pro Tyr Lys Lys Pro His Asp Leu Lys Lys Leu Trp Lys Ile Gly Val
 245 250 255

Leu Ile Gly Val Ile Arg His Met Ala Ser Asp Ile Ser Asn Ile Pro
 260 265 270

Asn Leu Val Arg Arg Ser Arg Ser Leu Gln Glu Lys Met Thr Ser Arg

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 340 345 350
 Tyr Pro Glu Phe Glu Asn Asn Tyr Asn Cys Val Tyr Lys Arg Lys Phe
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 405 410 415
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 Cys Pro Asp Tyr Asn Gly Met Gln Gln Gln Val Gln Ser Phe Gln Asp
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 164

Met Ser Val Ala Asp Ile Arg Met Glu Asn Glu Pro Asp Asp Leu Ala
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agt gat aat gtt gct gag att gat gtg agt gat gaa gag att gat gct
 212

Ser Asp Asn Val Ala Glu Ile Asp Val Ser Asp Glu Glu Ile Asp Ala
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gac gac ctt gag aga cgg atg tgg aaa gat cgt gtc agg ctt aaa aga
 260

Asp Asp Leu Glu Arg Arg Met Trp Lys Asp Arg Val Arg Leu Lys Arg
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atc aaa gag cga caa aaa gct ggc tct caa gga gct caa acg aag gag
 308

Ile Lys Glu Arg Gln Lys Ala Gly Ser Gln Gly Ala Gln Thr Lys Glu
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 356

Thr Pro Lys Lys Ile Ser Asp Gln Ala Gln Arg Lys Lys Met Ser Arg
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Ala Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Leu Met Glu Val Cys
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Lys Val Arg Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro
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Val Ser Gly Ser Ser Asp Asn Ile Arg Ala Trp Trp Lys Glu Lys Val
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Lys Phe Asp Lys Asn Gly Pro Ala Ala Ile Ala Lys Tyr Glu Glu Glu
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1845

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1905

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1965

tttgaataag ttgccagaag aactgctttg cccgttgtaa tggctctctag ggaaagcagt
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Val Arg Leu Lys Arg Ile Lys Glu Arg Gln Lys Ala Gly Ser Gln Gly
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Ala Gln Thr Lys Glu Thr Pro Lys Lys Ile Ser Asp Gln Ala Gln Arg
65 70 75 80

Lys Lys Met Ser Arg Ala Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys
85 90 95'

Leu Met Glu Val Cys Lys Val Arg Gly Phe Val Tyr Gly Ile Ile Pro
100 105 110

Glu Lys Gly Lys Pro Val Ser Gly Ser Ser Asp Asn Ile Arg Ala Trp
115 120 125

Trp Lys Glu Lys Val Lys Phe Asp Lys Asn Gly Pro Ala Ala Ile Ala
130 135 140

Lys Tyr Glu Glu Glu Cys Leu Ala Phe Gly Lys Ser Asp Gly Asn Arg
 145 150 155 160

Asn Ser Gln Phe Val Leu Gln Asp Leu Gln Asp Ala Thr Leu Gly Ser
 165 170 175

Leu Leu Ser Ser Leu Met Gln His Cys Asp Pro Pro Gln Arg Lys Tyr
 180 185 190

Pro Leu Glu Lys Gly Thr Pro Pro Pro Trp Trp Pro Thr Gly Asn Glu
 195 200 205

Glu Trp Trp Val Lys Leu Gly Leu Pro Lys Ser Gln Ser Pro Pro Tyr
 210 215 220

Arg Lys Pro His Asp Leu Lys Lys Met Trp Lys Val Gly Val Leu Thr
 225 230 235 240

Ala Val Ile Asn His Met Leu Pro Asp Ile Ala Lys Ile Lys Arg His
 245 250 255

Val Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser
 260 265 270

Ala Ile Trp Leu Ala Val Leu Asn Gln Glu Glu Ser Leu Ile Gln Gln
 275 280 285

Pro Ser Ser Asp Asn Gly Asn Ser Asn Val Thr Glu Thr His Arg Arg
 290 295 300

Gly Asn Asn Ala Asp Arg Arg Lys Pro Val Val Asn Ser Asp Ser Asp
 305 310 315 320

Tyr Asp Val Asp Gly Thr Glu Glu Ala Ser Gly Ser Val Ser Ser Lys
 325 330 335

Asp Ser Arg Arg Asn Gln Ile Gln Lys Glu Gln Pro Thr Ala Ile Ser
 340 345 350

His Ser Val Arg Asp Gln Asp Lys Ala Glu Lys His Arg Arg Arg Lys
 355 360 365

Arg Pro Arg Ile Arg Ser Gly Thr Val Asn Arg Gln Glu Glu Glu Gln
 370 375 380

Pro Glu Ala Gln Gln Arg Asn Ile Leu Pro Asp Met Asn His Val Asp
385 390 395 400

Ala Pro Leu Leu Glu Tyr Asn Ile Asn Gly Thr His Gln Glu Asp Asp
405 410 415

Val Val Asp Pro Asn Ile Ala Leu Gly Pro Glu Asp Asn Gly Leu Glu
420 425 430

Leu Val Val Pro Glu Phe Asn Asn Asn Tyr Thr Tyr Leu Pro Leu Val
435 440 445

Asn Glu Gln Thr Met Met Pro Val Asp Glu Arg Pro Met Leu Tyr Gly
450 455 460

Pro Asn Pro Asn Gln Glu Leu Gln Phe Gly Ser Gly Tyr Asn Phe Tyr
465 470 475 480

Asn Pro Ser Ala Val Phe Val His Asn Gln Glu Asp Asp Ile Leu His
485 490 495

Thr Gln Ile Glu Met Asn Thr Gln Ala Pro Pro His Asn Ser Gly Phe
500 505 510

Glu Glu Ala Pro Gly Gly Val Leu Gln Pro Leu Gly Leu Leu Gly Asn
515 520 525

Glu Asp Gly Val Thr Gly Ser Glu Leu Pro Gln Tyr Gln Ser Gly Ile
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105

Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp Gly Ser Trp Val

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201
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249
Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro Tyr Asn Pro Asn
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297
Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala Thr Leu Thr Ala
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345
Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met Thr Lys Gln Thr
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393
Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln Ser Ala Asp Ser
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gac ggt gtg acg gct aac gaa agt cat ttg aac aga gga gta acg gag
441
Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg Gly Val Thr Glu
      120              125              130

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489
Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn Met Gln Gln Asn
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537
Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met Ile Glu Glu Leu
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585
Leu His Tyr Gly Ser Ile Glu Leu Cys Ser Val Leu Pro Thr Gln Thr
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Leu

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701

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Glu Ala Ala Arg Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro
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Tyr Asn Pro Asn Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala
65 70 75 80

Thr Leu Thr Ala Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met
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Thr Lys Gln Thr Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln
100 105 110

Ser Ala Asp Ser Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg
115 120 125

Gly Val Thr Glu Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn
130 135 140

Met Gln Gln Asn Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met
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Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
 1 5 10 15

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 155

Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
 20 25 30

cca agg cct aaa cga gcc aaa agg gct aag aaa tct tct cct tct ggt
 203

Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly
 35 40 45

gat aaa tct cat aac ccg aca agc cct gct tct acc cga cgc agc tct
 251

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser
 50 55 60

atc tac aga gga gtc act aga cat aga tgg act ggg aga ttc gag gct
 299

Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala
 65 70 75 80

cat ctt tgg gac aaa agc tct tgg aat tgg att cag aac aag aaa ggc
 347

His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly
 85 90 95

aaa caa gtt tat ctg gga gca tat gac agt gaa gaa gca gca gca cat
 395

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His
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acg tac gat ctg gct gct ctc aag tac tgg gga ccc gac acc atc ttg
 443

Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu
 115 120 125

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Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg
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Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly
 145 150 155 160

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 587

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His
 165 170 175

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 Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr
 195 200 205
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 210 215 220
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 Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro
 225 230 235 240
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 Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala
 245 250 255
 aaa caa gaa gtt gaa acg aga gaa gcg aag gaa gag cct aga gaa gaa
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 260 265 270
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 Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Glu Lys
 275 280 285
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 290 295 300
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 305 310 315 320
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 340 345 350
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 Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe
 355 360 365

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 Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu
 370 375 380
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 1259
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 385 390 395 400
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 405 410 415
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 1352
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Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser
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Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala
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His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly
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Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His
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Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu
 115 120 125

Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg
 130 135 140

Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly
 145 150 155 160

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His
 165 170 175

Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr
 180 185 190

Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr
 195 200 205

Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe
 210 215 220

Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro
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 245 250 255

Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu
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Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Lys
 275 280 285

Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser
 290 295 300

Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met
 305 310 315 320

Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys
 325 330 335

Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala
 340 345 350

Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe

355 360 365
 Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu
 370 375 380
 Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro
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 Trp Thr Glu Glu Glu Asp Ala Lys Ile Leu Ala Tyr Val Ala Ile His
 20 25 30
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 144
 Gly Val Gly Asn Trp Ser Leu Ile Pro Lys Lys Ala Gly Leu Asn Arg
 35 40 45
 tgt gga aag agc tgt aga cta aga tgg act aat tac tta aga cct gac
 192
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60
 ctt aaa cat gac agc ttc tct acc caa gaa gaa gag ctt atc att gag
 240
 Leu Lys His Asp Ser Phe Ser Thr Gln Glu Glu Glu Leu Ile Ile Glu
 65 70 75 80
 tgt cat aga gcc att ggc agc agg tgg tct tcc att gca cga aag ctt
 288
 Cys His Arg Ala Ile Gly Ser Arg Trp Ser Ser Ile Ala Arg Lys Leu
 85 90 95
 cca gga aga acg gat aat gat gtg aag aat cac tgg aac aca aag ctg
 336
 Pro Gly Arg Thr Asp Asn Asp Val Lys Asn His Trp Asn Thr Lys Leu
 100 105 110
 aag aag aag ctg atg aaa atg ggg ata gac ccg gtg act cat aaa ccg
 384
 Lys Lys Lys Leu Met Lys Met Gly Ile Asp Pro Val Thr His Lys Pro

115	120	125
gtt tct caa ctc ctt gca gaa ttc aga aac att agc ggc cat gga aat 432		
Val Ser Gln Leu Leu Ala Glu Phe Arg Asn Ile Ser Gly His Gly Asn 130 135 140		
gca tcc ttc aaa aca gaa cca tct aac aac tct ata ctc aca caa tcc 480		
Ala Ser Phe Lys Thr Glu Pro Ser Asn Asn Ser Ile Leu Thr Gln Ser 145 150 155 160		
aac tca gct tgg gaa atg atg aga aac aca aca aca aac cat gag agt 528		
Asn Ser Ala Trp Glu Met Met Arg Asn Thr Thr Thr Asn His Glu Ser 165 170 175		
tat tac acc aac tct cca atg atg ttt aca aat tcc tct gag tac caa 576		
Tyr Tyr Thr Asn Ser Pro Met Met Phe Thr Asn Ser Ser Glu Tyr Gln 180 185 190		
act act cca ttt cat ttc tat agc cat cca aat cat ctg ctc aat gga 624		
Thr Thr Pro Phe His Phe Tyr Ser His Pro Asn His Leu Leu Asn Gly 195 200 205		
acc aca tct tca tgc tct tcc tca tca tct tct act agt atc act cag 672		
Thr Thr Ser Ser Cys Ser Ser Ser Ser Ser Ser Thr Ser Ile Thr Gln 210 215 220		
cca aac caa gta cct caa aca ccg gtt act aac ttc tac tgg agc gat 720		
Pro Asn Gln Val Pro Gln Thr Pro Val Thr Asn Phe Tyr Trp Ser Asp 225 230 235 240		
ttc ctt ctc tcg gac ccg gtt cct caa gta gtg gga tcc tca gct act 768		
Phe Leu Leu Ser Asp Pro Val Pro Gln Val Val Gly Ser Ser Ala Thr 245 250 255		
agc gac ctc act ttt acg cag aac gaa cat cat ttc aac atc gaa gcc 816		
Ser Asp Leu Thr Phe Thr Gln Asn Glu His His Phe Asn Ile Glu Ala 260 265 270		
gaa tac atc tct caa aac atc gat tca aag gcc tcg gga aca tgt cat 864		
Glu Tyr Ile Ser Gln Asn Ile Asp Ser Lys Ala Ser Gly Thr Cys His 275 280 285		
tcc gcg agt tcc ttc gtt gac gaa ata cta gat aaa gac caa gag atg 912		
Ser Ala Ser Ser Phe Val Asp Glu Ile Leu Asp Lys Asp Gln Glu Met 290 295 300		
ttg tca cag ttt cct caa ctc ttg aat gat ttc gat tat tag 954		
Leu Ser Gln Phe Pro Gln Leu Leu Asn Asp Phe Asp Tyr 305 310 315		

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Met Gly Arg Pro Pro Cys Cys Asp Lys Ser Asn Val Lys Lys Gly Leu
1 5 10 15

Trp Thr Glu Glu Glu Asp Ala Lys Ile Leu Ala Tyr Val Ala Ile His
20 25 30

Gly Val Gly Asn Trp Ser Leu Ile Pro Lys Lys Ala Gly Leu Asn Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys His Asp Ser Phe Ser Thr Gln Glu Glu Glu Leu Ile Ile Glu
65 70 75 80

Cys His Arg Ala Ile Gly Ser Arg Trp Ser Ser Ile Ala Arg Lys Leu
85 90 95

Pro Gly Arg Thr Asp Asn Asp Val Lys Asn His Trp Asn Thr Lys Leu
100 105 110

Lys Lys Lys Leu Met Lys Met Gly Ile Asp Pro Val Thr His Lys Pro
115 120 125

Val Ser Gln Leu Leu Ala Glu Phe Arg Asn Ile Ser Gly His Gly Asn
130 135 140

Ala Ser Phe Lys Thr Glu Pro Ser Asn Asn Ser Ile Leu Thr Gln Ser
145 150 155 160

Asn Ser Ala Trp Glu Met Met Arg Asn Thr Thr Thr Asn His Glu Ser
165 170 175

Tyr Tyr Thr Asn Ser Pro Met Met Phe Thr Asn Ser Ser Glu Tyr Gln
180 185 190

Thr Thr Pro Phe His Phe Tyr Ser His Pro Asn His Leu Leu Asn Gly
195 200 205

Thr Thr Ser Ser Cys Ser Ser Ser Ser Ser Thr Ser Ile Thr Gln
210 215 220

Pro Asn Gln Val Pro Gln Thr Pro Val Thr Asn Phe Tyr Trp Ser Asp
225 230 235 240

Phe Leu Leu Ser Asp Pro Val Pro Gln Val Val Gly Ser Ser Ala Thr
245 250 255

Ser Asp Leu Thr Phe Thr Gln Asn Glu His His Phe Asn Ile Glu Ala
260 265 270

Glu Tyr Ile Ser Gln Asn Ile Asp Ser Lys Ala Ser Gly Thr Cys His
275 280 285

Ser Ala Ser Ser Phe Val Asp Glu Ile Leu Asp Lys Asp Gln Glu Met
290 295 300

Leu Ser Gln Phe Pro Gln Leu Leu Asn Asp Phe Asp Tyr
305 310 315

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55

Met Asn Gly Leu Val
1 5

gac tct tct cga gat aag aag atg aaa aat ccg cga ttt tcg ttt cgc
103

Asp Ser Ser Arg Asp Lys Lys Met Lys Asn Pro Arg Phe Ser Phe Arg
10 15 20

aca aag agt gat gca gat att ctc gat gat ggt tat cga tgg aga aag
151

Thr Lys Ser Asp Ala Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys
25 30 35

tac ggt cag aaa tcc gtc aag aac agc ttg tat ccc agg agc tat tat
199

Tyr Gly Gln Lys Ser Val Lys Asn Ser Leu Tyr Pro Arg Ser Tyr Tyr
40 45 50

aga tgc aca caa cac atg tgt aac gtg aag aag caa gtt cag agg ctg
247

Arg Cys Thr Gln His Met Cys Asn Val Lys Lys Gln Val Gln Arg Leu
55 60 65

tcg aag gag acg agc att gtg gag aca act tat gaa gga atc cat aac
295

Ser Lys Glu Thr Ser Ile Val Glu Thr Thr Tyr Glu Gly Ile His Asn
70 75 80 85

cat cct tgt gag gag ctc atg caa acc cta act cct ctt ctt cat caa
343

His Pro Cys Glu Glu Leu Met Gln Thr Leu Thr Pro Leu Leu His Gln

90 95 100
 ttg cag ttc ctc tct aag ttc acc taa ttatgtttgt atatata
 390
 Leu Gln Phe Leu Ser Lys Phe Thr
 105
 acgttctaag agcatctcca atggaagtat ctcaatgaga tacctaacaa aagaaaaaaa
 450
 atttaaaaaa aaaaaaaaaa aaaaaa
 476
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 Met Asn Gly Leu Val Asp Ser Ser Arg Asp Lys Lys Met Lys Asn Pro
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 Arg Phe Ser Phe Arg Thr Lys Ser Asp Ala Asp Ile Leu Asp Asp Gly
 20 25 30
 Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys Asn Ser Leu Tyr
 35 40 45
 Pro Arg Ser Tyr Tyr Arg Cys Thr Gln His Met Cys Asn Val Lys Lys
 50 55 60
 Gln Val Gln Arg Leu Ser Lys Glu Thr Ser Ile Val Glu Thr Thr Tyr
 65 70 75 80
 Glu Gly Ile His Asn His Pro Cys Glu Glu Leu Met Gln Thr Leu Thr
 85 90 95
 Pro Leu Leu His Gln Leu Gln Phe Leu Ser Lys Phe Thr
 100 105
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 cactgaaacc caaagagatc caccatttgt tcttttttcc ttcacacaga gaactgtttt
 120
 cttccacact tcctttttac taggcagtgt taaccaattg agagagaaaa atg atg
 176
 Met
 1

gtt gat gaa aat gtg gaa acc aag gcc tct act tta gtg gca agt gtt
 224
 Val Asp Glu Asn Val Glu Thr Lys Ala Ser Thr Leu Val Ala Ser Val
 5 10 15

gat cat ggg ttt gga tcc ggg tcg ggt cat gat cat cat ggg tta tcg
 272
 Asp His Gly Phe Gly Ser Gly Ser Gly His Asp His His Gly Leu Ser
 20 25 30

gcg tct gtg cct ctt ctt ggt gtt aac tgg aag aag aga agg atg cct
 320
 Ala Ser Val Pro Leu Leu Gly Val Asn Trp Lys Lys Arg Arg Met Pro
 35 40 45

aga cag aga cga tct tct tct tcc ttt aac ctt ctc tct ttc cct cct
 368
 Arg Gln Arg Arg Ser Ser Ser Ser Phe Asn Leu Leu Ser Phe Pro Pro
 50 55 60 65

cct atg cct cct att tcc cac gtg cca act cct ctc ccc gca cgt aaa
 416
 Pro Met Pro Pro Ile Ser His Val Pro Thr Pro Leu Pro Ala Arg Lys
 70 75 80

att gac cca aga aag cta aga ttc ctc ttc caa aag gaa ctc aag aac
 464
 Ile Asp Pro Arg Lys Leu Arg Phe Leu Phe Gln Lys Glu Leu Lys Asn
 85 90 95

agt gac gtc agc tct ctc cga cgt atg ata ctc ccg aag aaa gcc gcg
 512
 Ser Asp Val Ser Ser Leu Arg Arg Met Ile Leu Pro Lys Lys Ala Ala
 100 105 110

gag gct cac ttg ccg gca ctt gaa tgc aag gaa ggg att cct ata aga
 560
 Glu Ala His Leu Pro Ala Leu Glu Cys Lys Glu Gly Ile Pro Ile Arg
 115 120 125

atg gaa gat ttg gac ggt ttt cac gtt tgg acc ttc aag tat agg tac
 608
 Met Glu Asp Leu Asp Gly Phe His Val Trp Thr Phe Lys Tyr Arg Tyr
 130 135 140 145

tgg cca aac aac aat agc aga atg tac gtg cta gaa aac aca ggc gat
 656
 Trp Pro Asn Asn Asn Ser Arg Met Tyr Val Leu Glu Asn Thr Gly Asp
 150 155 160

ttt gtg aat gct cat ggt ctg cag cta ggt gac ttc atc atg gtt tac
 704
 Phe Val Asn Ala His Gly Leu Gln Leu Gly Asp Phe Ile Met Val Tyr
 165 170 175

caa gat ctc tac tca aac aat tac gtt ata caa gca aga aaa gca tcg
 752
 Gln Asp Leu Tyr Ser Asn Asn Tyr Val Ile Gln Ala Arg Lys Ala Ser
 180 185 190

gaa gaa gaa gaa gta gac gta atc aat ctt gaa gaa gac gac gtt tac
 800
 Glu Glu Glu Glu Val Asp Val Ile Asn Leu Glu Glu Asp Asp Val Tyr
 195 200 205

 aca aac tta aca agg atc gaa aac act gtg gtt aac gat ctt ctc ctc
 848
 Thr Asn Leu Thr Arg Ile Glu Asn Thr Val Val Asn Asp Leu Leu Leu
 210 215 220 225

 caa gat ttt aat cat cac aac aac aac aac aac aac agc aac agc
 896
 Gln Asp Phe Asn His His Asn Asn Asn Asn Asn Asn Ser Asn Ser
 230 235 240

 aac agc aac aaa tgt tct tac tat tat cca gtc ata gat gat gtc acc
 944
 Asn Ser Asn Lys Cys Ser Tyr Tyr Tyr Pro Val Ile Asp Asp Val Thr
 245 250 255

 aca aac aca gag tct ttt gtc tac gac acg acg gct ctt acc tcc aac
 992
 Thr Asn Thr Glu Ser Phe Val Tyr Asp Thr Thr Ala Leu Thr Ser Asn
 260 265 270

 gat act cct ctc gat ttt ttg ggt gga cat acg acg act act aat aat
 1040
 Asp Thr Pro Leu Asp Phe Leu Gly Gly His Thr Thr Thr Thr Asn Asn
 275 280 285

 tat tac tcc aag ttc gga aca ttc gat ggt ttg ggc tcc gtt gag aat
 1088
 Tyr Tyr Ser Lys Phe Gly Thr Phe Asp Gly Leu Gly Ser Val Glu Asn
 290 295 300 305

 atc tct ctc gat gac ttc tac tag ataatacaatc gatgggctca tggattctt
 1142
 Ile Ser Leu Asp Asp Phe Tyr
 310

 gatgggtgatc agctatttaa tacccttata atatatataa gaattaaatg caatttgcac
 1202

 atatatattatc aagtgttgta atataacatt acagtttaaa aaaaaaaaaa aaaaa
 1257

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 Met Val Asp Glu Asn Val Glu Thr Lys Ala Ser Thr Leu Val Ala Ser
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 Val Asp His Gly Phe Gly Ser Gly Ser Gly His Asp His His Gly Leu
 20 25 30

 Ser Ala Ser Val Pro Leu Leu Gly Val Asn Trp Lys Lys Arg Arg Met
 35 40 45

Pro Arg Gln Arg Arg Ser Ser Ser Ser Phe Asn Leu Leu Ser Phe Pro
 50 55 60

Pro Pro Met Pro Pro Ile Ser His Val Pro Thr Pro Leu Pro Ala Arg
 65 70 75 80

Lys Ile Asp Pro Arg Lys Leu Arg Phe Leu Phe Gln Lys Glu Leu Lys
 85 90 95

Asn Ser Asp Val Ser Ser Leu Arg Arg Met Ile Leu Pro Lys Lys Ala
 100 105 110

Ala Glu Ala His Leu Pro Ala Leu Glu Cys Lys Glu Gly Ile Pro Ile
 115 120 125

Arg Met Glu Asp Leu Asp Gly Phe His Val Trp Thr Phe Lys Tyr Arg
 130 135 140

Tyr Trp Pro Asn Asn Asn Ser Arg Met Tyr Val Leu Glu Asn Thr Gly
 145 150 155 160

Asp Phe Val Asn Ala His Gly Leu Gln Leu Gly Asp Phe Ile Met Val
 165 170 175

Tyr Gln Asp Leu Tyr Ser Asn Asn Tyr Val Ile Gln Ala Arg Lys Ala
 180 185 190

Ser Glu Glu Glu Glu Val Asp Val Ile Asn Leu Glu Glu Asp Asp Val
 195 200 205

Tyr Thr Asn Leu Thr Arg Ile Glu Asn Thr Val Val Asn Asp Leu Leu
 210 215 220

Leu Gln Asp Phe Asn His His Asn Asn Asn Asn Asn Asn Ser Asn
 225 230 235 240

Ser Asn Ser Asn Lys Cys Ser Tyr Tyr Tyr Pro Val Ile Asp Asp Val
 245 250 255

Thr Thr Asn Thr Glu Ser Phe Val Tyr Asp Thr Thr Ala Leu Thr Ser
 260 265 270

Asn Asp Thr Pro Leu Asp Phe Leu Gly Gly His Thr Thr Thr Thr Asn
 275 280 285

Asn Tyr Tyr Ser Lys Phe Gly Thr Phe Asp Gly Leu Gly Ser Val Glu
 290 295 300

Asn Ile Ser Leu Asp Asp Phe Tyr
 305 310

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 <221> CDS <222> (51)..(863) <223> G1040

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 56 Met Met
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atg tta gag tca aga aac agt atg aga gct tca aac tca gtc cca gat
 104
 Met Leu Glu Ser Arg Asn Ser Met Arg Ala Ser Asn Ser Val Pro Asp
 5 10 15

ctg tct ctt cag atc agt ctt cct aac tat cac gcc gga aaa cct ctt
 152
 Leu Ser Leu Gln Ile Ser Leu Pro Asn Tyr His Ala Gly Lys Pro Leu
 20 25 30

cac gcc ggt gac cgg agc tcc aca agc agt gat tct gga agc agc ctc
 200
 His Gly Gly Asp Arg Ser Ser Thr Ser Ser Asp Ser Gly Ser Ser Leu
 35 40 45 50

agt gac ctg agc cat gag aac aac ttc ttc aac aaa cct ctc ttg agc
 248
 Ser Asp Leu Ser His Glu Asn Asn Phe Phe Asn Lys Pro Leu Leu Ser
 55 60 65

tta gga ttt gac cat cat cat caa agg cgc tca aac atg ttc caa cct
 296
 Leu Gly Phe Asp His His His Gln Arg Arg Ser Asn Met Phe Gln Pro
 70 75 80

caa atc tac ggt cga gat ttc aag aga agc tca tca tca atg gtt ggt
 344
 Gln Ile Tyr Gly Arg Asp Phe Lys Arg Ser Ser Ser Met Val Gly
 85 90 95

ctt aaa cga agc att cgt gct cca aga atg aga tgg act tct act ctt
 392
 Leu Lys Arg Ser Ile Arg Ala Pro Arg Met Arg Trp Thr Ser Thr Leu
 100 105 110

cat gct cac ttc gtc cat gct gtt caa ctt ctt ggc ggc cat gaa aga
 440
 His Ala His Phe Val His Ala Val Gln Leu Leu Gly Gly His Glu Arg
 115 120 125 130

gca acg cct aaa tca gtg ttg gag ctc atg aat gtg aag gat cta acc
 488
 Ala Thr Pro Lys Ser Val Leu Glu Leu Met Asn Val Lys Asp Leu Thr
 135 140 145

cta gct cat gtc aag agt cac ttg cag atg tat aga aca gtg aaa tgc
536

Leu Ala His Val Lys Ser His Leu Gln Met Tyr Arg Thr Val Lys Cys
150 155 160

act gat aaa gga tca cca gga gaa gga aag gta gag aaa gag gca gag
584

Thr Asp Lys Gly Ser Pro Gly Glu Gly Lys Val Glu Lys Glu Ala Glu
165 170 175

cag agg ata gag gac aat aat aat aat gaa gaa gct gat gaa gga act
632

Gln Arg Ile Glu Asp Asn Asn Asn Asn Glu Glu Ala Asp Glu Gly Thr
180 185 190

gac aca aat tcg cca aac tca tca tct gtg caa aag acc caa aga gct
680

Asp Thr Asn Ser Pro Asn Ser Ser Ser Val Gln Lys Thr Gln Arg Ala
195 200 205 210

tca tgg tca tcg aca aag gaa gta tct agg agc ata tct aca caa gca
728

Ser Trp Ser Ser Thr Lys Glu Val Ser Arg Ser Ile Ser Thr Gln Ala
215 220 225

tat tct cac ttg gga aca act cat cac act aag gcc aat gaa gag aaa
776

Tyr Ser His Leu Gly Thr Thr His His Thr Lys Ala Asn Glu Glu Lys
230 235 240

gag gat acc aac att cat ctc aat ttg gat ttc aca ttg ggc ggc cta
824

Glu Asp Thr Asn Ile His Leu Asn Leu Asp Phe Thr Leu Gly Gly Leu
245 250 255

gtt ggg gga tgg aat atg cgg aac cct cca gtg att taa cccttctcaa
873

Val Gly Gly Trp Asn Met Arg Asn Pro Pro Val Ile
260 265 270

gtgctaattg cottaagcta caacaaataa gtcagcttag gttaccagtt ttaacataat
933

tttaacttgt tttgatcata tgagcttcgg aagaatcata ttatcatcat atatgaactt
993

ctttccaaga atgttctatg agttttttga tatgtataat caagagaatc gtttgaagta
1053

aaaa
1057

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162

Met Met Met Leu Glu Ser Arg Asn Ser Met Arg Ala Ser Asn Ser Val
1 5 10 15

Pro Asp Leu Ser Leu Gln Ile Ser Leu Pro Asn Tyr His Ala Gly Lys
 20 25 30

Pro Leu His Gly Gly Asp Arg Ser Ser Thr Ser Ser Asp Ser Gly Ser
 35 40 45

Ser Leu Ser Asp Leu Ser His Glu Asn Asn Phe Phe Asn Lys Pro Leu
 50 55 60

Leu Ser Leu Gly Phe Asp His His His Gln Arg Arg Ser Asn Met Phe
 65 70 75 80

Gln Pro Gln Ile Tyr Gly Arg Asp Phe Lys Arg Ser Ser Ser Ser Met
 85 90 95

Val Gly Leu Lys Arg Ser Ile Arg Ala Pro Arg Met Arg Trp Thr Ser
 100 105 110

Thr Leu His Ala His Phe Val His Ala Val Gln Leu Leu Gly Gly His
 115 120 125

Glu Arg Ala Thr Pro Lys Ser Val Leu Glu Leu Met Asn Val Lys Asp
 130 135 140

Leu Thr Leu Ala His Val Lys Ser His Leu Gln Met Tyr Arg Thr Val
 145 150 155 160

Lys Cys Thr Asp Lys Gly Ser Pro Gly Glu Gly Lys Val Glu Lys Glu
 165 170 175

Ala Glu Gln Arg Ile Glu Asp Asn Asn Asn Asn Glu Glu Ala Asp Glu
 180 185 190

Gly Thr Asp Thr Asn Ser Pro Asn Ser Ser Ser Val Gln Lys Thr Gln
 195 200 205

Arg Ala Ser Trp Ser Ser Thr Lys Glu Val Ser Arg Ser Ile Ser Thr
 210 215 220

Gln Ala Tyr Ser His Leu Gly Thr Thr His His Thr Lys Ala Asn Glu
 225 230 235 240

Glu Lys Glu Asp Thr Asn Ile His Leu Asn Leu Asp Phe Thr Leu Gly
 245 250 255

Gly Leu Val Gly Gly Trp Asn Met Arg Asn Pro Pro Val Ile


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260                265                270

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52
                Met Gly Gly Gly Gly Asp Thr Thr Asp Thr
                1                5                10

aat atg atg cag aga gtt aat tct tct tct ggt aca tcg tct tct tcg
100
Asn Met Met Gln Arg Val Asn Ser Ser Ser Gly Thr Ser Ser Ser Ser
15                20                25

atc cct aaa cac aat ctt cac ttg aat cct gct ctt atc cgc tct cac
148
Ile Pro Lys His Asn Leu His Leu Asn Pro Ala Leu Ile Arg Ser His
30                35                40

cat cac ttc cgt cac cct ttc acc gga gct cct cca ccg ccg att cca
196
His His Phe Arg His Pro Phe Thr Gly Ala Pro Pro Pro Pro Ile Pro
45                50                55

ccc att tct cct tac tct cag atc ccg gcg act tta caa cct aga cat
244
Pro Ile Ser Pro Tyr Ser Gln Ile Pro Ala Thr Leu Gln Pro Arg His
60                65                70

tct cgc tct atg tcg caa ccg tct tct ttc ttc tcc ttt gat tca ttg
292
Ser Arg Ser Met Ser Gln Pro Ser Ser Phe Phe Ser Phe Asp Ser Leu
75                80                85                90

ccg ccg tta aat cct tct gct ccg tcg gtt tcg gtg tcg gtg gag gag
340
Pro Pro Leu Asn Pro Ser Ala Pro Ser Val Ser Val Ser Val Glu Glu
95                100                105

aaa acc ggt gcc gga ttt agt cct tcg ttg cct ccg tca ccg ttt acg
388
Lys Thr Gly Ala Gly Phe Ser Pro Ser Leu Pro Pro Ser Pro Phe Thr
110                115                120

atg tgt cat tct tct agc tct agg aac gcc gga gat gga gag aat cta
436
Met Cys His Ser Ser Ser Ser Arg Asn Ala Gly Asp Gly Glu Asn Leu
125                130                135

cct ccg aga aag tcg cat agg cgt tcg aat agt gat gtt act ttt ggg
484
Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Val Thr Phe Gly
140                145                150

ttt agt tca atg atg tct cag aat caa aag tct cct cct ttg agt tct
532
Phe Ser Ser Met Met Ser Gln Asn Gln Lys Ser Pro Pro Leu Ser Ser
155                160                165                170

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ttg gag aga tcg atc tct ggt gaa gat aca tca gat tgg tct aat ttg
 580
 Leu Glu Arg Ser Ile Ser Gly Glu Asp Thr Ser Asp Trp Ser Asn Leu
 175 180 185

gtg aag aaa gaa ccg aga gaa ggc ttc tac aag gga aga aaa cca gag
 628
 Val Lys Lys Glu Pro Arg Glu Gly Phe Tyr Lys Gly Arg Lys Pro Glu
 190 195 200

gtt gaa gca gct atg gac gat gtt ttc acg gct tat atg aat ctt gat
 676
 Val Glu Ala Ala Met Asp Asp Val Phe Thr Ala Tyr Met Asn Leu Asp
 205 210 215

aac att gat gtc ttg aat tct ttt gga ggt gaa gat ggc aag aat ggg
 724
 Asn Ile Asp Val Leu Asn Ser Phe Gly Gly Glu Asp Gly Lys Asn Gly
 220 225 230

aat gag aat gtg gag gag atg gag agt agt aga ggt agt ggt aca aag
 772
 Asn Glu Asn Val Glu Glu Met Glu Ser Ser Arg Gly Ser Gly Thr Lys
 235 240 245 250

aag acg aat ggt gga agt agt agt gat tct gaa gga gat agc agt gcg
 820
 Lys Thr Asn Gly Gly Ser Ser Ser Asp Ser Glu Gly Asp Ser Ser Ala
 255 260 265

agt ggg aat gtg aag gtt gcg ttg agt tct tct tct tca ggc gtg aag
 868
 Ser Gly Asn Val Lys Val Ala Leu Ser Ser Ser Ser Ser Gly Val Lys
 270 275 280

aga aga gca ggt gga gat att gct cct act ggt aga cat tac agg agt
 916
 Arg Arg Ala Gly Gly Asp Ile Ala Pro Thr Gly Arg His Tyr Arg Ser
 285 290 295

gtt tct atg gac agt tgt ttc atg ggg aag ttg aat ttc ggc gac gaa
 964
 Val Ser Met Asp Ser Cys Phe Met Gly Lys Leu Asn Phe Gly Asp Glu
 300 305 310

tca tcg cta aag ctt ccg cct tct tca tca gct aaa gtt tcc cca acc
 1012
 Ser Ser Leu Lys Leu Pro Pro Ser Ser Ser Ala Lys Val Ser Pro Thr
 315 320 325 330

aat tca ggt gaa ggg aat tca agt gct tat agt gtt gaa ttt gga aac
 1060
 Asn Ser Gly Glu Gly Asn Ser Ser Ala Tyr Ser Val Glu Phe Gly Asn
 335 340 345

agt gag ttt act gca gct gaa atg aag aag att gca gct gat gag aaa
 1108
 Ser Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Ala Ala Asp Glu Lys
 350 355 360

ctc gct gag att gta atg gct gac cct aag cgt gtt aaa aga atc ttg
 1156
 Leu Ala Glu Ile Val Met Ala Asp Pro Lys Arg Val Lys Arg Ile Leu
 365 370 375
 gcg aac cgc gta tct gct gca cgt tca aag gag cgg aag acg cga tac
 1204
 Ala Asn Arg Val Ser Ala Ala Arg Ser Lys Glu Arg Lys Thr Arg Tyr
 380 385 390
 atg gca gag ttg gaa cac aag gtg cag aca ctt cag act gaa gct act
 1252
 Met Ala Glu Leu Glu His Lys Val Gln Thr Leu Gln Thr Glu Ala Thr
 395 400 405 410
 aca tta tcg gct cag ctc aca cat ttg cag aga gat tct atg ggg ttg
 1300
 Thr Leu Ser Ala Gln Leu Thr His Leu Gln Arg Asp Ser Met Gly Leu
 415 420 425
 aca aac cag aac agt gag ctg aag ttt cgt ctt caa gct atg gag cag
 1348
 Thr Asn Gln Asn Ser Glu Leu Lys Phe Arg Leu Gln Ala Met Glu Gln
 430 435 440
 caa gca caa ctc cgc gat gct ctg tca gag aaa ctg aat gaa gaa gtc
 1396
 Gln Ala Gln Leu Arg Asp Ala Leu Ser Glu Lys Leu Asn Glu Glu Val
 445 450 455
 cag cgg ttg aaa ctg gtg ata ggg gag ccg aac cgc agg caa agt ggg
 1444
 Gln Arg Leu Lys Leu Val Ile Gly Glu Pro Asn Arg Arg Gln Ser Gly
 460 465 470
 agc agc agc agc gaa tca aag atg tca cta aac ccg gag atg ttt cag
 1492
 Ser Ser Ser Ser Glu Ser Lys Met Ser Leu Asn Pro Glu Met Phe Gln
 475 480 485 490
 cag ctt agc ata agt cag tta caa cac caa cag atg cag cat tcc aat
 1540
 Gln Leu Ser Ile Ser Gln Leu Gln His Gln Gln Met Gln His Ser Asn
 495 500 505
 cag tgt agc aca atg aaa gca aag cac act tca aac gac tag
 1582
 Gln Cys Ser Thr Met Lys Ala Lys His Thr Ser Asn Asp
 510 515
 ggtaagtaaa actgcgatcc gcagttgtct agttacatat atgataagaa tcttttgtgc
 1642
 agagttctgt ttttgggaagt tttaaagaaa catatataaa gattatgtcc gggaaatttg
 1702
 atcatatttc ctgaaacata cacacatata tatagtggta atggaggact ttctttctgg
 1762
 acca
 1766

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164

Met Gly Gly Gly Gly Asp Thr Thr Asp Thr Asn Met Met Gln Arg Val
1 5 10 15

Asn Ser Ser Ser Gly Thr Ser Ser Ser Ser Ile Pro Lys His Asn Leu
20 25 30

His Leu Asn Pro Ala Leu Ile Arg Ser His His His Phe Arg His Pro
35 40 45

Phe Thr Gly Ala Pro Pro Pro Pro Ile Pro Pro Ile Ser Pro Tyr Ser
50 55 60

Gln Ile Pro Ala Thr Leu Gln Pro Arg His Ser Arg Ser Met Ser Gln
65 70 75 80

Pro Ser Ser Phe Phe Ser Phe Asp Ser Leu Pro Pro Leu Asn Pro Ser
85 90 95

Ala Pro Ser Val Ser Val Ser Val Glu Glu Lys Thr Gly Ala Gly Phe
100 105 110

Ser Pro Ser Leu Pro Pro Ser Pro Phe Thr Met Cys His Ser Ser Ser
115 120 125

Ser Arg Asn Ala Gly Asp Gly Glu Asn Leu Pro Pro Arg Lys Ser His
130 135 140

Arg Arg Ser Asn Ser Asp Val Thr Phe Gly Phe Ser Ser Met Met Ser
145 150 155 160

Gln Asn Gln Lys Ser Pro Pro Leu Ser Ser Leu Glu Arg Ser Ile Ser
165 170 175

Gly Glu Asp Thr Ser Asp Trp Ser Asn Leu Val Lys Lys Glu Pro Arg
180 185 190

Glu Gly Phe Tyr Lys Gly Arg Lys Pro Glu Val Glu Ala Ala Met Asp
195 200 205

Asp Val Phe Thr Ala Tyr Met Asn Leu Asp Asn Ile Asp Val Leu Asn
210 215 220

Ser Phe Gly Gly Glu Asp Gly Lys Asn Gly Asn Glu Asn Val Glu Glu
 225 230 235 240

Met Glu Ser Ser Arg Gly Ser Gly Thr Lys Lys Thr Asn Gly Gly Ser
 245 250 255

Ser Ser Asp Ser Glu Gly Asp Ser Ser Ala Ser Gly Asn Val Lys Val
 260 265 270

Ala Leu Ser Ser Ser Ser Ser Gly Val Lys Arg Arg Ala Gly Gly Asp
 275 280 285

Ile Ala Pro Thr Gly Arg His Tyr Arg Ser Val Ser Met Asp Ser Cys
 290 295 300

Phe Met Gly Lys Leu Asn Phe Gly Asp Glu Ser Ser Leu Lys Leu Pro
 305 310 315 320

Pro Ser Ser Ser Ala Lys Val Ser Pro Thr Asn Ser Gly Glu Gly Asn
 325 330 335

Ser Ser Ala Tyr Ser Val Glu Phe Gly Asn Ser Glu Phe Thr Ala Ala
 340 345 350

Glu Met Lys Lys Ile Ala Ala Asp Glu Lys Leu Ala Glu Ile Val Met
 355 360 365

Ala Asp Pro Lys Arg Val Lys Arg Ile Leu Ala Asn Arg Val Ser Ala
 370 375 380

Ala Arg Ser Lys Glu Arg Lys Thr Arg Tyr Met Ala Glu Leu Glu His
 385 390 395 400

Lys Val Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu
 405 410 415

Thr His Leu Gln Arg Asp Ser Met Gly Leu Thr Asn Gln Asn Ser Glu
 420 425 430

Leu Lys Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Gln Leu Arg Asp
 435 440 445

Ala Leu Ser Glu Lys Leu Asn Glu Glu Val Gln Arg Leu Lys Leu Val
 450 455 460

Ile Gly Glu Pro Asn Arg Arg Gln Ser Gly Ser Ser Ser Ser Glu Ser

465 470 475 480
 Lys Met Ser Leu Asn Pro Glu Met Phe Gln Gln Leu Ser Ile Ser Gln
 485 490 495
 Leu Gln His Gln Gln Met Gln His Ser Asn Gln Cys Ser Thr Met Lys
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 Ala Lys His Thr Ser Asn Asp
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 120
 ccattaaatc tttatta atg gca caa ctt cct ccg aaa atc cca acc atg
 170
 Met Ala Gln Leu Pro Pro Lys Ile Pro Thr Met
 1 5 10
 acg acg cca aat tgg cct gac ttc tcc tcc cag aaa ctc cct tcc ata
 218
 Thr Thr Pro Asn Trp Pro Asp Phe Ser Ser Gln Lys Leu Pro Ser Ile
 15 20 25
 gcc gca acg gcg gca gcc gca gca acc gct gga cct caa caa caa aac
 266
 Ala Ala Thr Ala Ala Ala Ala Ala Thr Ala Gly Pro Gln Gln Gln Asn
 30 35 40
 cct tca tgg atg gat gag ttt ctc gac ttc tca gcg act cgc cgt ggg
 314
 Pro Ser Trp Met Asp Glu Phe Leu Asp Phe Ser Ala Thr Arg Arg Gly
 45 50 55
 act cac cgt cgt tct ata agc gac tcc att gct ttc ctt gaa cca cct
 362
 Thr His Arg Arg Ser Ile Ser Asp Ser Ile Ala Phe Leu Glu Pro Pro
 60 65 70 75
 tcc tcc ggc gtc gga aac cac cac ttc gat agg ttt gac gac gag caa
 410
 Ser Ser Gly Val Gly Asn His His Phe Asp Arg Phe Asp Asp Glu Gln
 80 85 90
 ttc atg tcc atg ttc aac gac gac gta cac aac aat aac cac aat cat
 458
 Phe Met Ser Met Phe Asn Asp Asp Val His Asn Asn Asn His Asn His
 95 100 105

cat cat cat cac agc atc aac ggc aat gtg ggt ccc acg cgt tca tcc
 506
 His His His His Ser Ile Asn Gly Asn Val Gly Pro Thr Arg Ser Ser
 110 115 120
 tcc aac acc tcc acg ccg tcc gat cat aat agc ctt agc gac gac gac
 554
 Ser Asn Thr Ser Thr Pro Ser Asp His Asn Ser Leu Ser Asp Asp Asp
 125 130 135
 aac aac aaa gaa gca cca ccg tcc gat cat gat cat cac atg gac aat
 602
 Asn Asn Lys Glu Ala Pro Pro Ser Asp His Asp His His Met Asp Asn
 140 145 150 155
 aat gta gcc aat caa aac aac gcc gcc ggt aac aat tac aac gaa tca
 650
 Asn Val Ala Asn Gln Asn Asn Ala Ala Gly Asn Asn Tyr Asn Glu Ser
 160 165 170
 gac gag gtc caa agc cag tgc aag acg gag cca caa gat ggt ccg tcg
 698
 Asp Glu Val Gln Ser Gln Cys Lys Thr Glu Pro Gln Asp Gly Pro Ser
 175 180 185
 gcg aat caa aac tcc ggt gga agc tcc ggt aat cgt att cac gac cct
 746
 Ala Asn Gln Asn Ser Gly Gly Ser Ser Gly Asn Arg Ile His Asp Pro
 190 195 200
 aaa agg gta aaa aga att tta gca aat agg caa tca gca cag aga tca
 794
 Lys Arg Val Lys Arg Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser
 205 210 215
 agg gtg agg aaa ttg caa tac ata tca gag ctt gaa agg agc gtt act
 842
 Arg Val Arg Lys Leu Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr
 220 225 230 235
 tca ttg cag act gaa gtg tca gtg tta tcg cca aga gtt gcg ttt ttg
 890
 Ser Leu Gln Thr Glu Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu
 240 245 250
 gat cat cag cga ttg ctt ctc aac gtc gac aat agt gct atc aag caa
 938
 Asp His Gln Arg Leu Leu Leu Asn Val Asp Asn Ser Ala Ile Lys Gln
 255 260 265
 cga atc gca gct tta gca caa gat aag att ttc aaa gac gct cat caa
 986
 Arg Ile Ala Ala Leu Ala Gln Asp Lys Ile Phe Lys Asp Ala His Gln
 270 275 280
 gaa gca ttg aag aga gaa ata gag aga ctt cga caa gta tat cat caa
 1034
 Glu Ala Leu Lys Arg Glu Ile Glu Arg Leu Arg Gln Val Tyr His Gln
 285 290 295

caa agc ctc aag aag atg gag aat aat gtc tcc gat caa tct ccg gcc
1082

Gln Ser Leu Lys Lys Met Glu Asn Asn Val Ser Asp Gln Ser Pro Ala
300 305 310 315

gat atc aaa ccg tcc gtt gag aag gaa cag ctc ctc aat gtc taa
1127

Asp Ile Lys Pro Ser Val Glu Lys Glu Gln Leu Leu Asn Val
320 325

agctgttcgt tcactaagat cttctttttc atggcgaaaa gattcttgac tataaaacct
1187

ctttgtgtca agaaattaat ttatcaaaga agatggcctt ttttatttga tctaatacaca
1247

tttttttaag ttgtgatgaa ttgtcttttg atgtatctgt tttttttttt ttttttt
1304

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166

Met Ala Gln Leu Pro Pro Lys Ile Pro Thr Met Thr Thr Pro Asn Trp
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Pro Asp Phe Ser Ser Gln Lys Leu Pro Ser Ile Ala Ala Thr Ala Ala
20 25 30

Ala Ala Ala Thr Ala Gly Pro Gln Gln Gln Asn Pro Ser Trp Met Asp
35 40 45

Glu Phe Leu Asp Phe Ser Ala Thr Arg Arg Gly Thr His Arg Arg Ser
50 55 60

Ile Ser Asp Ser Ile Ala Phe Leu Glu Pro Pro Ser Ser Gly Val Gly
65 70 75 80

Asn His His Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met Phe
85 90 95

Asn Asp Asp Val His Asn Asn Asn His Asn His His His His His Ser
100 105 110

Ile Asn Gly Asn Val Gly Pro Thr Arg Ser Ser Ser Asn Thr Ser Thr
115 120 125

Pro Ser Asp His Asn Ser Leu Ser Asp Asp Asp Asn Asn Lys Glu Ala
130 135 140

Pro Pro Ser Asp His Asp His His Met Asp Asn Asn Val Ala Asn Gln
145 150 155 160

Asn Asn Ala Ala Gly Asn Asn Tyr Asn Glu Ser Asp Glu Val Gln Ser
 165 170 175

Gln Cys Lys Thr Glu Pro Gln Asp Gly Pro Ser Ala Asn Gln Asn Ser
 180 185 190

Gly Gly Ser Ser Gly Asn Arg Ile His Asp Pro Lys Arg Val Lys Arg
 195 200 205

Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys Leu
 210 215 220

Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Thr Glu
 225 230 235 240

Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg Leu
 245 250 255

Leu Leu Asn Val Asp Asn Ser Ala Ile Lys Gln Arg Ile Ala Ala Leu
 260 265 270

Ala Gln Asp Lys Ile Phe Lys Asp Ala His Gln Glu Ala Leu Lys Arg
 275 280 285

Glu Ile Glu Arg Leu Arg Gln Val Tyr His Gln Gln Ser Leu Lys Lys
 290 295 300

Met Glu Asn Asn Val Ser Asp Gln Ser Pro Ala Asp Ile Lys Pro Ser
 305 310 315 320

Val Glu Lys Glu Gln Leu Leu Asn Val
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ctattgcttg agttctgatt gggcacagta gtaccattgc catttctctc acacataccg
 120

tctctttctc tcatcatcaa tcatcaatca tccaaaagaa aaaaccctaa aatttcactt
 180

gtaagctttt caccagtttc tctccatacc cattttatca gtttctccat atctttctct
 240

atg gat tct gac ata atg aac atg atg atg cat cag atg gag aag ctt
 288
 Met Asp Ser Asp Ile Met Asn Met Met Met His Gln Met Glu Lys Leu
 1 5 10 15
 cct gag ttt tgt aac cct aat tcc tct ttc ttc tct ccc gac cac aac
 336
 Pro Glu Phe Cys Asn Pro Asn Ser Ser Phe Phe Ser Pro Asp His Asn
 20 25 30
 aac act tac cct ttt ctc ttt aac tcc act cat tac cag tcc gat cac
 384
 Asn Thr Tyr Pro Phe Leu Phe Asn Ser Thr His Tyr Gln Ser Asp His
 35 40 45
 tca atg acc aac gaa cca ggt ttc cgc tac ggt tcc ggt tta ctc act
 432
 Ser Met Thr Asn Glu Pro Gly Phe Arg Tyr Gly Ser Gly Leu Leu Thr
 50 55 60
 aac cct tct tct atc tct ccc aac aca gct tac tct tcc gtt ttt ctt
 480
 Asn Pro Ser Ser Ile Ser Pro Asn Thr Ala Tyr Ser Ser Val Phe Leu
 65 70 75 80
 gac aaa aga aac aac agt aac aac aac aat aat ggc acg aac atg gca
 528
 Asp Lys Arg Asn Asn Ser Asn Asn Asn Asn Asn Gly Thr Asn Met Ala
 85 90 95
 gct atg cga gag atg atc ttc cgt atc gcc gtg atg caa ccg atc cat
 576
 Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His
 100 105 110
 atc gat ccc gag gcg gtt aag cca ccg aag agg agg aac gtc agg atc
 624
 Ile Asp Pro Glu Ala Val Lys Pro Pro Lys Arg Arg Asn Val Arg Ile
 115 120 125
 tct aaa gat cct caa agc gtg gcg gct agg cat aga agg gag aga ata
 672
 Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile
 130 135 140
 agc gag agg att cgg att ttg caa cgg ctt gtt cct ggt ggg acg aag
 720
 Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys
 145 150 155 160
 atg gat aca gct tcg atg ctc gat gaa gca att cat tat gtg aag ttt
 768
 Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe
 165 170 175
 tta aag aaa cag gtg cag tct ctg gag gag cag gcg gtg gtt act ggc
 816
 Leu Lys Lys Gln Val Gln Ser Leu Glu Glu Gln Ala Val Val Thr Gly
 180 185 190

gga ggg gga gga gga gga gga agg gtt ttg atc ggt gga ggt gga atg
 864
 Gly Gly Gly Gly Gly Gly Gly Arg Val Leu Ile Gly Gly Gly Gly Met
 195 200 205

acg gcg gcg agt ggt ggt ggt ggc ggc ggg gga gtg gtt atg aaa ggg
 912
 Thr Ala Ala Ser Gly Gly Gly Gly Gly Gly Val Val Met Lys Gly
 210 215 220

tgt gga aca gtg ggg act cat cag atg gtg ggc aat gca cag att ctt
 960
 Cys Gly Thr Val Gly Thr His Gln Met Val Gly Asn Ala Gln Ile Leu
 225 230 235 240

aga tga tgatgatttt taattttatt attattatat taatgttgga gaaaaagaga
 1016
 Arg

aaaatgattc tggagagggga agccaagtaa tttatgtgag agtctttaat ttaactttat
 1076

tttcttggtt agataatgtg taatgatggt ttttaaagcc aaagactctc catggttggt
 1136

ggagcgagtt tg
 1148

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Met Asp Ser Asp Ile Met Asn Met Met Met His Gln Met Glu Lys Leu
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Pro Glu Phe Cys Asn Pro Asn Ser Ser Phe Phe Ser Pro Asp His Asn
 20 25 30

Asn Thr Tyr Pro Phe Leu Phe Asn Ser Thr His Tyr Gln Ser Asp His
 35 40 45

Ser Met Thr Asn Glu Pro Gly Phe Arg Tyr Gly Ser Gly Leu Leu Thr
 50 55 60

Asn Pro Ser Ser Ile Ser Pro Asn Thr Ala Tyr Ser Ser Val Phe Leu
 65 70 75 80

Asp Lys Arg Asn Asn Ser Asn Asn Asn Asn Asn Gly Thr Asn Met Ala
 85 90 95

Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His
 100 105 110

Ile Asp Pro Glu Ala Val Lys Pro Pro Lys Arg Arg Asn Val Arg Ile
 115 120 125

Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile
 130 135 140

Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys
 145 150 155 160

Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe
 165 170 175

Leu Lys Lys Gln Val Gln Ser Leu Glu Glu Gln Ala Val Val Thr Gly
 180 185 190

Gly Gly Gly Gly Gly Gly Gly Arg Val Leu Ile Gly Gly Gly Gly Met
 195 200 205

Thr Ala Ala Ser Gly Gly Gly Gly Gly Gly Gly Val Val Met Lys Gly
 210 215 220

Cys Gly Thr Val Gly Thr His Gln Met Val Gly Asn Ala Gln Ile Leu
 225 230 235 240

Arg

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aatttataaa atatataaa aatagttata gctccccact tatat atg caa aag cca
 117

Met Gln Lys Pro
 1

aca tca agt atc tta aat gtc ata atg gac ggt gga gac agc gtc gga
 165
 Thr Ser Ser Ile Leu Asn Val Ile Met Asp Gly Gly Asp Ser Val Gly
 5 10 15 20

gga gga gga gga gat gat cac cac cgt cac ctc cac cat cac cac cgc
 213
 Gly Gly Gly Gly Asp Asp His His Arg His Leu His His His Arg
 25 30 35

cct act ttc cct ttt caa cta ctc gga aaa cac gac ccc gac gac aac
 261
 Pro Thr Phe Pro Phe Gln Leu Leu Gly Lys His Asp Pro Asp Asp Asn

40	45	50
cat caa caa caa cct tcc cct tcc tcc tcc tcc tct cta ttt tct ctc 309		
His Gln Gln Gln Pro Ser Pro Ser Ser Ser Ser Ser Leu Phe Ser Leu 55 60 65		
cat caa cac caa caa tta tct caa tog caa cct caa tcg caa tcg caa 357		
His Gln His Gln Gln Leu Ser Gln Ser Gln Pro Gln Ser Gln Ser Gln 70 75 80		
aag tca caa ccg cag aca acg caa aaa gag tta tta caa acg caa gag 405		
Lys Ser Gln Pro Gln Thr Thr Gln Lys Glu Leu Leu Gln Thr Gln Glu 85 90 95 100		
gaa tct gcg gtg gtg gca gct aaa aag cca ccg ttg aaa cga gcg tcg 453		
Glu Ser Ala Val Val Ala Ala Lys Lys Pro Pro Leu Lys Arg Ala Ser 105 110 115		
acg aaa gac cga cac acg aaa gta gac gga aga ggg agg aga ata agg 501		
Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly Arg Arg Ile Arg 120 125 130		
atg ccg gcg tta tgt gca gct agg gtt ttt cag cta acg cga gag cta 549		
Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu 135 140 145		
ggt cat aaa tcc gac ggt gag aca ata gag tgg ctt ctt caa caa gct 597		
Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala 150 155 160		
gaa cca tct gta atc gcc gcc acc gga acc gga aca atc ccg gcg aat 645		
Glu Pro Ser Val Ile Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala Asn 165 170 175 180		
ttc act tct tta aac atc tct ctc cgt tct tca ggc tct tcc atg tct 693		
Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly Ser Ser Met Ser 185 190 195		
ctt cct tct cat ttc cgc tcc gcc gct tcc act ttt agc cct aat aac 741		
Leu Pro Ser His Phe Arg Ser Ala Ala Ser Thr Phe Ser Pro Asn Asn 200 205 210		
ata ttt tct ccg gcg atg ctt caa caa caa caa caa caa caa cgt ggt 789		
Ile Phe Ser Pro Ala Met Leu Gln Gln Gln Gln Gln Gln Gln Arg Gly 215 220 225		
ggt ggt gtt ggg ttt cat cat ccc cat cta cag gga cgt gca cct acg 837		
Gly Gly Val Gly Phe His His Pro His Leu Gln Gly Arg Ala Pro Thr 230 235 240		

tcg tct ttg ttt cct ggt att gat aac ttc aca cca acg acg tcg ttt
 885
 Ser Ser Leu Phe Pro Gly Ile Asp Asn Phe Thr Pro Thr Thr Ser Phe
 245 250 255 260

ttg aac ttt cat aat cca aca aag caa gaa gga gat caa gat tct gaa
 933
 Leu Asn Phe His Asn Pro Thr Lys Gln Glu Gly Asp Gln Asp Ser Glu
 265 270 275

gag tta aac tcg gag aag aaa aga aga atc caa acg acg tcg gat ttg
 981
 Glu Leu Asn Ser Glu Lys Lys Arg Arg Ile Gln Thr Thr Ser Asp Leu
 280 285 290

cat caa caa caa caa caa cac caa cat gat caa atc gga gga tat aca
 1029
 His Gln Gln Gln Gln Gln His Gln His Asp Gln Ile Gly Gly Tyr Thr
 295 300 305

ctt caa tct agc aac agt gga tct acg gcc acc gca gcc gcc gcg caa
 1077
 Leu Gln Ser Ser Asn Ser Gly Ser Thr Ala Thr Ala Ala Ala Ala Gln
 310 315 320

caa ata ccg gga aat ttc tgg atg gtt gcg gcg gct gcg gct gca ggt
 1125
 Gln Ile Pro Gly Asn Phe Trp Met Val Ala Ala Ala Ala Ala Ala Gly
 325 330 335 340

ggt ggt ggt ggt aat aac aac caa aca ggt ggt ctt atg aca gct tct
 1173
 Gly Gly Gly Gly Asn Asn Asn Gln Thr Gly Gly Leu Met Thr Ala Ser
 345 350 355

att ggt act ggt ggc ggc ggt gga gag cct gtt tgg acg ttt cct tcc
 1221
 Ile Gly Thr Gly Gly Gly Gly Gly Glu Pro Val Trp Thr Phe Pro Ser
 360 365 370

att aac acg gca gcg gca gcg tta tat aga agt ggc gtt tcg ggc gtt
 1269
 Ile Asn Thr Ala Ala Ala Ala Leu Tyr Arg Ser Gly Val Ser Gly Val
 375 380 385

cca agc ggc gcg gtt tct agc ggt tta cat ttt atg aat ttc gca gcg
 1317
 Pro Ser Gly Ala Val Ser Ser Gly Leu His Phe Met Asn Phe Ala Ala
 390 395 400

cca atg gca ttt ctt act gga caa caa cag cta gca aca act agt aat
 1365
 Pro Met Ala Phe Leu Thr Gly Gln Gln Gln Leu Ala Thr Thr Ser Asn
 405 410 415 420

cat gag att aat gaa gat agt aat aat aat gaa gga gga aga agt gac
 1413
 His Glu Ile Asn Glu Asp Ser Asn Asn Asn Glu Gly Gly Arg Ser Asp
 425 430 435

ggt ggt ggt gat cat cat aat aca cag aga cat cat cat cat caa caa
1461

Gly Gly Gly Asp His His Asn Thr Gln Arg His His His His Gln Gln
440 445 450

caa cat cat cat aat att ctc tcc ggc ttg aac cag tac gga cgg caa
1509

Gln His His His Asn Ile Leu Ser Gly Leu Asn Gln Tyr Gly Arg Gln
455 460 465

gtt tcc ggc gac tct caa gct agt gga tca ctt gga ggt ggt gat gag
1557

Val Ser Gly Asp Ser Gln Ala Ser Gly Ser Leu Gly Gly Gly Asp Glu
470 475 480

gag gat cag caa gat tag acacacacaa aaacatttta atggtgggat
1605

Glu Asp Gln Gln Asp
485

tttctgccga cggcggtagc ggtgacggcg ttcggcggct gtgtaaaact tttgttttca
1665

ccgttaattt tttttatttt ctgtagtaat tttttttgct aagtaaaaaa aaaaaaaaaa
1725

aaa
1728

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170

Met Gln Lys Pro Thr Ser Ser Ile Leu Asn Val Ile Met Asp Gly Gly
1 5 10 15

Asp Ser Val Gly Gly Gly Gly Gly Asp Asp His His Arg His Leu His
20 25 30

His His His Arg Pro Thr Phe Pro Phe Gln Leu Leu Gly Lys His Asp
35 40 45

Pro Asp Asp Asn His Gln Gln Gln Pro Ser Pro Ser Ser Ser Ser
50 55 60

Leu Phe Ser Leu His Gln His Gln Gln Leu Ser Gln Ser Gln Pro Gln
65 70 75 80

Ser Gln Ser Gln Lys Ser Gln Pro Gln Thr Thr Gln Lys Glu Leu Leu
85 90 95

Gln Thr Gln Glu Glu Ser Ala Val Val Ala Ala Lys Lys Pro Pro Leu
100 105 110

Lys Arg Ala Ser Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly
 115 120 125

Arg Arg Ile Arg Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu
 130 135 140

Thr Arg Glu Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu
 145 150 155 160

Leu Gln Gln Ala Glu Pro Ser Val Ile Ala Ala Thr Gly Thr Gly Thr
 165 170 175

Ile Pro Ala Asn Phe Thr Ser Leu Asn Ile Ser Leu Arg Ser Ser Gly
 180 185 190

Ser Ser Met Ser Leu Pro Ser His Phe Arg Ser Ala Ala Ser Thr Phe
 195 200 205

Ser Pro Asn Asn Ile Phe Ser Pro Ala Met Leu Gln Gln Gln Gln Gln
 210 215 220

Gln Gln Arg Gly Gly Gly Val Gly Phe His His Pro His Leu Gln Gly
 225 230 235 240

Arg Ala Pro Thr Ser Ser Leu Phe Pro Gly Ile Asp Asn Phe Thr Pro
 245 250 255

Thr Thr Ser Phe Leu Asn Phe His Asn Pro Thr Lys Gln Glu Gly Asp
 260 265 270

Gln Asp Ser Glu Glu Leu Asn Ser Glu Lys Lys Arg Arg Ile Gln Thr
 275 280 285

Thr Ser Asp Leu His Gln Gln Gln Gln Gln His Gln His Asp Gln Ile
 290 295 300

Gly Gly Tyr Thr Leu Gln Ser Ser Asn Ser Gly Ser Thr Ala Thr Ala
 305 310 315 320

Ala Ala Ala Gln Gln Ile Pro Gly Asn Phe Trp Met Val Ala Ala Ala
 325 330 335

Ala Ala Ala Gly Gly Gly Gly Gly Asn Asn Asn Gln Thr Gly Gly Leu
 340 345 350

Met Thr Ala Ser Ile Gly Thr Gly Gly Gly Gly Glu Pro Val Trp

355 360 365
 Thr Phe Pro Ser Ile Asn Thr Ala Ala Ala Ala Leu Tyr Arg Ser Gly
 370 375 380
 Val Ser Gly Val Pro Ser Gly Ala Val Ser Ser Gly Leu His Phe Met
 385 390 395 400
 Asn Phe Ala Ala Pro Met Ala Phe Leu Thr Gly Gln Gln Gln Leu Ala
 405 410 415
 Thr Thr Ser Asn His Glu Ile Asn Glu Asp Ser Asn Asn Asn Glu Gly
 420 425 430
 Gly Arg Ser Asp Gly Gly Gly Asp His His Asn Thr Gln Arg His His
 435 440 445
 His His Gln Gln Gln His His His Asn Ile Leu Ser Gly Leu Asn Gln
 450 455 460
 Tyr Gly Arg Gln Val Ser Gly Asp Ser Gln Ala Ser Gly Ser Leu Gly
 465 470 475 480
 Gly Gly Asp Glu Glu Asp Gln Gln Asp
 485

<210> 171 <211> 1473 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (436)..(1371) <223> G1067

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 60
 atgcaaagaa gaagctactt ctttctcttg ccctaattaa tctacctaac tagggtttcc
 120
 tcttaccttt catgagagag atcatttaac ataagtcacc ttttttatat cttttgcttc
 180
 gtctttaatt tagttctgtt cttggctctgt ttctatatatt tgcggcttg cgtaaccgat
 240
 cacaccttaa tgcttttagct attgtttcct caaaatcatg agttttgact tctcgatctg
 300
 agttttcttt ttctctcttt acgctcttct tcacctagct accaatatat gaacgagcag
 360
 gatcaagaat cgagaaattg atttgagctg gcgaataagc agtggtggga tagggaatta
 420

gtagatgagg cgagg atg gaa ggc ggt tac gag caa ggc ggt gga gct tct
 471
 Met Glu Gly Gly Tyr Glu Gln Gly Gly Gly Ala Ser
 1 5 10

aga tac ttc cat aac ctc ttt aga ccg gag att cac cac caa cag ctt
 519
 Arg Tyr Phe His Asn Leu Phe Arg Pro Glu Ile His His Gln Gln Leu
 15 20 25

caa ccg cag ggc ggg atc aat ctt atc gac cag cat cat cat cag cac
 567
 Gln Pro Gln Gly Gly Ile Asn Leu Ile Asp Gln His His His Gln His
 30 35 40

cag caa cat caa caa caa caa ccg tcg gat gat tca aga gaa tct
 615
 Gln Gln His Gln Gln Gln Gln Pro Ser Asp Asp Ser Arg Glu Ser
 45 50 55 60

gac cat tca aac aaa gat cat cat caa cag ggt cga ccc gat tca gac
 663
 Asp His Ser Asn Lys Asp His His Gln Gln Gly Arg Pro Asp Ser Asp
 65 70 75

ccg aat aca tca agc tca gca ccg gga aaa cgt cca cgt gga cgt cca
 711
 Pro Asn Thr Ser Ser Ser Ala Pro Gly Lys Arg Pro Arg Gly Arg Pro
 80 85 90

cca gga tct aag aac aaa gcc aag cca ccg atc ata gta act cgt gat
 759
 Pro Gly Ser Lys Asn Lys Ala Lys Pro Pro Ile Ile Val Thr Arg Asp
 95 100 105

agc ccc aac gcg ctt aga tct cac gtt ctt gaa gta tct cct gga gct
 807
 Ser Pro Asn Ala Leu Arg Ser His Val Leu Glu Val Ser Pro Gly Ala
 110 115 120

gac ata gtt gag agt gtt tcc acg tac gct agg agg aga ggg aga ggc
 855
 Asp Ile Val Glu Ser Val Ser Thr Tyr Ala Arg Arg Arg Gly Arg Gly
 125 130 135 140

gtc tcc gtt tta gga gga aac ggc acc gta tct aac gtc act ctc cgt
 903
 Val Ser Val Leu Gly Gly Asn Gly Thr Val Ser Asn Val Thr Leu Arg
 145 150 155

cag cca gtc act cct gga aat ggc ggt ggt gtg tcc gga gga gga gga
 951
 Gln Pro Val Thr Pro Gly Asn Gly Gly Gly Val Ser Gly Gly Gly Gly
 160 165 170

gtt gtg act tta cat gga agg ttt gag att ctt tcg cta acg ggg act
 999
 Val Val Thr Leu His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr
 175 180 185

gtt ttg cca cct cct gca ccg cct ggt gcc ggt ggt ttg tct ata ttt
 1047
 Val Leu Pro Pro Pro Ala Pro Pro Gly Ala Gly Gly Leu Ser Ile Phe
 190 195 200

tta gcc gga ggg caa ggt cag gtg gtc gga gga agc gtt gtg gct ccc
 1095
 Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Ala Pro
 205 210 215 220

ctt att gca tca gct ccg gtt ata cta atg gcg gct tcg ttc tca aat
 1143
 Leu Ile Ala Ser Ala Pro Val Ile Leu Met Ala Ala Ser Phe Ser Asn
 225 230 235

gcg gtt ttc gag aga cta ccg att gag gag gag gaa gaa gaa ggt ggt
 1191
 Ala Val Phe Glu Arg Leu Pro Ile Glu Glu Glu Glu Glu Glu Gly Gly
 240 245 250

ggt ggc gga gga gga gga gga gga gga cca ccg cag atg caa caa gct
 1239
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro Pro Gln Met Gln Gln Ala
 255 260 265

cca tca gca tct ccg ccg tct gga gtg acc ggt cag gga cag tta gga
 1287
 Pro Ser Ala Ser Pro Pro Ser Gly Val Thr Gly Gln Gly Gln Leu Gly
 270 275 280

ggt aat gtg ggt ggt tat ggg ttt tct ggt gat cct cat ttg ctt gga
 1335
 Gly Asn Val Gly Gly Tyr Gly Phe Ser Gly Asp Pro His Leu Leu Gly
 285 290 295 300

tgg gga gct gga aca cct tca aga cca cct ttt taa ttgaatttta
 1381
 Trp Gly Ala Gly Thr Pro Ser Arg Pro Pro Phe
 305 310

atgtccggaa atttatgtgt ttttatcatc ttgaggagtc gtctttcctt tgggatattt
 1441

ggtgtttaat gtttagttga tatgcatatt tt
 1473

<210> 172 <211> 311 <212> PRT <213> Arabidopsis thaliana <400>
 172

Met Glu Gly Gly Tyr Glu Gln Gly Gly Gly Ala Ser Arg Tyr Phe His
 1 5 10 15

Asn Leu Phe Arg Pro Glu Ile His His Gln Gln Leu Gln Pro Gln Gly
 20 25 30

Gly Ile Asn Leu Ile Asp Gln His His His Gln His Gln Gln His Gln
 35 40 45

Gln Gln Gln Gln Pro Ser Asp Asp Ser Arg Glu Ser Asp His Ser Asn
 50 55 60

Lys Asp His His Gln Gln Gly Arg Pro Asp Ser Asp Pro Asn Thr Ser
 65 70 75 80

Ser Ser Ala Pro Gly Lys Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys
 85 90 95

Asn Lys Ala Lys Pro Pro Ile Ile Val Thr Arg Asp Ser Pro Asn Ala
 100 105 110

Leu Arg Ser His Val Leu Glu Val Ser Pro Gly Ala Asp Ile Val Glu
 115 120 125

Ser Val Ser Thr Tyr Ala Arg Arg Arg Gly Arg Gly Val Ser Val Leu
 130 135 140

Gly Gly Asn Gly Thr Val Ser Asn Val Thr Leu Arg Gln Pro Val Thr
 145 150 155 160

Pro Gly Asn Gly Gly Gly Val Ser Gly Gly Gly Val Val Thr Leu
 165 170 175

His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr Val Leu Pro Pro
 180 185 190

Pro Ala' Pro Pro Gly Ala Gly Gly Leu Ser Ile Phe Leu Ala Gly Gly
 195 200 205

Gln Gly Gln Val Val Gly Gly Ser Val Val Ala Pro Leu Ile Ala Ser
 210 215 220

Ala Pro Val Ile Leu Met Ala Ala Ser Phe Ser Asn Ala Val Phe Glu
 225 230 235 240

Arg Leu Pro Ile Glu Glu Glu Glu Glu Gly Gly Gly Gly Gly Gly
 245 250 255

Gly Gly Gly Gly Gly Pro Pro Gln Met Gln Gln Ala Pro Ser Ala Ser
 260 265 270

Pro Pro Ser Gly Val Thr Gly Gln Gly Gln Leu Gly Gly Asn Val Gly
 275 280 285

Gly Tyr Gly Phe Ser Gly Asp Pro His Leu Leu Gly Trp Gly Ala Gly
 290 295 300

Thr Pro Ser Arg Pro Pro Phe
 305 310

<210> 173 <211> 1295 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (170)..(1144) <223> G1070

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 60

gttttgacag caaaataaga agcaaaaaa aggtcaacta aaaaagatct gttcttagat
 120

cactctcttc ttcttttttt gatccaattc caccattgaa tcatagatc atg. gat cca
 178

Met Asp Pro
 1

gta caa tct cat gga tca caa agc tct cta cct cct cct ttc cac gca
 226

Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro Phe His Ala
 5 10 15

aga gac ttt caa tta cat ctt caa caa cag caa caa gag ttc ttc ctc
 274

Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Glu Phe Phe Leu
 20 25 30 35

cac cat cac cag caa caa aga aac caa acc gat ggt gac caa caa gga
 322

His His His Gln Gln Gln Arg Asn Gln Thr Asp Gly Asp Gln Gln Gly
 40 45 50

gga tca gga gga aac cga caa atc aag atg gat cgt gaa gag aca agc
 370

Gly Ser Gly Gly Asn Arg Gln Ile Lys Met Asp Arg Glu Glu Thr Ser
 55 60 65

gac aac ata gac aac ata gct aac aac agc ggt agt gaa ggt aaa gac
 418

Asp Asn Ile Asp Asn Ile Ala Asn Asn Ser Gly Ser Glu Gly Lys Asp
 70 75 80

ata gat ata cac ggt ggt tca gga gaa gga ggt ggt ggc tcc gga gga
 466

Ile Asp Ile His Gly Gly Ser Gly Glu Gly Gly Gly Gly Ser Gly Gly
 85 90 95

gat cat cag atg aca aga aga cca aga gga aga cca gcg gga tcc aag
 514

Asp His Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
 100 105 110 115

aac aaa cca aaa cca ccg att atc atc aca cgg gac agc gca aac gcg
 562

Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala

120 125 130
 ctt aga acc cac gtg atg gag atc gga gat ggc tgc gac tta gtc gaa
 610
 Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Leu Val Glu
 135 140 145
 agc gtt gcc act ttt gca cga aga cgc caa cgc ggc gtt tgc gtt atg
 658
 Ser Val Ala Thr Phe Ala Arg Arg Gln Arg Gly Val Cys Val Met
 150 155 160
 agc ggt act gga aat gtt act aac gtc act ata cgt cag cct gga tct
 706
 Ser Gly Thr Gly Asn Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser
 165 170 175
 cat cct tct cct ggc tcg gta gtt agt ctt cac gga agg ttc gag att
 754
 His Pro Ser Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile
 180 185 190 195
 cta tct ctc tca gga tct ttt ctc cct cct ccg gct cct cct aca gcc
 802
 Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Thr Ala
 200 205 210
 acc gga ttg agt gtt tac ctc gct gga gga caa gga cag gtg gtt gga
 850
 Thr Gly Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly
 215 220 225
 gga agc gta gtt ggt ccg ttg tta tgt gct ggt cct gtc gtt gtc atg
 898
 Gly Ser Val Val Gly Pro Leu Leu Cys Ala Gly Pro Val Val Val Met
 230 235 240
 gct gcg tct ttt agc aat gcg gcg tac gaa agg ttg cct tta gag gaa
 946
 Ala Ala Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu
 245 250 255
 gat gag atg cag acg ccg gtt cat ggc gga gga gga gga tca ttg
 994
 Asp Glu Met Gln Thr Pro Val His Gly Gly Gly Gly Gly Ser Leu
 260 265 270 275
 gag tcg ccg cca atg atg gga caa caa ctg caa cat cag caa caa gct
 1042
 Glu Ser Pro Pro Met Met Gly Gln Gln Leu Gln His Gln Gln Ala
 280 285 290
 atg tca ggt cat caa ggg tta cca cct aat ctt ctt ggt tcg gtt cag
 1090
 Met Ser Gly His Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln
 295 300 305
 ttg cag cag caa cat gat cag tct tat tgg tca acg gga cga cca ccg
 1138
 Leu Gln Gln Gln His Asp Gln Ser Tyr Trp Ser Thr Gly Arg Pro Pro
 310 315 320

tat tga tcaaataac acacacactc ataatcgttg ctagctagct aacgatgaat
 1194
 Tyr

catgagttta gtggatatat atatgattaa aagagggttag cttatgaaca ttaataagag
 1254

tttgattct atcgagcttc attatgtttg ggtcatcggt c
 1295

<210> 174 <211> 324 <212> PRT <213> Arabidopsis thaliana <400>
 174

Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro
 1 5 10 15

Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Glu
 20 25 30

Phe Phe Leu His His His Gln Gln Gln Arg Asn Gln Thr Asp Gly Asp
 35 40 45

Gln Gln Gly Gly Ser Gly Gly Asn Arg Gln Ile Lys Met Asp Arg Glu
 50 55 60

Glu Thr Ser Asp Asn Ile Asp Asn Ile Ala Asn Asn Ser Gly Ser Glu
 65 70 75 80

Gly Lys Asp Ile Asp Ile His Gly Gly Ser Gly Glu Gly Gly Gly Gly
 85 90 95

Ser Gly Gly Asp His Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala
 100 105 110

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser
 115 120 125

Ala Asn Ala Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp
 130 135 140

Ile Val Glu Ser Val Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val
 145 150 155 160

Cys Val Met Ser Gly Thr Gly Asn Val Thr Asn Val Thr Ile Arg Gln
 165 170 175

Pro Gly Ser His Pro Ser Pro Gly Ser Val Val Ser Leu His Gly Arg

180 185 190

Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro
195 200 205

Pro Thr Ala Thr Gly Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln
210 215 220

Val Val Gly Gly Ser Val Val Gly Pro Leu Leu Cys Ala Gly Pro Val
225 230 235 240

Val Val Met Ala Ala Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro
245 250 255

Leu Glu Glu Asp Glu Met Gln Thr Pro Val His Gly Gly Gly Gly Gly
260 265 270

Gly Ser Leu Glu Ser Pro Pro Met Met Gly Gln Gln Leu Gln His Gln
275 280 285

Gln Gln Ala Met Ser Gly His Gln Gly Leu Pro Pro Asn Leu Leu Gly
290 295 300

Ser Val Gln Leu Gln Gln Gln His Asp Gln Ser Tyr Trp Ser Thr Gly
305 310 315 320

Arg Pro Pro Tyr

<210> 175 <211> 1084 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (19)..(876) <223> G1075

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51
Met Ala Gly Leu Asp Leu Gly Thr Thr Ser Arg
1 5 10
tac gtc cac aac gtc gat ggt ggc ggc gga cag ttc acc acc gac
99
Tyr Val His Asn Val Asp Gly Gly Gly Gly Gln Phe Thr Thr Asp
15 20 25
aac cac cac gaa gat gac ggt ggc gct gga gga aac cac cat cat cac
147
Asn His His Glu Asp Asp Gly Gly Ala Gly Gly Asn His His His His
30 35 40
cat cat aat cat aat cac cat caa ggt tta gat tta ata gct tct aat
195
His His Asn His Asn His His Gln Gly Leu Asp Leu Ile Ala Ser Asn

45	50	55
gat aac tct gga cta ggc ggc ggt gga gga gga ggg agc ggt gac ctc 243		
Asp Asn Ser Gly Leu Gly Gly Gly Gly Gly Gly Ser Gly Asp Leu 60 65 70 75		
gtc atg cgt cgg cca cgt ggc cgt cca gct gga tcg aag aac aaa ccg 291		
Val Met Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro 80 85 90		
aag ccg ccg gtg att gtc acg cgc gag agc gca aac act ctt agg gct 339		
Lys Pro Pro Val Ile Val Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala 95 100 105		
cac att ctt gaa gtt gga agt ggc tgc gac gtt ttc gaa tgt atc tcc 387		
His Ile Leu Glu Val Gly Ser Gly Cys Asp Val Phe Glu Cys Ile Ser 110 115 120		
act tac gct cgt cgg aga cag cgc ggg att tgc gtt tta tcc ggg acg 435		
Thr Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Thr 125 130 135		
gga acc gtc act aac gtc agc atc cgt cag cct acg gcg gcc gga gct 483		
Gly Thr Val Thr Asn Val Ser Ile Arg Gln Pro Thr Ala Ala Gly Ala 140 145 150 155		
gtt gtg act ctg cgg ggt act ttt gag att ctt tcc ctc tcc gga tct 531		
Val Val Thr Leu Arg Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser 160 165 170		
ttt ctt ccg cca cct gct cct cca ggg gcg act agc ttg acg ata ttc 579		
Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe 175 180 185		
ctc gct gga gct caa gga cag gtc gtc gga ggt aac gta gtt ggt gag 627		
Leu Ala Gly Ala Gln Gly Gln Val Val Gly Gly Asn Val Val Gly Glu 190 195 200		
tta atg gcg gcg ggg ccg gta atg gtc atg gca gcg tct ttt aca aac 675		
Leu Met Ala Ala Gly Pro Val Met Val Met Ala Ala Ser Phe Thr Asn 205 210 215		
gtg gct tac gaa agg ttg cct ttg gac gag cat gag gag cac ttg caa 723		
Val Ala Tyr Glu Arg Leu Pro Leu Asp Glu His Glu Glu His Leu Gln 220 225 230 235		
agt ggc ggc ggc gga ggt gga ggg aat atg tac tcg gaa gcc act ggc 771		
Ser Gly Gly Gly Gly Gly Gly Gly Asn Met Tyr Ser Glu Ala Thr Gly 240 245 250		

ggt ggc gga ggg ttg cct ttc ttt aat ttg ccg atg agt atg cct cag
 819
 Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu Pro Met Ser Met Pro Gln
 255 260 265

att gga gtt gaa agt tgg cag ggg aat cac gcc gcc ggt agg gct
 867
 Ile Gly Val Glu Ser Trp Gln Gly Asn His Ala Gly Ala Gly Arg Ala
 270 275 280

ccg ttt tag caatttaaga aactttaatt gttttttcca cttttttggt
 916
 Pro Phe
 285

tttctccgaa ttttatgaaa ttatgattta agaaaaaaaa cgatattggt catgtattga
 976

ccctcttact gcatggtttc ttctattggg ttaattggct agctcataag aattgtttaa
 1036

tttggttatt gtcacaaat ttgccacat ataaagcttc tagcaaat
 1084

<210> 176 <211> 285 <212> PRT <213> Arabidopsis thaliana <400>
 176

Met Ala Gly Leu Asp Leu Gly Thr Thr Ser Arg Tyr Val His Asn Val
 1 5 10 15

Asp Gly Gly Gly Gly Gly Gln Phe Thr Thr Asp Asn His His Glu Asp
 20 25 30

Asp Gly Gly Ala Gly Gly Asn His His His His His His Asn His Asn
 35 40 45

His His Gln Gly Leu Asp Leu Ile Ala Ser Asn Asp Asn Ser Gly Leu
 50 55 60

Gly Gly Gly Gly Gly Gly Gly Ser Gly Asp Leu Val Met Arg Arg Pro
 65 70 75 80

Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro Val Ile
 85 90 95

Val Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His Ile Leu Glu Val
 100 105 110

Gly Ser Gly Cys Asp Val Phe Glu Cys Ile Ser Thr Tyr Ala Arg Arg
 115 120 125

Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Thr Gly Thr Val Thr Asn
 130 135 140

Val Ser Ile Arg Gln Pro Thr Ala Ala Gly Ala Val Val Thr Leu Arg
 145 150 155 160

Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro
 165 170 175

Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe Leu Ala Gly Ala Gln
 180 185 190

Gly Gln Val Val Gly Gly Asn Val Val Gly Glu Leu Met Ala Ala Gly
 195 200 205

Pro Val Met Val Met Ala Ala Ser Phe Thr Asn Val Ala Tyr Glu Arg
 210 215 220

Leu Pro Leu Asp Glu His Glu Glu His Leu Gln Ser Gly Gly Gly Gly
 225 230 235 240

Gly Gly Gly Asn Met Tyr Ser Glu Ala Thr Gly Gly Gly Gly Gly Leu
 245 250 255

Pro Phe Phe Asn Leu Pro Met Ser Met Pro Gln Ile Gly Val Glu Ser
 260 265 270

Trp Gln Gly Asn His Ala Gly Ala Gly Arg Ala Pro Phe
 275 280 285

<210> 177 <211> 2663 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (31)..(2427) <223> G1089

<400> 177
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 54

Met Gly Cys Ala Gln Ser Lys Ile
 1 5

gag aac gaa gaa gca gtt act cgt tgc aaa gaa cga aaa caa ttg atg
 102

Glu Asn Glu Glu Ala Val Thr Arg Cys Lys Glu Arg Lys Gln Leu Met
 10 15 20

aaa gac gcc gtc act gct cgt aac gct ttc gcc gcc gct cac tca gct
 150

Lys Asp Ala Val Thr Ala Arg Asn Ala Phe Ala Ala Ala His Ser Ala
 25 30 35 40

tac gct atg gct ctt aaa aac acc gga gct gct ctt tcc gat tac tct
 198

Tyr Ala Met Ala Leu Lys Asn Thr Gly Ala Ala Leu Ser Asp Tyr Ser
 45 50 55
 cac ggc gag ttt tta gtc tct aat cac tcg tct tcc tcc gca gct gca
 246
 His Gly Glu Phe Leu Val Ser Asn His Ser Ser Ser Ser Ala Ala Ala
 60 65 70
 gca atc gct tct act tct tct ctt ccc act gct ata tct cct cct ctt
 294
 Ala Ile Ala Ser Thr Ser Ser Leu Pro Thr Ala Ile Ser Pro Pro Leu
 75 80 85
 cct tct tcc acc gct ccg gtt tct aat tca acc gct tct tct tcc tcc
 342
 Pro Ser Ser Thr Ala Pro Val Ser Asn Ser Thr Ala Ser Ser Ser Ser
 90 95 100
 gct gcg gtt cct cag ccg att cct gat act ctt cct cct cct cct
 390
 Ala Ala Val Pro Gln Pro Ile Pro Asp Thr Leu Pro Pro Pro Pro Pro
 105 110 115 120
 cca cca ccg ctt cct ctt caa cgt gct gct act atg ccg gag atg aac
 438
 Pro Pro Pro Leu Pro Leu Gln Arg Ala Ala Thr Met Pro Glu Met Asn
 125 130 135
 ggt aga tcc ggt ggt ggt cat gct ggt agt gga ctc aac gga att gaa
 486
 Gly Arg Ser Gly Gly Gly His Ala Gly Ser Gly Leu Asn Gly Ile Glu
 140 145 150
 gaa gat gga gcc cta gat aac gat gat gat gac gat gat gat gat
 534
 Glu Asp Gly Ala Leu Asp Asn Asp Asp Asp Asp Asp Asp Asp Asp
 155 160 165
 gac tct gaa atg gag aat cgt gat cgt ttg att agg aaa tcg aga agc
 582
 Asp Ser Glu Met Glu Asn Arg Asp Arg Leu Ile Arg Lys Ser Arg Ser
 170 175 180
 cgt gga ggt agt act aga gga aat agg acg acg att gaa gat cat cat
 630
 Arg Gly Gly Ser Thr Arg Gly Asn Arg Thr Thr Ile Glu Asp His His
 185 190 195 200
 ctt cag gag gag aaa gct ccg cca cct ccc cct ttg gcg aat tcg cgg
 678
 Leu Gln Glu Glu Lys Ala Pro Pro Pro Pro Leu Ala Asn Ser Arg
 205 210 215
 cca att ccg ccg cca cgt cag cat cag cat caa cat cag caa cag caa
 726
 Pro Ile Pro Pro Pro Arg Gln His Gln His Gln His Gln Gln Gln
 220 225 230
 caa caa cct ttc tac gat tac ttc ttc cct aat gtt gag aat atg cct
 774
 Gln Gln Pro Phe Tyr Asp Tyr Phe Phe Pro Asn Val Glu Asn Met Pro

235	240	245
gga act act tta gaa gat act cct cca caa cca caa cca cca aca		
822		
Gly Thr Thr Leu Glu Asp Thr Pro Pro Gln Pro Gln Pro Gln Pro Thr		
250	255	260
agg cct gtg cct cct caa cca cat tca cca gtc gtt act gag gat gac		
870		
Arg Pro Val Pro Pro Gln Pro His Ser Pro Val Val Thr Glu Asp Asp		
265	270	275 280
gaa gat gag gag gag gaa gag gag gaa gag gag gag gaa gag gag acg		
918		
Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Thr		
	285	290 295
gtg att gaa cgg aaa cca ctg gtg gag gaa aga ccg aag aga gta gag		
966		
Val Ile Glu Arg Lys Pro Leu Val Glu Glu Arg Pro Lys Arg Val Glu		
	300	305 310
gaa gtg acg att gaa ttg gaa aaa gtt act aat ttg aga ggg atg aag		
1014		
Glu Val Thr Ile Glu Leu Glu Lys Val Thr Asn Leu Arg Gly Met Lys		
	315	320 325
aag agt aaa ggg ata ggg att ccc gga gag agg aga gga atg cga atg		
1062		
Lys Ser Lys Gly Ile Gly Ile Pro Gly Glu Arg Arg Gly Met Arg Met		
	330	335 340
ccg gtg act gcg acg cat ttg gcg aat gta ttc att gag ctt gat gat		
1110		
Pro Val Thr Ala Thr His Leu Ala Asn Val Phe Ile Glu Leu Asp Asp		
345	350	355 360
aat ttc ttg aaa gct tct gaa agt gct cat gat gtt tct aag atg ctt		
1158		
Asn Phe Leu Lys Ala Ser Glu Ser Ala His Asp Val Ser Lys Met Leu		
	365	370 375
gaa gct act agg ctc cat tac cat tct aat ttt gca gat aac cga gga		
1206		
Glu Ala Thr Arg Leu His Tyr His Ser Asn Phe Ala Asp Asn Arg Gly		
	380	385 390
cat att gat cac tct gct aga gtg atg cgt gta att aca tgg aat aga		
1254		
His Ile Asp His Ser Ala Arg Val Met Arg Val Ile Thr Trp Asn Arg		
	395	400 405
tca ttt aga gga ata cca aat gct gat gat ggg aaa gat gat gtt gat		
1302		
Ser Phe Arg Gly Ile Pro Asn Ala Asp Asp Gly Lys Asp Asp Val Asp		
	410	415 420
ttg gaa gag aat gaa act cat gct act gtt ctt gac aaa ttg cta gca		
1350		
Leu Glu Glu Asn Glu Thr His Ala Thr Val Leu Asp Lys Leu Leu Ala		
425	430	435 440

tgg gaa aag aag ctc tat gac gaa gtc aag gct ggc gaa ctc atg aaa
 1398
 Trp Glu Lys Lys Leu Tyr Asp Glu Val Lys Ala Gly Glu Leu Met Lys
 445 450 455

atc gag tac cag aaa aag gtt gct cat tta aat cgg gtg aag aaa cga
 1446
 Ile Glu Tyr Gln Lys Lys Val Ala His Leu Asn Arg Val Lys Lys Arg
 460 465 470

ggt ggc cac tcg gat tca tta gag aga gct aaa gca gca gta agt cat
 1494
 Gly Gly His Ser Asp Ser Leu Glu Arg Ala Lys Ala Val Ser His
 475 480 485

ttg cat aca aga tat ata gtt gat atg caa tcc atg gac tcc aca gtt
 1542
 Leu His Thr Arg Tyr Ile Val Asp Met Gln Ser Met Asp Ser Thr Val
 490 495 500

tca gaa atc aat cgt ctt agg gat gaa caa cta tac cta aag ctc gtt
 1590
 Ser Glu Ile Asn Arg Leu Arg Asp Glu Gln Leu Tyr Leu Lys Leu Val
 505 510 515 520

cac ctt gtt gag gcg atg ggg aag atg tgg gaa atg atg caa ata cat
 1638
 His Leu Val Glu Ala Met Gly Lys Met Trp Glu Met Met Gln Ile His
 525 530 535

cat caa aga caa gct gag atc tca aag gtg ttg aga tct cta gat gtt
 1686
 His Gln Arg Gln Ala Glu Ile Ser Lys Val Leu Arg Ser Leu Asp Val
 540 545 550

tca caa gcg gtg aaa gaa aca aat gat cat cat cac gaa cgc acc atc
 1734
 Ser Gln Ala Val Lys Glu Thr Asn Asp His His His Glu Arg Thr Ile
 555 560 565

cag ctc ttg gca gtg gtt caa gaa tgg cac acg cag ttt tgc agg atg
 1782
 Gln Leu Leu Ala Val Val Gln Glu Trp His Thr Gln Phe Cys Arg Met
 570 575 580

ata gat cat cag aaa gaa tac ata aaa gca ctt ggc gga tgg cta aag
 1830
 Ile Asp His Gln Lys Glu Tyr Ile Lys Ala Leu Gly Gly Trp Leu Lys
 585 590 595 600

cta aat ctc atc cct atc gaa agc aca ctc aag gag aaa gta tct tcg
 1878
 Leu Asn Leu Ile Pro Ile Glu Ser Thr Leu Lys Glu Lys Val Ser Ser
 605 610 615

cct cct cga gtt ccc aat ccc gca atc caa aaa ctc ctc cac gct tgg
 1926
 Pro Pro Arg Val Pro Asn Pro Ala Ile Gln Lys Leu Leu His Ala Trp
 620 625 630

tat gac cgt tta gac aaa atc ccc gac gaa atg gct aaa agt gcc ata
 1974
 Tyr Asp Arg Leu Asp Lys Ile Pro Asp Glu Met Ala Lys Ser Ala Ile
 635 640 645

atc aat ttc gca gcg gtt gta agc acg ata atg cag cag caa gaa gac
 2022
 Ile Asn Phe Ala Ala Val Val Ser Thr Ile Met Gln Gln Gln Glu Asp
 650 655 660

gag ata agt ctc aga aac aaa tgc gaa gag aca aga aaa gaa ttg gga
 2070
 Glu Ile Ser Leu Arg Asn Lys Cys Glu Glu Thr Arg Lys Glu Leu Gly
 665 670 675 680

aga aaa att aga cag ttt gag gat tgg tac cac aaa tac atc cag aag
 2118
 Arg Lys Ile Arg Gln Phe Glu Asp Trp Tyr His Lys Tyr Ile Gln Lys
 685 690 695

aga gga ccg gag ggg atg aat ccg gat gaa gcg gat aac gat cat aat
 2166
 Arg Gly Pro Glu Gly Met Asn Pro Asp Glu Ala Asp Asn Asp His Asn
 700 705 710

gat gag gtc gct gtg agg caa ttc aat gta gaa caa att aag aag agg
 2214
 Asp Glu Val Ala Val Arg Gln Phe Asn Val Glu Gln Ile Lys Lys Arg
 715 720 725

ttg gaa gaa gaa gaa gaa gct tac cat aga caa agc cat caa gtt aga
 2262
 Leu Glu Glu Glu Glu Glu Ala Tyr His Arg Gln Ser His Gln Val Arg
 730 735 740

gag aag tca ctg gct agt ctt cga act cgc ctc ccc gag ctt ttt cag
 2310
 Glu Lys Ser Leu Ala Ser Leu Arg Thr Arg Leu Pro Glu Leu Phe Gln
 745 750 755 760

gca atg tcc gag gtt gcg tat tca tgt tcg gat atg tat aga gct ata
 2358
 Ala Met Ser Glu Val Ala Tyr Ser Cys Ser Asp Met Tyr Arg Ala Ile
 765 770 775

acg tat gcg agt aag cgg caa agc caa agc gaa cgg cat cag aaa cct
 2406
 Thr Tyr Ala Ser Lys Arg Gln Ser Gln Ser Glu Arg His Gln Lys Pro
 780 785 790

agc cag gga cag agt tcg taa gaactaatgt aagatcagag taatgtcttc
 2457
 Ser Gln Gly Gln Ser Ser
 795

ttcttctttg atcttgaata tttaagcaca cacatacata caacgtatag ctaaatcttt
 2517

atcattgctt tcttatatta aggttttggc ttttgtaaga aggtttctta catatgagat
 2577

tcatatagtg ttgtattcctt aaggaactgt tctgttgagt aataagaaag ttgtgtattg
2637

aaatagagtt gcatttggtta attttg
2663

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178

Met Gly Cys Ala Gln Ser Lys Ile Glu Asn Glu Glu Ala Val Thr Arg
1 5 10 15

Cys Lys Glu Arg Lys Gln Leu Met Lys Asp Ala Val Thr Ala Arg Asn
20 25 30

Ala Phe Ala Ala Ala His Ser Ala Tyr Ala Met Ala Leu Lys Asn Thr
35 40 45

Gly Ala Ala Leu Ser Asp Tyr Ser His Gly Glu Phe Leu Val Ser Asn
50 55 60

His Ser Ser Ser Ser Ala Ala Ala Ala Ile Ala Ser Thr Ser Ser Leu
65 70 75 80

Pro Thr Ala Ile Ser Pro Pro Leu Pro Ser Ser Thr Ala Pro Val Ser
85 90 95

Asn Ser Thr Ala Ser Ser Ser Ser Ala Ala Val Pro Gln Pro Ile Pro
100 105 110

Asp Thr Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro Leu Gln Arg
115 120 125

Ala Ala Thr Met Pro Glu Met Asn Gly Arg Ser Gly Gly Gly His Ala
130 135 140

Gly Ser Gly Leu Asn Gly Ile Glu Glu Asp Gly Ala Leu Asp Asn Asp
145 150 155 160

Asp Asp Asp Asp Asp Asp Asp Asp Asp Ser Glu Met Glu Asn Arg Asp
165 170 175

Arg Leu Ile Arg Lys Ser Arg Ser Arg Gly Gly Ser Thr Arg Gly Asn
180 185 190

Arg Thr Thr Ile Glu Asp His His Leu Gln Glu Glu Lys Ala Pro Pro
195 200 205

Pro Pro Pro Leu Ala Asn Ser Arg Pro Ile Pro Pro Pro Arg Gln His
 210 215 220
 Gln His Gln His Gln Gln Gln Gln Gln Pro Phe Tyr Asp Tyr Phe
 225 230 235 240
 Phe Pro Asn Val Glu Asn Met Pro Gly Thr Thr Leu Glu Asp Thr Pro
 245 250 255
 Pro Gln Pro Gln Pro Gln Pro Thr Arg Pro Val Pro Pro Gln Pro His
 260 265 270
 Ser Pro Val Val Thr Glu Asp Asp Glu Asp Glu Glu Glu Glu Glu
 275 280 285
 Glu Glu Glu Glu Glu Glu Glu Thr Val Ile Glu Arg Lys Pro Leu Val
 290 295 300
 Glu Glu Arg Pro Lys Arg Val Glu Glu Val Thr Ile Glu Leu Glu Lys
 305 310 315 320
 Val Thr Asn Leu Arg Gly Met Lys Lys Ser Lys Gly Ile Gly Ile Pro
 325 330 335
 Gly Glu Arg Arg Gly Met Arg Met Pro Val Thr Ala Thr His Leu Ala
 340 345 350
 Asn Val Phe Ile Glu Leu Asp Asp Asn Phe Leu Lys Ala Ser Glu Ser
 355 360 365
 Ala His Asp Val Ser Lys Met Leu Glu Ala Thr Arg Leu His Tyr His
 370 375 380
 Ser Asn Phe Ala Asp Asn Arg Gly His Ile Asp His Ser Ala Arg Val
 385 390 395 400
 Met Arg Val Ile Thr Trp Asn Arg Ser Phe Arg Gly Ile Pro Asn Ala
 405 410 415
 Asp Asp Gly Lys Asp Asp Val Asp Leu Glu Glu Asn Glu Thr His Ala
 420 425 430
 Thr Val Leu Asp Lys Leu Leu Ala Trp Glu Lys Lys Leu Tyr Asp Glu
 435 440 445

Val Lys Ala Gly Glu Leu Met Lys Ile Glu Tyr Gln Lys Lys Val Ala
 450 455 460

His Leu Asn Arg Val Lys Lys Arg Gly Gly His Ser Asp Ser Leu Glu
 465 470 475 480

Arg Ala Lys Ala Ala Val Ser His Leu His Thr Arg Tyr Ile Val Asp
 485 490 495

Met Gln Ser Met Asp Ser Thr Val Ser Glu Ile Asn Arg Leu Arg Asp
 500 505 510

Glu Gln Leu Tyr Leu Lys Leu Val His Leu Val Glu Ala Met Gly Lys
 515 520 525

Met Trp Glu Met Met Gln Ile His His Gln Arg Gln Ala Glu Ile Ser
 530 535 540

Lys Val Leu Arg Ser Leu Asp Val Ser Gln Ala Val Lys Glu Thr Asn
 545 550 555 560

Asp His His His Glu Arg Thr Ile Gln Leu Leu Ala Val Val Gln Glu
 565 570 575

Trp His Thr Gln Phe Cys Arg Met Ile Asp His Gln Lys Glu Tyr Ile
 580 585 590

Lys Ala Leu Gly Gly Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser
 595 600 605

Thr Leu Lys Glu Lys Val Ser Ser Pro Pro Arg Val Pro Asn Pro Ala
 610 615 620

Ile Gln Lys Leu Leu His Ala Trp Tyr Asp Arg Leu Asp Lys Ile Pro
 625 630 635 640

Asp Glu Met Ala Lys Ser Ala Ile Ile Asn Phe Ala Ala Val Val Ser
 645 650 655

Thr Ile Met Gln Gln Gln Glu Asp Glu Ile Ser Leu Arg Asn Lys Cys
 660 665 670

Glu Glu Thr Arg Lys Glu Leu Gly Arg Lys Ile Arg Gln Phe Glu Asp
 675 680 685

Trp Tyr His Lys Tyr Ile Gln Lys Arg Gly Pro Glu Gly Met Asn Pro

690 695 700
 Asp Glu Ala Asp Asn Asp His Asn Asp Glu Val Ala Val Arg Gln Phe
 705 710 715 720
 Asn Val Glu Gln Ile Lys Lys Arg Leu Glu Glu Glu Glu Ala Tyr
 725 730 735
 His Arg Gln Ser His Gln Val Arg Glu Lys Ser Leu Ala Ser Leu Arg
 740 745 750
 Thr Arg Leu Pro Glu Leu Phe Gln Ala Met Ser Glu Val Ala Tyr Ser
 755 760 765
 Cys Ser Asp Met Tyr Arg Ala Ile Thr Tyr Ala Ser Lys Arg Gln Ser
 770 775 780
 Gln Ser Glu Arg His Gln Lys Pro Ser Gln Gly Gln Ser Ser
 785 790 795

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 48
 Met Asp Leu Thr Asp Arg Arg Asn Pro Phe Asn Asn Leu Val Phe Pro
 1 5 10 15
 ccg ccg cct ccg ccg cca tcc acg acc ttc aca agc cct ata ttc cca
 96
 Pro Pro Pro Pro Pro Pro Ser Thr Thr Phe Thr Ser Pro Ile Phe Pro
 20 25 30
 cga aca agc tct tcc ggc acc aat ttc ccc att ctg gcc atc gca gtg
 144
 Arg Thr Ser Ser Ser Gly Thr Asn Phe Pro Ile Leu Ala Ile Ala Val
 35 40 45
 att gga atc tta gcc act gcg ttc tta ctt gta agt tac tac atc ttc
 192
 Ile Gly Ile Leu Ala Thr Ala Phe Leu Leu Val Ser Tyr Tyr Ile Phe
 50 55 60
 gtg atc aaa tgc tgt ctt aat tgg cac caa atc gac atc ttt cgc cgc
 240
 Val Ile Lys Cys Cys Leu Asn Trp His Gln Ile Asp Ile Phe Arg Arg
 65 70 75 80
 cgc aga cga agc agt gac caa aac cct cta atg att tac tct cct cat
 288
 Arg Arg Arg Ser Ser Asp Gln Asn Pro Leu Met Ile Tyr Ser Pro His
 85 90 95

gag gta aac aga gga cta gac gaa tcc gcc att aga gct atc cca gtc
 336
 Glu Val Asn Arg Gly Leu Asp Glu Ser Ala Ile Arg Ala Ile Pro Val
 100 105 110

ttc aaa ttc aag aag aga gac gtt gtt gca gga gaa gaa gat cag agt
 384
 Phe Lys Phe Lys Lys Arg Asp Val Val Ala Gly Glu Glu Asp Gln Ser
 115 120 125

aag aac tct caa gaa tgc tct gtt tgt tta aac gag ttt caa gaa gac
 432
 Lys Asn Ser Gln Glu Cys Ser Val Cys Leu Asn Glu Phe Gln Glu Asp
 130 135 140

gag aag cta agg att att cct aac tgc tgc cac gtg ttt cac att gat
 480
 Glu Lys Leu Arg Ile Ile Pro Asn Cys Cys His Val Phe His Ile Asp
 145 150 155 160

tgc att gat atc tgg ctt cag ggc aac gca aat tgt ccc ttg tgc aga
 528
 Cys Ile Asp Ile Trp Leu Gln Gly Asn Ala Asn Cys Pro Leu Cys Arg
 165 170 175

acc agc gtt tct tgc gaa gca agt ttc act ctt gac cta atc tct gca
 576
 Thr Ser Val Ser Cys Glu Ala Ser Phe Thr Leu Asp Leu Ile Ser Ala
 180 185 190

ccg agc tct cct cgg gag aat agc cct cat tct cgg aac agg aat ctc
 624
 Pro Ser Ser Pro Arg Glu Asn Ser Pro His Ser Arg Asn Arg Asn Leu
 195 200 205

gaa ccc ggc ctg gtt cta gga ggc gat gat gac ttc gtc gtc ata gag
 672
 Glu Pro Gly Leu Val Leu Gly Gly Asp Asp Asp Phe Val Val Ile Glu
 210 215 220

ctt ggg gcc agt aat ggt aac aac aga gaa agc gtg aga aac ata gac
 720
 Leu Gly Ala Ser Asn Gly Asn Asn Arg Glu Ser Val Arg Asn Ile Asp
 225 230 235 240

ttc ctt acg gag caa gaa agg gtt acc tcg aat gag gtc tcg acc gga
 768
 Phe Leu Thr Glu Gln Glu Arg Val Thr Ser Asn Glu Val Ser Thr Gly
 245 250 255

aac agc ccg aaa tcg gtg agt cct ttg cct ata aag ttt ggt aat cgg
 816
 Asn Ser Pro Lys Ser Val Ser Pro Leu Pro Ile Lys Phe Gly Asn Arg
 260 265 270

gga atg tat aag aaa gaa agg aaa ttt cac aaa gtg acg agt atg gga
 864
 Gly Met Tyr Lys Lys Glu Arg Lys Phe His Lys Val Thr Ser Met Gly
 275 280 285

gac gaa tgt atc gat act aga ggc aaa gat ggt cat ttt ggt gaa att
912

Asp Glu Cys Ile Asp Thr Arg Gly Lys Asp Gly His Phe Gly Glu Ile
290 295 300

cag ccc ata aga aga tcg atc tcg atg gat tca tca gtg gat cgt cag
960

Gln Pro Ile Arg Arg Ser Ile Ser Met Asp Ser Ser Val Asp Arg Gln
305 310 315 320

ctg tac ttg gcg gtc caa gag gaa atc agc cgg aga aac agg cag att
1008

Leu Tyr Leu Ala Val Gln Glu Glu Ile Ser Arg Arg Asn Arg Gln Ile
325 330 335

ccg gta gct gga gac ggt gaa gat agt agc agt agt ggt ggt ggt aat
1056

Pro Val Ala Gly Asp Gly Glu Asp Ser Ser Ser Ser Gly Gly Gly Asn
340 345 350

agc aga gtc atg aag aga tgt ttc ttc tct ttt gga agt agt aga act
1104

Ser Arg Val Met Lys Arg Cys Phe Phe Ser Phe Gly Ser Ser Arg Thr
355 360 365

tca aaa agt tct tca ata tta cct gtt tat ttg gaa ccc taa
1146

Ser Lys Ser Ser Ser Ile Leu Pro Val Tyr Leu Glu Pro
370 375 380

<210> 180 <211> 381 <212> PRT <213> Arabidopsis thaliana <400>
180

Met Asp Leu Thr Asp Arg Arg Asn Pro Phe Asn Asn Leu Val Phe Pro
1 5 10 15

Pro Pro Pro Pro Pro Pro Ser Thr Thr Phe Thr Ser Pro Ile Phe Pro
20 25 30

Arg Thr Ser Ser Ser Gly Thr Asn Phe Pro Ile Leu Ala Ile Ala Val
35 40 45

Ile Gly Ile Leu Ala Thr Ala Phe Leu Leu Val Ser Tyr Tyr Ile Phe
50 55 60

Val Ile Lys Cys Cys Leu Asn Trp His Gln Ile Asp Ile Phe Arg Arg
65 70 75 80

Arg Arg Arg Ser Ser Asp Gln Asn Pro Leu Met Ile Tyr Ser Pro His
85 90 95

Glu Val Asn Arg Gly Leu Asp Glu Ser Ala Ile Arg Ala Ile Pro Val
100 105 110

Phe Lys Phe Lys Lys Arg Asp Val Val Ala Gly Glu Glu Asp Gln Ser
 115 120 125
 Lys Asn Ser Gln Glu Cys Ser Val Cys Leu Asn Glu Phe Gln Glu Asp
 130 135 140
 Glu Lys Leu Arg Ile Ile Pro Asn Cys Cys His Val Phe His Ile Asp
 145 150 155 160
 Cys Ile Asp Ile Trp Leu Gln Gly Asn Ala Asn Cys Pro Leu Cys Arg
 165 170 175
 Thr Ser Val Ser Cys Glu Ala Ser Phe Thr Leu Asp Leu Ile Ser Ala
 180 185 190
 Pro Ser Ser Pro Arg Glu Asn Ser Pro His Ser Arg Asn Arg Asn Leu
 195 200 205
 Glu Pro Gly Leu Val Leu Gly Gly Asp Asp Asp Phe Val Val Ile Glu
 210 215 220
 Leu Gly Ala Ser Asn Gly Asn Asn Arg Glu Ser Val Arg Asn Ile Asp
 225 230 235 240
 Phe Leu Thr Glu Gln Glu Arg Val Thr Ser Asn Glu Val Ser Thr Gly
 245 250 255
 Asn Ser Pro Lys Ser Val Ser Pro Leu Pro Ile Lys Phe Gly Asn Arg
 260 265 270
 Gly Met Tyr Lys Lys Glu Arg Lys Phe His Lys Val Thr Ser Met Gly
 275 280 285
 Asp Glu Cys Ile Asp Thr Arg Gly Lys Asp Gly His Phe Gly Glu Ile
 290 295 300
 Gln Pro Ile Arg Arg Ser Ile Ser Met Asp Ser Ser Val Asp Arg Gln
 305 310 315 320
 Leu Tyr Leu Ala Val Gln Glu Glu Ile Ser Arg Arg Asn Arg Gln Ile
 325 330 335
 Pro Val Ala Gly Asp Gly Glu Asp Ser Ser Ser Ser Gly Gly Gly Asn
 340 345 350

Ser Arg Val Met Lys Arg Cys Phe Phe Ser Phe Gly Ser Ser Arg Thr
 355 360 365

Ser Lys Ser Ser Ser Ile Leu Pro Val Tyr Leu Glu Pro
 370 375 380

<210> 181 <211> 1064 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (61)..(849) <223> G1134

<400> 181
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 60

atg caa cca aca tcc gtc ggt agt agc ggc ggt ggt gac gac gga gga
 108

Met Gln Pro Thr Ser Val Gly Ser Ser Gly Gly Gly Asp Asp Gly Gly
 1 5 10 15

ggc aga gga gga gga gga ggg cta agt aga agt gga cta tct cgg atc
 156

Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile
 20 25 30

cgt tca gct cca gcg act tgg ctt gaa gct tta ctt gag gaa gat gaa
 204

Arg Ser Ala Pro Ala Thr Trp Leu Glu Ala Leu Leu Glu Glu Asp Glu
 35 40 45

gaa gag tct ttg aaa cct aat ctt ggt ctc acc gat ttg ctt acc ggg
 252

Glu Glu Ser Leu Lys Pro Asn Leu Gly Leu Thr Asp Leu Leu Thr Gly
 50 55 60

aac tcg aac gat tta ccg aca agt cgc ggc tcg ttc gag ttc ccg att
 300

Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile
 65 70 75 80

cct gtt gag caa ggg ttg tat caa caa ggt ggg ttt cac cga cag aat
 348

Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn
 85 90 95

agt act ccg gcg gat ttt ctt agt ggt tct gat gga ttt atc caa agc
 396

Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser
 100 105 110

ttt ggg att cag gcg aat tac gat tac tta tcg ggg aat atc gat gtt
 444

Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val
 115 120 125

tct ccg gga agt aag cgg tct aga gaa atg gaa gca ctc ttc tct tct
 492

Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser
 130 135 140

cct gag ttt act tct caa atg aaa gga gag caa agc agc ggt caa gtt
 540
 Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val
 145 150 155 160

cct acc gga gta tca agc atg tcg gat atg aac atg gag aac ctt atg
 588
 Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met
 165 170 175

gag gac tct gtt gct ttt agg gtt cgg gct aaa cgt ggt tgc gca act
 636
 Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr
 180 185 190

cat ccc cgc agc att gcc gag agg gta cga agg acg cgg att agt gat
 684
 His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp
 195 200 205

cgg ata agg aag cta caa gag ctt gta cct aac atg gac aag caa acc
 732
 Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr
 210 215 220

aac act gca gac atg tta gaa gaa gca gta gaa tac gtg aaa gtt ctt
 780
 Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu
 225 230 235 240

caa agg cag atc cag gag tta aca gaa gaa cag aag agg tgc aca tgc
 828
 Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys
 245 250 255

ata cct aag gaa gaa caa taa gggttgcctc tgatttggtt tatatttgct
 879
 Ile Pro Lys Glu Glu Gln
 260

taacggcaat gatctgatcg aaaaattcga aagatgatct tagcttgaat ttagatggat
 939

gtcatgttga aaagtatatt atttgataaa tggatgtagg tgtaataataa aatttttgta
 999

caataatgaa gaaagttaaa aagaattaat gaaaacatat attcctttatg atataaaaaa
 1059

aaaaa
 1064

<210> 182 <211> 262 <212> PRT <213> Arabidopsis thaliana <400>
 182

Met Gln Pro Thr Ser Val Gly Ser Ser Gly Gly Gly Asp Asp Gly Gly
 1 5 10 15

Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile

20	25	30
Arg Ser Ala Pro Ala Thr Trp Leu Glu Ala Leu Leu Glu Glu Asp Glu		
35	40	45
Glu Glu Ser Leu Lys Pro Asn Leu Gly Leu Thr Asp Leu Leu Thr Gly		
50	55	60
Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile		
65	70	75
Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn		
85	90	95
Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser		
100	105	110
Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val		
115	120	125
Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser		
130	135	140
Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val		
145	150	155
Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met		
165	170	175
Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr		
180	185	190
His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp		
195	200	205
Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr		
210	215	220
Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu		
225	230	235
Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys		
245	250	255
Ile Pro Lys Glu Glu Gln		
260		

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 <221> CDS <222> (46)..(807) <223> G1142

<400> 183

attaattaac aaaaaaccaa aagaaggcgg cgcaaacaaa agata atg caa cca gag
 57

Met Gln Pro Glu
 1

acc tca gat cag atg ttg tac tcg ttt ctt gcc gga aac gaa gtc ggc
 105

Thr Ser Asp Gln Met Leu Tyr Ser Phe Leu Ala Gly Asn Glu Val Gly
 5 10 15 20

ggt gga ggg tac tgc gtc tcc ggc gac tac atg acg act atg cag agc
 153

Gly Gly Gly Tyr Cys Val Ser Gly Asp Tyr Met Thr Thr Met Gln Ser
 25 30 35

tta tgt ggg tct tcg tcg tcg acg tca tcg tat tac cca ctg gcg atc
 201

Leu Cys Gly Ser Ser Ser Ser Thr Ser Ser Tyr Tyr Pro Leu Ala Ile
 40 45 50

tcc ggc atc gga gaa acg atg gct caa gac aga gct tta gct gct ttg
 249

Ser Gly Ile Gly Glu Thr Met Ala Gln Asp Arg Ala Leu Ala Ala Leu
 55 60 65

agg aac cac aaa gaa gct gag aga aga agg aga gag agg atc aat tct
 297

Arg Asn His Lys Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile Asn Ser
 70 75 80

cat ctc aac aag ctt cgt aac gta ctc tct tgt aat tct aag acc gat
 345

His Leu Asn Lys Leu Arg Asn Val Leu Ser Cys Asn Ser Lys Thr Asp
 85 90 95 100

aaa gcc aca ctg ctc gcc aaa gta gtt caa cga gtc aga gaa ctt aaa
 393

Lys Ala Thr Leu Leu Ala Lys Val Val Gln Arg Val Arg Glu Leu Lys
 105 110 115

cag caa acc cta gag acc tcc gac tcc gac caa aca tta tta cca tca
 441

Gln Gln Thr Leu Glu Thr Ser Asp Ser Asp Gln Thr Leu Leu Pro Ser
 120 125 130

gag acc gac gaa att agt gtt cta cac ttt gga gac tat tca aac gac
 489

Glu Thr Asp Glu Ile Ser Val Leu His Phe Gly Asp Tyr Ser Asn Asp
 135 140 145

ggt cat ata atc ttc aaa gcc tct cta tgt tgt gaa gat aga tca gat
 537

Gly His Ile Ile Phe Lys Ala Ser Leu Cys Cys Glu Asp Arg Ser Asp
 150 155 160

ctc ttg ccg gac ctt atg gag att ctc aag tct ctt aac atg aag act
585

Leu Leu Pro Asp Leu Met Glu Ile Leu Lys Ser Leu Asn Met Lys Thr
165 170 175 180

ctc cga gct gag atg gta acc att ggt ggt cgg aca aga agt gtt ctt
633

Leu Arg Ala Glu Met Val Thr Ile Gly Gly Arg Thr Arg Ser Val Leu
185 190 195

gtc gta gct gct gac aaa gag atg cac ggc gtc gag tct gtg cat ttt
681

Val Val Ala Ala Asp Lys Glu Met His Gly Val Glu Ser Val His Phe
200 205 210

ttg caa aat gct ctc aag tcg ctg ctt gag cgg tca agc aag tcg ttg
729

Leu Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Leu
215 220 225

atg gaa cgt agt tct ggt ggt gga gga gga gaa cgg tca aag cgg cgt
777

Met Glu Arg Ser Ser Gly Gly Gly Gly Gly Glu Arg Ser Lys Arg Arg
230 235 240

cgt gcg ctg gat cac atc ata atg gtg tga aatgatgaga attgagcaca
827

Arg Ala Leu Asp His Ile Ile Met Val
245 250

ctaaaaagtc tataattgat taatatatat agggatgat cataattaac ttggttataa
887

ttacccaaaac cttttttatt cctctttaat aatatatatg ttatatggtt ttagttacta
947

agtcttgga gtgtaagcaa atgttgtaag taggtttggt gtgttctttt tcttttcttt
1007

tttttttctt tttcaaaaaa aaaaaaaaaa
1037

<210> 184 <211> 253 <212> PRT <213> Arabidopsis thaliana <400>
184

Met Gln Pro Glu Thr Ser Asp Gln Met Leu Tyr Ser Phe Leu Ala Gly
1 5 10 15

Asn Glu Val Gly Gly Gly Gly Tyr Cys Val Ser Gly Asp Tyr Met Thr
20 25 30

Thr Met Gln Ser Leu Cys Gly Ser Ser Ser Ser Thr Ser Ser Tyr Tyr
35 40 45

Pro Leu Ala Ile Ser Gly Ile Gly Glu Thr Met Ala Gln Asp Arg Ala
50 55 60

Leu Ala Ala Leu Arg Asn His Lys Glu Ala Glu Arg Arg Arg Arg Glu
65 70 75 80

Arg Ile Asn Ser His Leu Asn Lys Leu Arg Asn Val Leu Ser Cys Asn
85 90 95

Ser Lys Thr Asp Lys Ala Thr Leu Leu Ala Lys Val Val Gln Arg Val
100 105 110

Arg Glu Leu Lys Gln Gln Thr Leu Glu Thr Ser Asp Ser Asp Gln Thr
115 120 125

Leu Leu Pro Ser Glu Thr Asp Glu Ile Ser Val Leu His Phe Gly Asp
130 135 140

Tyr Ser Asn Asp Gly His Ile Ile Phe Lys Ala Ser Leu Cys Cys Glu
145 150 155 160

Asp Arg Ser Asp Leu Leu Pro Asp Leu Met Glu Ile Leu Lys Ser Leu
165 170 175

Asn Met Lys Thr Leu Arg Ala Glu Met Val Thr Ile Gly Gly Arg Thr
180 185 190

Arg Ser Val Leu Val Val Ala Ala Asp Lys Glu Met His Gly Val Glu
195 200 205

Ser Val His Phe Leu Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser
210 215 220

Ser Lys Ser Leu Met Glu Arg Ser Ser Gly Gly Gly Gly Glu Arg
225 230 235 240

Ser Lys Arg Arg Arg Ala Leu Asp His Ile Ile Met Val
245 250

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58

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gga aac tat cgg tgg ccg tca aag cta tca aag tta tca ctc aga gca
106
Gly Asn Tyr Arg Trp Pro Ser Lys Leu Ser Lys Leu Ser Leu Arg Ala

	5	10	15
aaa caa acg aat ctg tac cgc gtc att cta atc gcg atc ctc tgc gtc			
154			
Lys Gln Thr Asn Leu Tyr Arg Val Ile Leu Ile Ala Ile Leu Cys Val			
20 25 30			
acc ttt tac ttc gtc gga gta tgg caa cac tcc ggc aga gga atc tca			
202			
Thr Phe Tyr Phe Val Gly Val Trp Gln His Ser Gly Arg Gly Ile Ser			
35 40 45			
cgc tct tcc att tct aac cac gag ctc acg tcc gtg ccc tgc acg ttt			
250			
Arg Ser Ser Ile Ser Asn His Glu Leu Thr Ser Val Pro Cys Thr Phe			
50 55 60 65			
cct cac caa acc aca ccg att ctc aac ttc gcc tcc cgt cac aca gcc			
298			
Pro His Gln Thr Thr Pro Ile Leu Asn Phe Ala Ser Arg His Thr Ala			
70 75 80			
cct gac ctt cct ccg acg ata acg gac gcg cgt gtt gtt caa atc ccg			
346			
Pro Asp Leu Pro Pro Thr Ile Thr Asp Ala Arg Val Val Gln Ile Pro			
85 90 95			
tcg tgc ggc gtt gaa ttc tcg gag tac acg ccc tgc gag ttc gtg aat			
394			
Ser Cys Gly Val Glu Phe Ser Glu Tyr Thr Pro Cys Glu Phe Val Asn			
100 105 110			
cgg tct ttg aat ttc cca aga gag agg ctt ata tac aga gag aga cac			
442			
Arg Ser Leu Asn Phe Pro Arg Glu Arg Leu Ile Tyr Arg Glu Arg His			
115 120 125			
tgt ccg gaa aaa cac gag ata gtc agg tgt cgg att cca gcg ccg tac			
490			
Cys Pro Glu Lys His Glu Ile Val Arg Cys Arg Ile Pro Ala Pro Tyr			
130 135 140 145			
ggt tac agt tta cct ttt cgg tgg ccg gag agc cgt gac gtg gcg tgg			
538			
Gly Tyr Ser Leu Pro Phe Arg Trp Pro Glu Ser Arg Asp Val Ala Trp			
150 155 160			
ttt gct aac gtg ccg cat acg gaa cta acg gtg gag aag aag aat cag			
586			
Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn Gln			
165 170 175			
aac tgg gta agg tat gag aag gat agg ttt tta ttt cct ggt ggt ggt			
634			
Asn Trp Val Arg Tyr Glu Lys Asp Arg Phe Leu Phe Pro Gly Gly Gly			
180 185 190			
acg atg ttt cca cgt gga gct gat gct tac atc gac gag atc gga cgg			
682			
Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Glu Ile Gly Arg			
195 200 205			

ttg ata aat ctc aaa gat gga tca att cgg aca gcc att gat act gga
 730
 Leu Ile Asn Leu Lys Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr Gly
 210 215 220 225
 tgt ggg gta gcg agc ttt ggg gcg tat cta atg tcg agg aac ata gta
 778
 Cys Gly Val Ala Ser Phe Gly Ala Tyr Leu Met Ser Arg Asn Ile Val
 230 235 240
 acg atg tcg ttt gca cca aga gac aca cac gaa gct cag gtt cag ttc
 826
 Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln Phe
 245 250 255
 gca ctt gag aga gga gtc cct gcc atc ata gga gtg tta gcc tct att
 874
 Ala Leu Glu Arg Gly Val Pro Ala Ile Ile Gly Val Leu Ala Ser Ile
 260 265 270
 agg ctc cca ttt ccg gcc aga gcc ttc gac att gct cat tgc tct cga
 922
 Arg Leu Pro Phe Pro Ala Arg Ala Phe Asp Ile Ala His Cys Ser Arg
 275 280 285
 tgt ctc att cct tgg ggc caa tac aac ggg acg tat ctc ata gaa gtg
 970
 Cys Leu Ile Pro Trp Gly Gln Tyr Asn Gly Thr Tyr Leu Ile Glu Val
 290 295 300 305
 gat agg gta ctg aga ccg ggg ggg tat tgg att ttg tcg gga ccg ccg
 1018
 Asp Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro Pro
 310 315 320
 att aac tgg cag aga cac tgg aag ggt tgg gaa aga act aga gac gat
 1066
 Ile Asn Trp Gln Arg His Trp Lys Gly Trp Glu Arg Thr Arg Asp Asp
 325 330 335
 ctc aac tcg gag cag tct cag atc gag agg gtg gct agg agc ttg tgt
 1114
 Leu Asn Ser Glu Gln Ser Gln Ile Glu Arg Val Ala Arg Ser Leu Cys
 340 345 350
 tgg agg aaa ttg gtg cag aga gag gat ctt gcg gtt tgg cag aaa cct
 1162
 Trp Arg Lys Leu Val Gln Arg Glu Asp Leu Ala Val Trp Gln Lys Pro
 355 360 365
 acc aac cat gtt cac tgt aag cgc aat cgg ata gct tta gga cgc cct
 1210
 Thr Asn His Val His Cys Lys Arg Asn Arg Ile Ala Leu Gly Arg Pro
 370 375 380 385
 ccg ttc tgc cac ccg aca cta ccc aac cag ggc tgg tac act aag ctt
 1258
 Pro Phe Cys His Arg Thr Leu Pro Asn Gln Gly Trp Tyr Thr Lys Leu
 390 395 400

gaa acc tgt ttg acg ccg ttg ccg gaa gta aca gga tct gag atc aaa
 1306
 Glu Thr Cys Leu Thr Pro Leu Pro Glu Val Thr Gly Ser Glu Ile Lys
 405 410 415

gaa gta gcg ggt gga cag ttg gcg aga tgg cct gag aga ttg aat gct
 1354
 Glu Val Ala Gly Gly Gln Leu Ala Arg Trp Pro Glu Arg Leu Asn Ala
 420 425 430

ctt cct ccg agg atc aaa agt gga agc ttg gaa ggg atc act gag gat
 1402
 Leu Pro Pro Arg Ile Lys Ser Gly Ser Leu Glu Gly Ile Thr Glu Asp
 435 440 445

gaa ttt gtc agc aac aca gag aaa tgg cag aga aga gtg tct tac tac
 1450
 Glu Phe Val Ser Asn Thr Glu Lys Trp Gln Arg Arg Val Ser Tyr Tyr
 450 455 460 465

aag aaa tat gac caa cag cta gcg gag acg gga aga tac aga aac ttt
 1498
 Lys Lys Tyr Asp Gln Gln Leu Ala Glu Thr Gly Arg Tyr Arg Asn Phe
 470 475 480

ctc gac atg aac gct cat ctt gga ggt ttc gcc tca gcc tta gtc gat
 1546
 Leu Asp Met Asn Ala His Leu Gly Gly Phe Ala Ser Ala Leu Val Asp
 485 490 495

gat cct gta tgg gtc atg aat gtt gtc ccc gtg gag gcc agt gtt aac
 1594
 Asp Pro Val Trp Val Met Asn Val Val Pro Val Glu Ala Ser Val Asn
 500 505 510

acc ctt gga gtt atc tat gag cga gga ttg att gga acg tat caa aac
 1642
 Thr Leu Gly Val Ile Tyr Glu Arg Gly Leu Ile Gly Thr Tyr Gln Asn
 515 520 525

tgg tgt gaa gca atg tca act tac cca agg aca tac gat ttc atc cat
 1690
 Trp Cys Glu Ala Met Ser Thr Tyr Pro Arg Thr Tyr Asp Phe Ile His
 530 535 540 545

gcc gat tcg gtg ttc agt ctg tac aaa gac aga tgt gac atg gaa gat
 1738
 Ala Asp Ser Val Phe Ser Leu Tyr Lys Asp Arg Cys Asp Met Glu Asp
 550 555 560

atc ttg cta gaa atg gac agg att cta aga cca aag gga agc gtg atc
 1786
 Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Lys Gly Ser Val Ile
 565 570 575

atc aga gac gac att gat gtg cta acc aaa gtg aag aag att aca gat
 1834
 Ile Arg Asp Asp Ile Asp Val Leu Thr Lys Val Lys Lys Ile Thr Asp
 580 585 590

gcg atg caa tgg gaa ggg agg ata gga gat cat gaa aac gga cct ctt
1882

Ala Met Gln Trp Glu Gly Arg Ile Gly Asp His Glu Asn Gly Pro Leu
595 600 605

gaa aga gag aag att ttg ttt ctt gtg aag gag tac tgg acc gca cct
1930

Glu Arg Glu Lys Ile Leu Phe Leu Val Lys Glu Tyr Trp Thr Ala Pro
610 615 620 625

gcg cct gat cag tca tca gat cct tga tcaagcttgg aataattcat
1977

Ala Pro Asp Gln Ser Ser Asp Pro
630

aaaatttgta gctccattct tttttcttca aatgttttgt acacactaat cgactttggg
2037

ggaaagaaga aacaaacacc cgctaaattg tttcaaaccg gagattcatt gcgactttgt
2097

gagaaaaatga actagagagt ttactacaaa
2127

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186

Met Gly Asn Tyr Arg Trp Pro Ser Lys Leu Ser Lys Leu Ser Leu Arg
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Ala Lys Gln Thr Asn Leu Tyr Arg Val Ile Leu Ile Ala Ile Leu Cys
20 25 30

Val Thr Phe Tyr Phe Val Gly Val Trp Gln His Ser Gly Arg Gly Ile
35 40 45

Ser Arg Ser Ser Ile Ser Asn His Glu Leu Thr Ser Val Pro Cys Thr
50 55 60

Phe Pro His Gln Thr Thr Pro Ile Leu Asn Phe Ala Ser Arg His Thr
65 70 75 80

Ala Pro Asp Leu Pro Pro Thr Ile Thr Asp Ala Arg Val Val Gln Ile
85 90 95

Pro Ser Cys Gly Val Glu Phe Ser Glu Tyr Thr Pro Cys Glu Phe Val
100 105 110

Asn Arg Ser Leu Asn Phe Pro Arg Glu Arg Leu Ile Tyr Arg Glu Arg
115 120 125

His Cys Pro Glu Lys His Glu Ile Val Arg Cys Arg Ile Pro Ala Pro

130 135 140
 Tyr Gly Tyr Ser Leu Pro Phe Arg Trp Pro Glu Ser Arg Asp Val Ala
 145 150 155 160
 Trp Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn
 165 170 175
 Gln Asn Trp Val Arg Tyr Glu Lys Asp Arg Phe Leu Phe Pro Gly Gly
 180 185 190
 Gly Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Glu Ile Gly
 195 200 205
 Arg Leu Ile Asn Leu Lys Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr
 210 215 220
 Gly Cys Gly Val Ala Ser Phe Gly Ala Tyr Leu Met Ser Arg Asn Ile
 225 230 235 240
 Val Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln
 245 250 255
 Phe Ala Leu Glu Arg Gly Val Pro Ala Ile Ile Gly Val Leu Ala Ser
 260 265 270
 Ile Arg Leu Pro Phe Pro Ala Arg Ala Phe Asp Ile Ala His Cys Ser
 275 280 285
 Arg Cys Leu Ile Pro Trp Gly Gln Tyr Asn Gly Thr Tyr Leu Ile Glu
 290 295 300
 Val Asp Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro
 305 310 315 320
 Pro Ile Asn Trp Gln Arg His Trp Lys Gly Trp Glu Arg Thr Arg Asp
 325 330 335
 Asp Leu Asn Ser Glu Gln Ser Gln Ile Glu Arg Val Ala Arg Ser Leu
 340 345 350
 Cys Trp Arg Lys Leu Val Gln Arg Glu Asp Leu Ala Val Trp Gln Lys
 355 360 365
 Pro Thr Asn His Val His Cys Lys Arg Asn Arg Ile Ala Leu Gly Arg
 370 375 380

Pro Pro Phe Cys His Arg Thr Leu Pro Asn Gln Gly Trp Tyr Thr Lys
 385 390 395 400
 Leu Glu Thr Cys Leu Thr Pro Leu Pro Glu Val Thr Gly Ser Glu Ile
 405 410 415
 Lys Glu Val Ala Gly Gly Gln Leu Ala Arg Trp Pro Glu Arg Leu Asn
 420 425 430
 Ala Leu Pro Pro Arg Ile Lys Ser Gly Ser Leu Glu Gly Ile Thr Glu
 435 440 445
 Asp Glu Phe Val Ser Asn Thr Glu Lys Trp Gln Arg Arg Val Ser Tyr
 450 455 460
 Tyr Lys Lys Tyr Asp Gln Gln Leu Ala Glu Thr Gly Arg Tyr Arg Asn
 465 470 475 480
 Phe Leu Asp Met Asn Ala His Leu Gly Gly Phe Ala Ser Ala Leu Val
 485 490 495
 Asp Asp Pro Val Trp Val Met Asn Val Val Pro Val Glu Ala Ser Val
 500 505 510
 Asn Thr Leu Gly Val Ile Tyr Glu Arg Gly Leu Ile Gly Thr Tyr Gln
 515 520 525
 Asn Trp Cys Glu Ala Met Ser Thr Tyr Pro Arg Thr Tyr Asp Phe Ile
 530 535 540
 His Ala Asp Ser Val Phe Ser Leu Tyr Lys Asp Arg Cys Asp Met Glu
 545 550 555 560
 Asp Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Lys Gly Ser Val
 565 570 575
 Ile Ile Arg Asp Asp Ile Asp Val Leu Thr Lys Val Lys Lys Ile Thr
 580 585 590
 Asp Ala Met Gln Trp Glu Gly Arg Ile Gly Asp His Glu Asn Gly Pro
 595 600 605
 Leu Glu Arg Glu Lys Ile Leu Phe Leu Val Lys Glu Tyr Trp Thr Ala
 610 615 620

Pro Ala Pro Asp Gln Ser Ser Asp Pro
625 630

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caaccataag acaaaacaac gaacgaggaa gagagagaga gaaggatata tctctaataca
120

cg atg cag gag ata ata ccg gat ttt ctt gaa gag tgt gaa ttt gtc
167

Met Gln Glu Ile Ile Pro Asp Phe Leu Glu Glu Cys Glu Phe Val
1 5 10 15

gac act tca cta gcc gga gat gat cta ttt gcc atc tta gag agt ctt
215

Asp Thr Ser Leu Ala Gly Asp Asp Leu Phe Ala Ile Leu Glu Ser Leu
20 25 30

gaa ggt gcc gga gag ata tct ccg aca gct gca tct aca cct aaa gat
263

Glu Gly Ala Gly Glu Ile Ser Pro Thr Ala Ala Ser Thr Pro Lys Asp
35 40 45

gga acc aca agt tcc aag gag tta gtt aag gat caa gat tat gaa aac
311

Gly Thr Thr Ser Ser Lys Glu Leu Val Lys Asp Gln Asp Tyr Glu Asn
50 55 60

tca tct cct aag agg aaa aag caa aga cta gaa acc agg aaa gaa gag
359

Ser Ser Pro Lys Arg Lys Lys Gln Arg Leu Glu Thr Arg Lys Glu Glu
65 70 75

gac gaa gaa gaa gaa gac gga gac gga gaa gca gaa gaa gat aat aag
407

Asp Glu Glu Glu Glu Asp Gly Asp Gly Glu Ala Glu Glu Asp Asn Lys
80 85 90 95

caa gat ggg caa caa aag atg tct cat gta acc gtg gaa cgt aac cgg
455

Gln Asp Gly Gln Gln Lys Met Ser His Val Thr Val Glu Arg Asn Arg
100 105 110

aga aag caa atg aac gag cac tta acc gtt ttg cgt tct ctt atg cct
503

Arg Lys Gln Met Asn Glu His Leu Thr Val Leu Arg Ser Leu Met Pro
115 120 125

tgt ttc tac gtc aaa cgg ggg gac caa gca tcg atc ata gga gga gtt
551

Cys Phe Tyr Val Lys Arg Gly Asp Gln Ala Ser Ile Ile Gly Gly Val
130 135 140

gtg gag tac ata agc gag tta caa caa gtt ctc caa tct ttg gaa gcc
 599
 Val Glu Tyr Ile Ser Glu Leu Gln Gln Val Leu Gln Ser Leu Glu Ala
 145 150 155
 aag aaa caa cgt aaa acc tac gcc gaa gtc cta agc ccg aga gtt gtc
 647
 Lys Lys Gln Arg Lys Thr Tyr Ala Glu Val Leu Ser Pro Arg Val Val
 160 165 170 175
 ccg agc cct cgt cct tca ccg cct gtt cta agc cca aga aaa ccg cct
 695
 Pro Ser Pro Arg Pro Ser Pro Pro Val Leu Ser Pro Arg Lys Pro Pro
 180 185 190
 ctt agc ccg cgc atc aac cac cac cag att cac cac cac cta ctt ctc
 743
 Leu Ser Pro Arg Ile Asn His His Gln Ile His His His Leu Leu Leu
 195 200 205
 cct ccc ata agt cct cga aca cct cag cca aca agc cca tac cgg gcc
 791
 Pro Pro Ile Ser Pro Arg Thr Pro Gln Pro Thr Ser Pro Tyr Arg Ala
 210 215 220
 att cca ccg caa cta cca ctc atc cca cag cct ccg ctt cgc tct tac
 839
 Ile Pro Pro Gln Leu Pro Leu Ile Pro Gln Pro Pro Leu Arg Ser Tyr
 225 230 235
 agc tca ttg gcc agt tgc agc agc tta gga gat cca cct cca tac tct
 887
 Ser Ser Leu Ala Ser Cys Ser Ser Leu Gly Asp Pro Pro Pro Tyr Ser
 240 245 250 255
 cct gct tca tct tct tca tct cct tca gtt agt agt aac cat gag agt
 935
 Pro Ala Ser Ser Ser Ser Ser Pro Ser Val Ser Ser Asn His Glu Ser
 260 265 270
 agt gtg atc aat gag ctt gtt gct aac tca aaa tcg gct ttg gct gat
 983
 Ser Val Ile Asn Glu Leu Val Ala Asn Ser Lys Ser Ala Leu Ala Asp
 275 280 285
 gtg gaa gtg aag ttt tca gga gct aac gtg ctg ctc aaa acg gtg tcg
 1031
 Val Glu Val Lys Phe Ser Gly Ala Asn Val Leu Leu Lys Thr Val Ser
 290 295 300
 cat aag atc ccg gga caa gtt atg aag ata att gct gct ctt gaa gat
 1079
 His Lys Ile Pro Gly Gln Val Met Lys Ile Ile Ala Ala Leu Glu Asp
 305 310 315
 ttg gct ctt gag att ctt cag gtt aat att aac acc gtc gac gaa acc
 1127
 Leu Ala Leu Glu Ile Leu Gln Val Asn Ile Asn Thr Val Asp Glu Thr
 320 325 330 335

atg ctt aat tct ttc acc atc aag att gga att gag tgc caa cta agt
1175

Met Leu Asn Ser Phe Thr Ile Lys Ile Gly Ile Glu Cys Gln Leu Ser
340 345 350

gca gaa gaa ctg gct caa caa att cag caa aca ttc tgc tag
1217

Ala Glu Glu Leu Ala Gln Gln Ile Gln Gln Thr Phe Cys
355 360

taaagaagga tttaatatag ctctgtataa accttaacga gagagcagta cgtactcact
1277

ttctctcctt agtatccctt taattatctt ttcagttttc tgcaaagata tggagtttaa
1337

aaaaataaaa ttgttatcta aagttttaat caaatattga ttaattataa ctaatatagg
1397

tataagttag ttttaaagat tatcagcttc ataacagcca tcgtcatggt tactttcttt
1457

taaatttttag aatttagacg tactcctacc atgtaatttt atttctgtca ttacatcaag
1517

cattgtagct gtaattgcat atgaatgaac aatagtgtat gagtgatctc atgaataata
1577

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1604

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20 25 30

Gly Ala Gly Glu Ile Ser Pro Thr Ala Ala Ser Thr Pro Lys Asp Gly
35 40 45

Thr Thr Ser Ser Lys Glu Leu Val Lys Asp Gln Asp Tyr Glu Asn Ser
50 55 60

Ser Pro Lys Arg Lys Lys Gln Arg Leu Glu Thr Arg Lys Glu Glu Asp
65 70 75 80

Glu Glu Glu Glu Asp Gly Asp Gly Glu Ala Glu Glu Asp Asn Lys Gln
85 90 95

Asp Gly Gln Gln Lys Met Ser His Val Thr Val Glu Arg Asn Arg Arg
100 105 110

Lys Gln Met Asn Glu His Leu Thr Val Leu Arg Ser Leu Met Pro Cys
 115 120 125

Phe Tyr Val Lys Arg Gly Asp Gln Ala Ser Ile Ile Gly Gly Val Val
 130 135 140

Glu Tyr Ile Ser Glu Leu Gln Gln Val Leu Gln Ser Leu Glu Ala Lys
 145 150 155 160

Lys Gln Arg Lys Thr Tyr Ala Glu Val Leu Ser Pro Arg Val Val Pro
 165 170 175

Ser Pro Arg Pro Ser Pro Pro Val Leu Ser Pro Arg Lys Pro Pro Leu
 180 185 190

Ser Pro Arg Ile Asn His His Gln Ile His His His Leu Leu Leu Pro
 195 200 205

Pro Ile Ser Pro Arg Thr Pro Gln Pro Thr Ser Pro Tyr Arg Ala Ile
 210 215 220

Pro Pro Gln Leu Pro Leu Ile Pro Gln Pro Pro Leu Arg Ser Tyr Ser
 225 230 235 240

Ser Leu Ala Ser Cys Ser Ser Leu Gly Asp Pro Pro Pro Tyr Ser Pro
 245 250 255

Ala Ser Ser Ser Ser Ser Pro Ser Val Ser Ser Asn His Glu Ser Ser
 260 265 270

Val Ile Asn Glu Leu Val Ala Asn Ser Lys Ser Ala Leu Ala Asp Val
 275 280 285

Glu Val Lys Phe Ser Gly Ala Asn Val Leu Leu Lys Thr Val Ser His
 290 295 300

Lys Ile Pro Gly Gln Val Met Lys Ile Ile Ala Ala Leu Glu Asp Leu
 305 310 315 320

Ala Leu Glu Ile Leu Gln Val Asn Ile Asn Thr Val Asp Glu Thr Met
 325 330 335

Leu Asn Ser Phe Thr Ile Lys Ile Gly Ile Glu Cys Gln Leu Ser Ala
 340 345 350

Glu Glu Leu Ala Gln Gln Ile Gln Gln Thr Phe Cys
355 360

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120

gaaacttttg acgagtgggt tcaaatttct ggtgaaaacg accagcaaga agttgttcaa
180

caacttcaca aggttctgcg accatttctt cttcggaggt taaaatcaga ttagagaaaa
240

ggcttacctc caaaaaagga gacaatactc aaagtggc atg tct caa atg caa
294

Met Ser Gln Met Gln
1 5

aaa cag tac tac aag gct tta ctg cag aag gat ctt gaa gtg gtt aat
342

Lys Gln Tyr Tyr Lys Ala Leu Leu Gln Lys Asp Leu Glu Val Val Asn
10 15 20

ggt ggt gga gaa cgc aaa cgt ctg ttg aac ata gca atg caa ttg cgg
390

Gly Gly Gly Glu Arg Lys Arg Leu Leu Asn Ile Ala Met Gln Leu Arg
25 30 35

aaa tgc tgc aat cac cct tat ctc ttc cag ggt gcg gag cct ggt ccc
438

Lys Cys Cys Asn His Pro Tyr Leu Phe Gln Gly Ala Glu Pro Gly Pro
40 45 50

cca tat act aca gga gat cac ctt gta aca aac gca ggt aag atg gtt
486

Pro Tyr Thr Thr Gly Asp His Leu Val Thr Asn Ala Gly Lys Met Val
55 60 65

ctc tta gat aaa ttg cta cct aag ttg aag gat cga gat tca agg gtt
534

Leu Leu Asp Lys Leu Leu Pro Lys Leu Lys Asp Arg Asp Ser Arg Val
70 75 80 85

ctg ata ttt tct cag atg aca agg ctt ttg gat att ctc gag gat tac
582

Leu Ile Phe Ser Gln Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr
90 95 100

cta atg tat cgt ggt tac cag tac tgc cgt att gat gga aat act ggt
630

Leu Met Tyr Arg Gly Tyr Gln Tyr Cys Arg Ile Asp Gly Asn Thr Gly
105 110 115

ggt gac gaa cga gat gct tcc ata gaa gcc tat aac aag cca gga agt
 678
 Gly Asp Glu Arg Asp Ala Ser Ile Glu Ala Tyr Asn Lys Pro Gly Ser
 120 125 130

gag aaa ttc gtt ttc ttg tta tcc act aga gct gga gga ctt ggt atc
 726
 Glu Lys Phe Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile
 135 140 145

aat ctt gct act gca gat gtt gtg atc ctc tat gat agt gac tgg aac
 774
 Asn Leu Ala Thr Ala Asp Val Val Ile Leu Tyr Asp Ser Asp Trp Asn
 150 155 160 165

cct caa gtt gac ttg caa gct cag gat cgt gca cat agg att ggt caa
 822
 Pro Gln Val Asp Leu Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln
 170 175 180

aaa aaa gaa gtt caa gtg ttc cgg ttc tgc acc gag aat gct att gag
 870
 Lys Lys Glu Val Gln Val Phe Arg Phe Cys Thr Glu Asn Ala Ile Glu
 185 190 195

gct aaa gtc att gag aga gct tac aag aag ttg gca ctt gat gct ctg
 918
 Ala Lys Val Ile Glu Arg Ala Tyr Lys Lys Leu Ala Leu Asp Ala Leu
 200 205 210

gtt att cag caa ggg aga ttg gca gaa cag aaa act gtt aat aag gat
 966
 Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys Thr Val Asn Lys Asp
 215 220 225

gag ttg ctt caa atg gtg aga tat ggt gct gaa atg gtg ttt agt tct
 1014
 Glu Leu Leu Gln Met Val Arg Tyr Gly Ala Glu Met Val Phe Ser Ser
 230 235 240 245

aaa gat agc aca att acg gat gag gat att gac aga atc att gcc aaa
 1062
 Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg Ile Ile Ala Lys
 250 255 260

gga gaa gag gca acg gct gaa ctt gat gcc aag atg aag aaa ttt act
 1110
 Gly Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys Met Lys Lys Phe Thr
 265 270 275

gaa gat gca ata cag ttt aaa atg gat gac agt gct gac ttt tat gat
 1158
 Glu Asp Ala Ile Gln Phe Lys Met Asp Asp Ser Ala Asp Phe Tyr Asp
 280 285 290

ttt gac gat gac aac aag gat gag agc aag gtg gat ttt aaa aag att
 1206
 Phe Asp Asp Asp Asn Lys Asp Glu Ser Lys Val Asp Phe Lys Lys Ile
 295 300 305

gtg agt gaa aat tgg aat gat cca cca aaa aga gag aga aag cgc aac
 1254
 Val Ser Glu Asn Trp Asn Asp Pro Pro Lys Arg Glu Arg Lys Arg Asn
 310 315 320 325

tac tct gaa gtt gaa tac ttc aag caa acg ttg cga caa ggt gct cca
 1302
 Tyr Ser Glu Val Glu Tyr Phe Lys Gln Thr Leu Arg Gln Gly Ala Pro
 330 335 340

gct aaa cct aaa gag cct aga att cca cgc atg ccc caa ttg cat gat
 1350
 Ala Lys Pro Lys Glu Pro Arg Ile Pro Arg Met Pro Gln Leu His Asp
 345 350 355

ttt cag ttc ttt aac att cag agg ctg act gag ctg tat gaa aaa gaa
 1398
 Phe Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu Leu Tyr Glu Lys Glu
 360 365 370

gtg cga tac ctt atg caa gca cat cag aaa act caa atg aaa gac aca
 1446
 Val Arg Tyr Leu Met Gln Ala His Gln Lys Thr Gln Met Lys Asp Thr
 375 380 385

att gag gtt gat gaa cct gaa gaa gtt gga gat ccc tta act gct gaa
 1494
 Ile Glu Val Asp Glu Pro Glu Glu Val Gly Asp Pro Leu Thr Ala Glu
 390 395 400 405

gaa gtg gaa gaa aag gag cta ttg ctg gaa gag ggt ttc tca aca tgg
 1542
 Glu Val Glu Glu Lys Glu Leu Leu Leu Glu Glu Gly Phe Ser Thr Trp
 410 415 420

agc aga aga gac ttc aat gcc ttc att agg gct tgt gag aag tat ggc
 1590
 Ser Arg Arg Asp Phe Asn Ala Phe Ile Arg Ala Cys Glu Lys Tyr Gly
 425 430 435

cgg aac gac ata aag agt att gcc tct gag atg gaa ggg aaa act gag
 1638
 Arg Asn Asp Ile Lys Ser Ile Ala Ser Glu Met Glu Gly Lys Thr Glu
 440 445 450

gaa gag gtt gaa cga tat gct caa gtt ttc caa gtg cga tat aaa gag
 1686
 Glu Glu Val Glu Arg Tyr Ala Gln Val Phe Gln Val Arg Tyr Lys Glu
 455 460 465

ctg aat gat tac gac aga atc atc aag aat att gag aga ggg gaa gca
 1734
 Leu Asn Asp Tyr Asp Arg Ile Ile Lys Asn Ile Glu Arg Gly Glu Ala
 470 475 480 485

aga atc tct agg aaa gat gaa atc atg aaa gct att ggg aag aaa ctg
 1782
 Arg Ile Ser Arg Lys Asp Glu Ile Met Lys Ala Ile Gly Lys Lys Leu
 490 495 500

gat cgc tac aga aac ccg tgg ctg gaa ctg aag att caa tat ggt cag
 1830
 Asp Arg Tyr Arg Asn Pro Trp Leu Glu Leu Lys Ile Gln Tyr Gly Gln
 505 510 515

aac aaa ggg aag ctg tac aat gaa gag tgc gac cgt ttc atg ata tgc
 1878
 Asn Lys Gly Lys Leu Tyr Asn Glu Glu Cys Asp Arg Phe Met Ile Cys
 520 525 530

atg gtc cat aaa ctt ggg tat gga aac tgg gat gag cta aag gca gcg
 1926
 Met Val His Lys Leu Gly Tyr Gly Asn Trp Asp Glu Leu Lys Ala Ala
 535 540 545

ttt cgg aca tcc ccc ttg ttt agg ttt gac tgg ttt gta aaa tcc cgc
 1974
 Phe Arg Thr Ser Pro Leu Phe Arg Phe Asp Trp Phe Val Lys Ser Arg
 550 555 560 565

aca act cag gaa ctt gca agg aga tgt gac aca cta atc agg ttg att
 2022
 Thr Thr Gln Glu Leu Ala Arg Arg Cys Asp Thr Leu Ile Arg Leu Ile
 570 575 580

gag aaa gag aat caa gaa ttt gat gag aga gag agg caa gcc cga aaa
 2070
 Glu Lys Glu Asn Gln Glu Phe Asp Glu Arg Glu Arg Gln Ala Arg Lys
 585 590 595

gag aag aag ctt tca aag agt gca acg cca tca aaa cga cct tcg ggt
 2118
 Glu Lys Lys Leu Ser Lys Ser Ala Thr Pro Ser Lys Arg Pro Ser Gly
 600 605 610

agg caa gca aat gag agc cct tca tct ctt ctg aag aaa cga aag cag
 2166
 Arg Gln Ala Asn Glu Ser Pro Ser Ser Leu Leu Lys Lys Arg Lys Gln
 615 620 625

ctg tca atg gat gat tat gga aag cgt agg aaa taa gaaggcttgt
 2212
 Leu Ser Met Asp Asp Tyr Gly Lys Arg Arg Lys
 630 635 640

gttgaatcca tcactaagta atcagaaaga tttatgatca cttctagggt tgattccgaa
 2272

tcggagaatt agttagaaga agctccttag agacaaggat ctaatatattt gtaccgcgaa
 2332

gcatactgc attgtctccg acttctctta tttcttcaac gtgtatttta ctctattttg
 2392

tttgtagaaa tattcaccac attcctagta gtgcgttttt agtaaattctc aaatgaactt
 2452

ttgtggtcgg atttgaacaa aaaaaaaaaa
 2481

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190 .

Met Ser Gln Met Gln Lys Gln Tyr Tyr Lys Ala Leu Leu Gln Lys Asp
1 5 10 15

Leu Glu Val Val Asn Gly Gly Gly Glu Arg Lys Arg Leu Leu Asn Ile
20 25 30

Ala Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Gln Gly
35 40 45

Ala Glu Pro Gly Pro Pro Tyr Thr Thr Gly Asp His Leu Val Thr Asn
50 55 60

Ala Gly Lys Met Val Leu Leu Asp Lys Leu Leu Pro Lys Leu Lys Asp
65 70 75 80

Arg Asp Ser Arg Val Leu Ile Phe Ser Gln Met Thr Arg Leu Leu Asp
85 90 95

Ile Leu Glu Asp Tyr Leu Met Tyr Arg Gly Tyr Gln Tyr Cys Arg Ile
100 105 110

Asp Gly Asn Thr Gly Gly Asp Glu Arg Asp Ala Ser Ile Glu Ala Tyr
115 120 125

Asn Lys Pro Gly Ser Glu Lys Phe Val Phe Leu Leu Ser Thr Arg Ala
130 135 140

Gly Gly Leu Gly Ile Asn Leu Ala Thr Ala Asp Val Val Ile Leu Tyr
145 150 155 160

Asp Ser Asp Trp Asn Pro Gln Val Asp Leu Gln Ala Gln Asp Arg Ala
165 170 175

His Arg Ile Gly Gln Lys Lys Glu Val Gln Val Phe Arg Phe Cys Thr
180 185 190

Glu Asn Ala Ile Glu Ala Lys Val Ile Glu Arg Ala Tyr Lys Lys Leu
195 200 205

Ala Leu Asp Ala Leu Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys
210 215 220

Thr Val Asn Lys Asp Glu Leu Leu Gln Met Val Arg Tyr Gly Ala Glu
225 230 235 240

Met Val Phe Ser Ser Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp
245 250 255

Arg Ile Ile Ala Lys Gly Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys
260 265 270

Met Lys Lys Phe Thr Glu Asp Ala Ile Gln Phe Lys Met Asp Asp Ser
275 280 285

Ala Asp Phe Tyr Asp Phe Asp Asp Asp Asn Lys Asp Glu Ser Lys Val
290 295 300

Asp Phe Lys Lys Ile Val Ser Glu Asn Trp Asn Asp Pro Pro Lys Arg
305 310 315 320

Glu Arg Lys Arg Asn Tyr Ser Glu Val Glu Tyr Phe Lys Gln Thr Leu
325 330 335

Arg Gln Gly Ala Pro Ala Lys Pro Lys Glu Pro Arg Ile Pro Arg Met
340 345 350

Pro Gln Leu His Asp Phe Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu
355 360 365

Leu Tyr Glu Lys Glu Val Arg Tyr Leu Met Gln Ala His Gln Lys Thr
370 375 380

Gln Met Lys Asp Thr Ile Glu Val Asp Glu Pro Glu Glu Val Gly Asp
385 390 395 400

Pro Leu Thr Ala Glu Glu Val Glu Glu Lys Glu Leu Leu Leu Glu Glu
405 410 415

Gly Phe Ser Thr Trp Ser Arg Arg Asp Phe Asn Ala Phe Ile Arg Ala
420 425 430

Cys Glu Lys Tyr Gly Arg Asn Asp Ile Lys Ser Ile Ala Ser Glu Met
435 440 445

Glu Gly Lys Thr Glu Glu Glu Val Glu Arg Tyr Ala Gln Val Phe Gln
450 455 460

Val Arg Tyr Lys Glu Leu Asn Asp Tyr Asp Arg Ile Ile Lys Asn Ile
465 470 475 480

Glu Arg Gly Glu Ala Arg Ile Ser Arg Lys Asp Glu Ile Met Lys Ala
 485 490 495

Ile Gly Lys Lys Leu Asp Arg Tyr Arg Asn Pro Trp Leu Glu Leu Lys
 500 505 510

Ile Gln Tyr Gly Gln Asn Lys Gly Lys Leu Tyr Asn Glu Glu Cys Asp
 515 520 525

Arg Phe Met Ile Cys Met Val His Lys Leu Gly Tyr Gly Asn Trp Asp
 530 535 540

Glu Leu Lys Ala Ala Phe Arg Thr Ser Pro Leu Phe Arg Phe Asp Trp
 545 550 555 560

Phe Val Lys Ser Arg Thr Thr Gln Glu Leu Ala Arg Arg Cys Asp Thr
 565 570 575

Leu Ile Arg Leu Ile Glu Lys Glu Asn Gln Glu Phe Asp Glu Arg Glu
 580 585 590

Arg Gln Ala Arg Lys Glu Lys Lys Leu Ser Lys Ser Ala Thr Pro Ser
 595 600 605

Lys Arg Pro Ser Gly Arg Gln Ala Asn Glu Ser Pro Ser Ser Leu Leu
 610 615 620

Lys Lys Arg Lys Gln Leu Ser Met Asp Asp Tyr Gly Lys Arg Arg Lys
 625 630 635 640

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 60

c atg gat cca ttt tta att cag tcc cca ttc tcc ggc ttc tca ccg gaa
 109

Met Asp Pro Phe Leu Ile Gln Ser Pro Phe Ser Gly Phe Ser Pro Glu
 1 5 10 15

tat tct atc gga tct tct cca gat tct ttc tca tcc tct tct tct aac
 157

Tyr Ser Ile Gly Ser Ser Pro Asp Ser Phe Ser Ser Ser Ser Ser Asn
 20 25 30

aat tac tct ctt ccc ttc aac gag aac gac tca gag gaa atg ttt ctc
 205

Asn Tyr Ser Leu Pro Phe Asn Glu Asn Asp Ser Glu Glu Met Phe Leu

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35          40          45
tac ggt cta atc gag cag tcc acg caa caa acc tat att gac tcg gat
253
Tyr Gly Leu Ile Glu Gln Ser Thr Gln Gln Thr Tyr Ile Asp Ser Asp
50          55          60
agt caa gac ctt ccg atc aaa tcc gta agc tca aga aag tca gag aag
301
Ser Gln Asp Leu Pro Ile Lys Ser Val Ser Ser Arg Lys Ser Glu Lys
65          70          75          80
tct tac aga ggc gta aga cga cgg cca tgg ggg aaa ttc gcg gcg gag
349
Ser Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu
85          90          95
ata aga gat tcg act aga aac ggt att agg gtt tgg ctc ggg acg ttc
397
Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp Leu Gly Thr Phe
100          105          110
gaa agc gcg gaa gag gcg gct tta gcc tac gat caa gct gct ttc tcg
445
Glu Ser Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala Phe Ser
115          120          125
atg aga ggg tcc tcg gcg att ctc aat ttt tcg gcg gag aga gtt caa
493
Met Arg Gly Ser Ser Ala Ile Leu Asn Phe Ser Ala Glu Arg Val Gln
130          135          140
gag tcg ctt tcg gag att aaa tat acc tac gag gat ggt tgt tct ccg
541
Glu Ser Leu Ser Glu Ile Lys Tyr Thr Tyr Glu Asp Gly Cys Ser Pro
145          150          155          160
gtt gtg gcg ttg aag agg aaa cac tcg atg aga cgg aga atg acc aat
589
Val Val Ala Leu Lys Arg Lys His Ser Met Arg Arg Arg Met Thr Asn
165          170          175
aag aag acg aaa gat agt gac ttt gat cac cgc tcc gtg aag tta gat
637
Lys Lys Thr Lys Asp Ser Asp Phe Asp His Arg Ser Val Lys Leu Asp
180          185          190
aat gta gtt gtc ttt gag gat ttg gga gaa cag tac ctt gag gag ctt
685
Asn Val Val Val Phe Glu Asp Leu Gly Glu Gln Tyr Leu Glu Glu Leu
195          200          205
ttg ggg tct tct gaa aat agt ggg act tgg tga aagattagga tttgtattag
738
Leu Gly Ser Ser Glu Asn Ser Gly Thr Trp
210          215
ggaccttaag tttgaagtgg ttgattaatt ttaaccctaa tatgtttttt gtttgcttaa
798

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atatttgatt ctattgagaa acatcgaaaa cagtttgat gtacttttgt gatacttggc
858

g
859

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192

Met Asp Pro Phe Leu Ile Gln Ser Pro Phe Ser Gly Phe Ser Pro Glu
1 5 10 15

Tyr Ser Ile Gly Ser Ser Pro Asp Ser Phe Ser Ser Ser Ser Ser Asn
20 25 30

Asn Tyr Ser Leu Pro Phe Asn Glu Asn Asp Ser Glu Glu Met Phe Leu
35 40 45

Tyr Gly Leu Ile Glu Gln Ser Thr Gln Gln Thr Tyr Ile Asp Ser Asp
50 55 60

Ser Gln Asp Leu Pro Ile Lys Ser Val Ser Ser Arg Lys Ser Glu Lys
65 70 75 80

Ser Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu
85 90 95

Ile Arg Asp Ser Thr Arg Asn Gly Ile Arg Val Trp Leu Gly Thr Phe
100 105 110

Glu Ser Ala Glu Glu Ala Ala Leu Ala Tyr Asp Gln Ala Ala Phe Ser
115 120 125

Met Arg Gly Ser Ser Ala Ile Leu Asn Phe Ser Ala Glu Arg Val Gln
130 135 140

Glu Ser Leu Ser Glu Ile Lys Tyr Thr Tyr Glu Asp Gly Cys Ser Pro
145 150 155 160

Val Val Ala Leu Lys Arg Lys His Ser Met Arg Arg Arg Met Thr Asn
165 170 175

Lys Lys Thr Lys Asp Ser Asp Phe Asp His Arg Ser Val Lys Leu Asp
180 185 190

Asn Val Val Val Phe Glu Asp Leu Gly Glu Gln Tyr Leu Glu Glu Leu
195 200 205

Leu Gly Ser Ser Glu Asn Ser Gly Thr Trp
210 215

<210> 193 <211> 1072 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (152)..(967) <223> G1267

<400> 193

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60

atcaccaccc tctccggctc tcaacagaac aacaacaaaa aaacagcttc cgtgtcctg
120

ttccggcgaa atcggacggt cgagatcaat c atg cat cgt aga gca gca att
172

Met His Arg Arg Ala Ala Ile
1 5

caa gaa tcg gat gac gaa gaa gat gag act tac aac gac gtc gtt cct
220

Gln Glu Ser Asp Asp Glu Glu Asp Glu Thr Tyr Asn Asp Val Val Pro
10 15 20

gaa tct cct tct tct tgt gaa gac tca aag atc tca aaa cca act cca
268

Glu Ser Pro Ser Ser Cys Glu Asp Ser Lys Ile Ser Lys Pro Thr Pro
25 30 35

aag aaa agg agg aac gta gag aag aga gtt gtc tca gtt ccg ata gct
316

Lys Lys Arg Arg Asn Val Glu Lys Arg Val Val Ser Val Pro Ile Ala
40 45 50 55

gac gtg gaa gga tct aag agc aga ggc gaa gta tat cca ccg tcc gat
364

Asp Val Glu Gly Ser Lys Ser Arg Gly Glu Val Tyr Pro Pro Ser Asp
60 65 70

tca tgg gcc tgg aga aag tac gga caa aaa ccg atc aaa ggc tcg cct
412

Ser Trp Ala Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro
75 80 85

tat ccc agg gga tat tac aga tgt agt agc tca aaa gga tgt ccg gcg
460

Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser Ser Ser Lys Gly Cys Pro Ala
90 95 100

agg aag cag gtg gag aga agc cgt gtg gac cct tct aag ctt atg att
508

Arg Lys Gln Val Glu Arg Ser Arg Val Asp Pro Ser Lys Leu Met Ile
105 110 115

act tac gcc tgc gac cac aat cac cct ttc cct tcc tcc tcc gct aac
556

Thr Tyr Ala Cys Asp His Asn His Pro Phe Pro Ser Ser Ser Ala Asn
120 125 130 135

acc aaa tcc cac cac cgc tcc tcc gtc gtc ctc aaa acc gca aag aaa
 604
 Thr Lys Ser His His Arg Ser Ser Val Val Leu Lys Thr Ala Lys Lys
 140 145 150
 gag gaa gaa tac gaa gag gag gaa gaa gaa cta acc gtc acc gcc gca
 652
 Glu Glu Glu Tyr Glu Glu Glu Glu Glu Glu Leu Thr Val Thr Ala Ala
 155 160 165
 gag gaa cca ccg gcg gga ctt gat cta agc cac gta gac tca ccg ttg
 700
 Glu Glu Pro Pro Ala Gly Leu Asp Leu Ser His Val Asp Ser Pro Leu
 170 175 180
 cta tta ggc ggc tgc tac agc gaa atc gga gag ttc ggg tgg ttc tac
 748
 Leu Leu Gly Gly Cys Tyr Ser Glu Ile Gly Glu Phe Gly Trp Phe Tyr
 185 190 195
 gac gcg tcg atc tca tca tca tct ggt tct tcg aat ttc ctc gac gta
 796
 Asp Ala Ser Ile Ser Ser Ser Ser Gly Ser Ser Asn Phe Leu Asp Val
 200 205 210 215
 act cta gag aga ggt ttt tca gta ggc caa gag gaa gat gag tct ttg
 844
 Thr Leu Glu Arg Gly Phe Ser Val Gly Gln Glu Glu Asp Glu Ser Leu
 220 225 230
 ttc ggt gat ctc ggt gat tta cct gat tgc gcc tcc gtg ttc cgc cgt
 892
 Phe Gly Asp Leu Gly Asp Leu Pro Asp Cys Ala Ser Val Phe Arg Arg
 235 240 245
 ggg act gtt gcg acg gag gag caa cat cga aga tgt gat ttt ggc gcc
 940
 Gly Thr Val Ala Thr Glu Glu Gln His Arg Arg Cys Asp Phe Gly Ala
 250 255 260
 att cct ttc tgt gat agt tct aga tga gttgtgtgt gttagcaaaa
 987
 Ile Pro Phe Cys Asp Ser Ser Arg
 265 270
 ccaaaagaaa aaaacacaat ttttttattt tccactgtaa aggtgtatca atggtggatt
 1047
 cattttttta aaaaaaaaaa aaaaa
 1072

<210> 194 <211> 271 <212> PRT <213> Arabidopsis thaliana <400>
 194

Met His Arg Arg Ala Ala Ile Gln Glu Ser Asp Asp Glu Glu Asp Glu
 1 5 10 15

Thr Tyr Asn Asp Val Val Pro Glu Ser Pro Ser Ser Cys Glu Asp Ser
 20 25 30

Lys Ile Ser Lys Pro Thr Pro Lys Lys Arg Arg Asn Val Glu Lys Arg
 35 40 45
 Val Val Ser Val Pro Ile Ala Asp Val Glu Gly Ser Lys Ser Arg Gly
 50 55 60
 Glu Val Tyr Pro Pro Ser Asp Ser Trp Ala Trp Arg Lys Tyr Gly Gln
 65 70 75 80
 Lys Pro Ile Lys Gly Ser Pro Tyr Pro Arg Gly Tyr Tyr Arg Cys Ser
 85 90 95
 Ser Ser Lys Gly Cys Pro Ala Arg Lys Gln Val Glu Arg Ser Arg Val
 100 105 110
 Asp Pro Ser Lys Leu Met Ile Thr Tyr Ala Cys Asp His Asn His Pro
 115 120 125
 Phe Pro Ser Ser Ser Ala Asn Thr Lys Ser His His Arg Ser Ser Val
 130 135 140
 Val Leu Lys Thr Ala Lys Lys Glu Glu Glu Tyr Glu Glu Glu Glu Glu
 145 150 155 160
 Glu Leu Thr Val Thr Ala Ala Glu Glu Pro Pro Ala Gly Leu Asp Leu
 165 170 175
 Ser His Val Asp Ser Pro Leu Leu Leu Gly Gly Cys Tyr Ser Glu Ile
 180 185 190
 Gly Glu Phe Gly Trp Phe Tyr Asp Ala Ser Ile Ser Ser Ser Ser Gly
 195 200 205
 Ser Ser Asn Phe Leu Asp Val Thr Leu Glu Arg Gly Phe Ser Val Gly
 210 215 220
 Gln Glu Glu Asp Glu Ser Leu Phe Gly Asp Leu Gly Asp Leu Pro Asp
 225 230 235 240
 Cys Ala Ser Val Phe Arg Arg Gly Thr Val Ala Thr Glu Glu Gln His
 245 250 255
 Arg Arg Cys Asp Phe Gly Ala Ile Pro Phe Cys Asp Ser Ser Arg
 260 265 270

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 <221> CDS <222> (58)..(579) <223> G1275

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 57

atg aat gat gca gac aca aac ttg ggg agt agt ttc agc gat gat act
 105

Met Asn Asp Ala Asp Thr Asn Leu Gly Ser Ser Phe Ser Asp Asp Thr
 1 5 10 15

cac tct gtg ttc gag ttt ccg gag cta gac ttg tca gat gaa tgg atg
 153

His Ser Val Phe Glu Phe Pro Glu Leu Asp Leu Ser Asp Glu Trp Met
 20 25 30

gat gat gat ctt gtg tct gcg gtt tcc ggg atg aat cag tct tat ggt
 201

Asp Asp Asp Leu Val Ser Ala Val Ser Gly Met Asn Gln Ser Tyr Gly
 35 40 45

tat cag act agt gat gtt gct ggt gct tta ttc tca ggt tct tct agc
 249

Tyr Gln Thr Ser Asp Val Ala Gly Ala Leu Phe Ser Gly Ser Ser Ser
 50 55 60

tgt ttc agt cat cct gaa tct cca agt acc aaa act tat gtt gct gct
 297

Cys Phe Ser His Pro Glu Ser Pro Ser Thr Lys Thr Tyr Val Ala Ala
 65 70 75 80

aca gcc act gct tct gcc gac aac caa aac aag aaa gaa aag aaa aaa
 345

Thr Ala Thr Ala Ser Ala Asp Asn Gln Asn Lys Lys Glu Lys Lys Lys
 85 90 95

att aaa ggg aga gtt gcg ttc aag aca cgg tcc gag gtg gaa gtg ctt
 393

Ile Lys Gly Arg Val Ala Phe Lys Thr Arg Ser Glu Val Glu Val Leu
 100 105 110

gac gac ggg ttc aag tgg aga aag tat ggg aag aag atg gtg aag aac
 441

Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn
 115 120 125

agc cca cat cca aga aac tac tac aaa tgt tca gtt gat ggc tgt ccc
 489

Ser Pro His Pro Arg Asn Tyr Tyr Lys Cys Ser Val Asp Gly Cys Pro
 130 135 140

gtg aag aaa agg gtt gaa cga gac aga gat gat ccg agc ttt gtg ata
 537

Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ser Phe Val Ile
 145 150 155 160

aca act tac gag ggt tcc cac aat cac tca agc atg aac taa
 579

Thr Thr Tyr Glu Gly Ser His Asn His Ser Ser Met Asn

165

170

gactcgaact aaggctcaag gcgaccatgc tatattcagc acatcttatt ttctatgggt
639

acgaacgata cttaaaactg cttctagttc ttatatcca ttgtaaaactg gttgcaggtt
699

cacaaatttt gagaggttta tgacattcta aatctgtagt acttatata
748

<210> 196 <211> 173 <212> PRT <213> Arabidopsis thaliana <400>
196

Met Asn Asp Ala Asp Thr Asn Leu Gly Ser Ser Phe Ser Asp Asp Thr
1 5 10 15

His Ser Val Phe Glu Phe Pro Glu Leu Asp Leu Ser Asp Glu Trp Met
20 25 30

Asp Asp Asp Leu Val Ser Ala Val Ser Gly Met Asn Gln Ser Tyr Gly
35 40 45

Tyr Gln Thr Ser Asp Val Ala Gly Ala Leu Phe Ser Gly Ser Ser Ser
50 55 60

Cys Phe Ser His Pro Glu Ser Pro Ser Thr Lys Thr Tyr Val Ala Ala
65 70 75 80

Thr Ala Thr Ala Ser Ala Asp Asn Gln Asn Lys Lys Glu Lys Lys Lys
85 90 95

Ile Lys Gly Arg Val Ala Phe Lys Thr Arg Ser Glu Val Glu Val Leu
100 105 110

Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn
115 120 125

Ser Pro His Pro Arg Asn Tyr Tyr Lys Cys Ser Val Asp Gly Cys Pro
130 135 140

Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ser Phe Val Ile
145 150 155 160

Thr Thr Tyr Glu Gly Ser His Asn His Ser Ser Met Asn
165 170

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55 Met Asp Phe Lys Lys
1 5

gaa gaa aca ctt cgt aga ggg cca tgg ctc gaa gaa gaa gac gaa cgg
103
Glu Glu Thr Leu Arg Arg Gly Pro Trp Leu Glu Glu Glu Asp Glu Arg
10 15 20

cta gtg aag gtc att agt ctt ttg gga gaa cgt cgt tgg gat tct tta
151
Leu Val Lys Val Ile Ser Leu Leu Gly Glu Arg Arg Trp Asp Ser Leu
25 30 35

gca ata gtt tcc ggt ttg aag agg agt ggt aag agt tgc agg cta agg
199
Ala Ile Val Ser Gly Leu Lys Arg Ser Gly Lys Ser Cys Arg Leu Arg
40 45 50

tgg atg aac tat ctg aat ccg act ctg aag cgt gga ccg atg agt caa
247
Trp Met Asn Tyr Leu Asn Pro Thr Leu Lys Arg Gly Pro Met Ser Gln
55 60 65

gaa gaa gag aga atc atc ttt cag ctc cat gct cta tgg ggt aac aag
295
Glu Glu Glu Arg Ile Ile Phe Gln Leu His Ala Leu Trp Gly Asn Lys
70 75 80 85

tgg tcg aag att gcg aga aga tta ccc ggt agg act gat aac gag ata
343
Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile
90 95 100

aag aac tat tgg aga act cat tat aga aag aaa cag gaa gct caa aac
391
Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys Gln Glu Ala Gln Asn
105 110 115

tat gga aag ctc ttt gag tgg aga gga aat aca gga gaa gaa ttg ttg
439
Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr Gly Glu Glu Leu Leu
120 125 130

cac aag tat aag gaa aca gag atc act agg aca aag acg acg tct caa
487
His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr Lys Thr Thr Ser Gln
135 140 145

gaa cat ggt ttt gtt gaa gtt gtg agc atg gaa agt ggt aaa gaa gcc
535
Glu His Gly Phe Val Glu Val Val Ser Met Glu Ser Gly Lys Glu Ala
150 155 160 165

aac ggt ggt gtt ggt gga aga gaa agc ttc ggt gtt atg aaa tca ccg
583
Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly Val Met Lys Ser Pro
170 175 180

tat gaa aat cgg att tcg gat tgg ata tca gag att tct act gac cag
631

Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu Ile Ser Thr Asp Gln
185 190 195

agt gaa gca aat ctt tca gaa gat cac agc agc aat agc tgc agt gag
679

Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser Asn Ser Cys Ser Glu
200 205 210

aac aat att aac att ggt act tgg tgg ttt caa gag act agg gac ttt
727

Asn Asn Ile Asn Ile Gly Thr Trp Trp Phe Gln Glu Thr Arg Asp Phe
215 220 225

gag gag ttt tca tgt tct cta tgg tca taa ttctaaagtt gggtttattta
777

Glu Glu Phe Ser Cys Ser Leu Trp Ser
230 235

ctttttaaaa aaaaaaaaaa aaa
800

<210> 198 <211> 238 <212> PRT <213> Arabidopsis thaliana <400>
198

Met Asp Phe Lys Lys Glu Glu Thr Leu Arg Arg Gly Pro Trp Leu Glu
1 5 10 15

Glu Glu Asp Glu Arg Leu Val Lys Val Ile Ser Leu Leu Gly Glu Arg
20 25 30

Arg Trp Asp Ser Leu Ala Ile Val Ser Gly Leu Lys Arg Ser Gly Lys
35 40 45

Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Asn Pro Thr Leu Lys Arg
50 55 60

Gly Pro Met Ser Gln Glu Glu Glu Arg Ile Ile Phe Gln Leu His Ala
65 70 75 80

Leu Trp Gly Asn Lys Trp Ser Lys Ile Ala Arg Arg Leu Pro Gly Arg
85 90 95

Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Tyr Arg Lys Lys
100 105 110

Gln Glu Ala Gln Asn Tyr Gly Lys Leu Phe Glu Trp Arg Gly Asn Thr
115 120 125

Gly Glu Glu Leu Leu His Lys Tyr Lys Glu Thr Glu Ile Thr Arg Thr

130 135 140
 Lys Thr Thr Ser Gln Glu His Gly Phe Val Glu Val Val Ser Met Glu
 145 150 155 160
 Ser Gly Lys Glu Ala Asn Gly Gly Val Gly Gly Arg Glu Ser Phe Gly
 165 170 175
 Val Met Lys Ser Pro Tyr Glu Asn Arg Ile Ser Asp Trp Ile Ser Glu
 180 185 190
 Ile Ser Thr Asp Gln Ser Glu Ala Asn Leu Ser Glu Asp His Ser Ser
 195 200 205
 Asn Ser Cys Ser Glu Asn Asn Ile Asn Ile Gly Thr Trp Trp Phe Gln
 210 215 220
 Glu Thr Arg Asp Phe Glu Glu Phe Ser Cys Ser Leu Trp Ser
 225 230 235
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 Met Arg Lys Pro Glu Val Ala Ile Ala Ala Ser Thr His Gln
 1 5 10
 gta aag aag atg aag aag gga ctt tgg tct cct gag gaa gac tca aag
 96
 Val Lys Lys Met Lys Lys Gly Leu Trp Ser Pro Glu Glu Asp Ser Lys
 15 20 25 30
 ctg atg caa tac atg tta agc aat gga caa gga tgt tgg agt gat gtt
 144
 Leu Met Gln Tyr Met Leu Ser Asn Gly Gln Gly Cys Trp Ser Asp Val
 35 40 45
 gcg aaa aac gca gga ctt caa aga tgt ggc aaa agc tgc cgt ctt cgt
 192
 Ala Lys Asn Ala Gly Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg
 50 55 60
 tgg atc aac tat ctt cgt cct gac ctc aag cgt ggc gct ttc tct cct
 240
 Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Ala Phe Ser Pro
 65 70 75
 caa gaa gag gat ctc atc att cgc ttt cat tcc atc ctc ggc aac agg
 288
 Gln Glu Glu Asp Leu Ile Ile Arg Phe His Ser Ile Leu Gly Asn Arg
 80 85 90

tgg tct cag att gca gca cga ttg cct ggt cgg acc gat aac gag atc
 336
 Trp Ser Gln Ile Ala Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile
 95 100 105 110
 aag aat ttc tgg aac tca aca ata aag aaa agg cta aag aag atg tcc
 384
 Lys Asn Phe Trp Asn Ser Thr Ile Lys Lys Arg Leu Lys Lys Met Ser
 115 120 125
 gat acc tcc aac tta atc aac aac tca tcc tca tca ccc aac aca gca
 432
 Asp Thr Ser Asn Leu Ile Asn Asn Ser Ser Ser Ser Pro Asn Thr Ala
 130 135 140
 agc gat tcc tct tct aat tcc gca tct tct ttg gat att aaa gac att
 480
 Ser Asp Ser Ser Ser Asn Ser Ala Ser Ser Leu Asp Ile Lys Asp Ile
 145 150 155
 ata gga agc ttc atg tcc tta caa gaa caa ggc ttc gtc aac cct tcc
 528
 Ile Gly Ser Phe Met Ser Leu Gln Glu Gln Gly Phe Val Asn Pro Ser
 160 165 170
 ttg acc cac ata caa acc aac aat cca ttt cca acg gga aac atg atc
 576
 Leu Thr His Ile Gln Thr Asn Asn Pro Phe Pro Thr Gly Asn Met Ile
 175 180 185 190
 agc cac ccg tgc aat gac gat ttt acc cct tat gta gat ggt atc tat
 624
 Ser His Pro Cys Asn Asp Asp Phe Thr Pro Tyr Val Asp Gly Ile Tyr
 195 200 205
 gga gta aac gca ggg gta caa ggg gaa ctc tac ttc cca cct ttg gaa
 672
 Gly Val Asn Ala Gly Val Gln Gly Glu Leu Tyr Phe Pro Pro Leu Glu
 210 215 220
 tgt gaa gaa ggt gat tgg tac aat gca aat ata aac aac cac tta gac
 720
 Cys Glu Glu Gly Asp Trp Tyr Asn Ala Asn Ile Asn Asn His Leu Asp
 225 230 235
 gag ttg aac act aat gga tcc gga aac gca cct gag ggt atg aga cca
 768
 Glu Leu Asn Thr Asn Gly Ser Gly Asn Ala Pro Glu Gly Met Arg Pro
 240 245 250
 gtg gaa gaa ttt tgg gac ctt gac cag ttg atg aac act gag gtt cct
 816
 Val Glu Glu Phe Trp Asp Leu Asp Gln Leu Met Asn Thr Glu Val Pro
 255 260 265 270
 tcg ttt tac ttc aac ttc aaa caa agc ata tga atatttttac gtcatttat
 869
 Ser Phe Tyr Phe Asn Phe Lys Gln Ser Ile
 275 280

tcttttttct attgcggttt atactcaaga ttcttagcca cacacacata aatgcaaata
929

tatatacatt gttagagagt attttgtatt tcgtataatc ttttcgtact agggcttgag
989

ccttgaggtc ccatgtaacg attagtcaat gtaaaacata tctcctataa taaataaata
1049

aaagaaataa taagcacata aaaaaaaaaa aa
1081

<210> 200 <211> 280 <212> PRT <213> Arabidopsis thaliana <400>
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Met Arg Lys Pro Glu Val Ala Ile Ala Ala Ser Thr His Gln Val Lys
1 5 10 15

Lys Met Lys Lys Gly Leu Trp Ser Pro Glu Glu Asp Ser Lys Leu Met
20 25 30

Gln Tyr Met Leu Ser Asn Gly Gln Gly Cys Trp Ser Asp Val Ala Lys
35 40 45

Asn Ala Gly Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile
50 55 60

Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Ala Phe Ser Pro Gln Glu
65 70 75 80

Glu Asp Leu Ile Ile Arg Phe His Ser Ile Leu Gly Asn Arg Trp Ser
85 90 95

Gln Ile Ala Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn
100 105 110

Phe Trp Asn Ser Thr Ile Lys Lys Arg Leu Lys Lys Met Ser Asp Thr
115 120 125

Ser Asn Leu Ile Asn Asn Ser Ser Ser Ser Pro Asn Thr Ala Ser Asp
130 135 140

Ser Ser Ser Asn Ser Ala Ser Ser Leu Asp Ile Lys Asp Ile Ile Gly
145 150 155 160

Ser Phe Met Ser Leu Gln Glu Gln Gly Phe Val Asn Pro Ser Leu Thr
165 170 175

His Ile Gln Thr Asn Asn Pro Phe Pro Thr Gly Asn Met Ile Ser His

180 185 190

Pro Cys Asn Asp Asp Phe Thr Pro Tyr Val Asp Gly Ile Tyr Gly Val
195 200 205

Asn Ala Gly Val Gln Gly Glu Leu Tyr Phe Pro Pro Leu Glu Cys Glu
210 215 220

Glu Gly Asp Trp Tyr Asn Ala Asn Ile Asn Asn His Leu Asp Glu Leu
225 230 235 240

Asn Thr Asn Gly Ser Gly Asn Ala Pro Glu Gly Met Arg Pro Val Glu
245 250 255

Glu Phe Trp Asp Leu Asp Gln Leu Met Asn Thr Glu Val Pro Ser Phe
260 265 270

Tyr Phe Asn Phe Lys Gln Ser Ile -
275 280

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60

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110

Met Ile Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu
1 5 10

gac gag aag ctc aag gat ctt gtc gaa caa tac ggt cct cac aat tgg
158

Asp Glu Lys Leu Lys Asp Leu Val Glu Gln Tyr Gly Pro His Asn Trp
15 20 25

aac gcc att gct ctc aag ctt cct ggt cgc tct ggt aag agt tgt aga
206

Asn Ala Ile Ala Leu Lys Leu Pro Gly Arg Ser Gly Lys Ser Cys Arg
30 35 40 45

ttg aga tgg ttt aat caa ttg gat cca agg atc aac cga aac cct ttc
254

Leu Arg Trp Phe Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe
50 55 60

acg gaa gaa gaa gaa gaa aga ctt tta gcg gct cat cgg atc cat ggg
302

Thr Glu Glu Glu Glu Glu Arg Leu Leu Ala Ala His Arg Ile His Gly
65 70 75

aac aga tgg tcc atc atc gca agg ctt ttc cct gga aga act gat aac
350

Asn Arg Trp Ser Ile Ile Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn
 80 85 90
 gcc gtc aag aac cat tgg cac gtc atc atg gct cgt cgc aca cgc caa
 398
 Ala Val Lys Asn His Trp His Val Ile Met Ala Arg Arg Thr Arg Gln
 95 100 105
 acc tct aag cct cgt ctt ctt ccc tcg acg act tcg tct tct tct tta
 446
 Thr Ser Lys Pro Arg Leu Leu Pro Ser Thr Thr Ser Ser Ser Ser Leu
 110 115 120 125
 atg gcg agt gaa caa atc atg atg agt tct ggt ggt tat aat cat aat
 494
 Met Ala Ser Glu Gln Ile Met Met Ser Ser Gly Gly Tyr Asn His Asn
 130 135 140
 tat agt tcc gat gat cgg aag aaa ata ttt cca gca gac ttt ata aat
 542
 Tyr Ser Ser Asp Asp Arg Lys Lys Ile Phe Pro Ala Asp Phe Ile Asn
 145 150 155
 ttc cct tac aaa ttc tct cat atc aat cat ctt cac ttc cta aag gag
 590
 Phe Pro Tyr Lys Phe Ser His Ile Asn His Leu His Phe Leu Lys Glu
 160 165 170
 ttt ttc ccc gga aag atc gct tta agt cac aaa gca aat cag agt aag
 638
 Phe Phe Pro Gly Lys Ile Ala Leu Ser His Lys Ala Asn Gln Ser Lys
 175 180 185
 aag cct atg gag ttc tac aat ttt cta caa gta aac aca gat tca aac
 686
 Lys Pro Met Glu Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Asn
 190 195 200 205
 aag agc gag att ata gat caa gat tca ggt caa agc aaa cgc agt gac
 734
 Lys Ser Glu Ile Ile Asp Gln Asp Ser Gly Gln Ser Lys Arg Ser Asp
 210 215 220
 tcg gac acc aaa cat gaa agt cat gtt cca ttc ttc gac ttt tta tcc
 782
 Ser Asp Thr Lys His Glu Ser His Val Pro Phe Phe Asp Phe Leu Ser
 225 230 235
 gtt gga aac tct gcc tcc tag gattagtttt ttgcagtaa ctctaaatt
 833
 Val Gly Asn Ser Ala Ser
 240
 tctagattaa ctatttagtc cgtatacgta cgagattatc taggtcgta gcatgtatgc
 893
 ttgatgtgta taatcactaa ctagttagct attacctgcg aaaattgtaa gaaaaataca
 953
 taatgttgat gtatcacaca ttctcaatgt ctgtaaaatt tccatcgagt tgtaactat
 1013

caaagttatc cgtttgaaaa aaaaaaaa
1041

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Leu Lys Asp Leu Val Glu Gln Tyr Gly Pro His Asn Trp Asn Ala Ile
20 25 30

Ala Leu Lys Leu Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
35 40 45

Phe Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu
50 55 60

Glu Glu Glu Arg Leu Leu Ala Ala His Arg Ile His Gly Asn Arg Trp
65 70 75 80

Ser Ile Ile Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn Ala Val Lys
85 90 95

Asn His Trp His Val Ile Met Ala Arg Arg Thr Arg Gln Thr Ser Lys
100 105 110

Pro Arg Leu Leu Pro Ser Thr Thr Ser Ser Ser Ser Leu Met Ala Ser
115 120 125

Glu Gln Ile Met Met Ser Ser Gly Gly Tyr Asn His Asn Tyr Ser Ser
130 135 140

Asp Asp Arg Lys Lys Ile Phe Pro Ala Asp Phe Ile Asn Phe Pro Tyr
145 150 155 160

Lys Phe Ser His Ile Asn His Leu His Phe Leu Lys Glu Phe Phe Pro
165 170 175

Gly Lys Ile Ala Leu Ser His Lys Ala Asn Gln Ser Lys Lys Pro Met
180 185 190

Glu Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Asn Lys Ser Glu
195 200 205

Ile Ile Asp Gln Asp Ser Gly Gln Ser Lys Arg Ser Asp Ser Asp Thr

210

215

220

Lys His Glu Ser His Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn
 225 230 235 240

Ser Ala Ser

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 57

Met Gly Lys
 1

gga aga gca cca tgt tgt gac aaa acc aaa gtg aag aga gga cca tgg
 105

Gly Arg Ala Pro Cys Cys Asp Lys Thr Lys Val Lys Arg Gly Pro Trp
 5 10 15

agc cat gat gaa gac ttg aaa ctc atc tct ttc att cac aag aat ggt
 153

Ser His Asp Glu Asp Leu Lys Leu Ile Ser Phe Ile His Lys Asn Gly
 20 25 30 35

cat gag aat tgg aga tct ctc cca aag caa gct gga ttg ttg agg tgt
 201

His Glu Asn Trp Arg Ser Leu Pro Lys Gln Ala Gly Leu Leu Arg Cys
 40 45 50

ggc aag agt tgt cgt ctg cga tgg att aat tac ctc aga cct gat gtg
 249

Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Val
 55 60 65

aaa cgt ggc aat ttc agt gca gag gaa gaa gac acc atc atc aaa ctt
 297

Lys Arg Gly Asn Phe Ser Ala Glu Glu Glu Asp Thr Ile Ile Lys Leu
 70 75 80

cac cag agc ttt ggt aac aag tgg tcg aag att gct tct aag ctg cct
 345

His Gln Ser Phe Gly Asn Lys Trp Ser Lys Ile Ala Ser Lys Leu Pro
 85 90 95

gga aga aca gac aat gag atc aag aat gtg tgg cat aca cat ctc aag
 393

Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu Lys
 100 105 110 115

aaa aga ttg agc tcg gaa act aac ctt aat gcc gat gaa gcg ggt tca
 441

Lys Arg Leu Ser Ser Glu Thr Asn Leu Asn Ala Asp Glu Ala Gly Ser
 120 125 130

aaa ggt tct ttg aat gaa gaa gag aac tct caa gag tca tct cca aat
 489
 Lys Gly Ser Leu Asn Glu Glu Glu Asn Ser Gln Glu Ser Ser Pro Asn
 135 140 145

 gct tca atg tct ttt gct ggt tcc aac att tca agc aaa gac gat gat
 537
 Ala Ser Met Ser Phe Ala Gly Ser Asn Ile Ser Ser Lys Asp Asp Asp
 150 155 160

 gca cag ata agt caa atg ttt gag cac att cta act tat agc gag ttt
 585
 Ala Gln Ile Ser Gln Met Phe Glu His Ile Leu Thr Tyr Ser Glu Phe
 165 170 175

 acg ggg atg tta caa gag gta gac aaa cca gag ctg ctg gag atg cct
 633
 Thr Gly Met Leu Gln Glu Val Asp Lys Pro Glu Leu Leu Glu Met Pro
 180 185 190 195

 ttt gat tta gat cct gac att tgg agt ttc ata gat ggt tca gac tca
 681
 Phe Asp Leu Asp Pro Asp Ile Trp Ser Phe Ile Asp Gly Ser Asp Ser
 200 205 210

 ttc caa caa cca gag aac aga gct ctt caa gag tct gaa gaa gat gaa
 729
 Phe Gln Gln Pro Glu Asn Arg Ala Leu Gln Glu Ser Glu Glu Asp Glu
 215 220 225

 gtt gat aaa tgg ttt aag cac ctg gaa agc gaa ctc ggg tta gaa gaa
 777
 Val Asp Lys Trp Phe Lys His Leu Glu Ser Glu Leu Gly Leu Glu Glu
 230 235 240

 aac gat aac caa caa caa caa cag cat aaa cag gga aca gaa gat gaa
 825
 Asn Asp Asn Gln Gln Gln Gln Gln His Lys Gln Gly Thr Glu Asp Glu
 245 250 255

 cat tca tca tca ctc ttg gag agt tac gag ctc ctc ata cat taa
 870
 His Ser Ser Ser Leu Leu Glu Ser Tyr Glu Leu Leu Ile His
 260 265 270

 tgaagccata aagcaagtca ttttcacctt gaaaatggaa ttattagcta acttattggc
 930

 attattagta tataagcaag atcagatagg cgcattgtagt agcaacaacg aagaaacgtc
 990

 gaattgtaga caaatgtag atattacaga gttgaaagat tgtattttgc aaatgattgc
 1050

 tttgtagtga aatcaagtta tcacaaaaaa aaaaaaaa
 1088

 <210> . 204 <211> 273 <212> PRT <213> Arabidopsis thaliana <400>
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Met Gly Lys Gly Arg Ala Pro Cys Cys Asp Lys Thr Lys Val Lys Arg
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 Gly Pro Trp Ser His Asp Glu Asp Leu Lys Leu Ile Ser Phe Ile His
 20 25 30
 Lys Asn Gly His Glu Asn Trp Arg Ser Leu Pro Lys Gln Ala Gly Leu
 35 40 45
 Leu Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg
 50 55 60
 Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Glu Glu Glu Asp Thr Ile
 65 70 75 80
 Ile Lys Leu His Gln Ser Phe Gly Asn Lys Trp Ser Lys Ile Ala Ser
 85 90 95
 Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr
 100 105 110
 His Leu Lys Lys Arg Leu Ser Ser Glu Thr Asn Leu Asn Ala Asp Glu
 115 120 125
 Ala Gly Ser Lys Gly Ser Leu Asn Glu Glu Glu Asn Ser Gln Glu Ser
 130 135 140
 Ser Pro Asn Ala Ser Met Ser Phe Ala Gly Ser Asn Ile Ser Ser Lys
 145 150 155 160
 Asp Asp Asp Ala Gln Ile Ser Gln Met Phe Glu His Ile Leu Thr Tyr
 165 170 175
 Ser Glu Phe Thr Gly Met Leu Gln Glu Val Asp Lys Pro Glu Leu Leu
 180 185 190
 Glu Met Pro Phe Asp Leu Asp Pro Asp Ile Trp Ser Phe Ile Asp Gly
 195 200 205
 Ser Asp Ser Phe Gln Gln Pro Glu Asn Arg Ala Leu Gln Glu Ser Glu
 210 215 220
 Glu Asp Glu Val Asp Lys Trp Phe Lys His Leu Glu Ser Glu Leu Gly
 225 230 235 240
 Leu Glu Glu Asn Asp Asn Gln Gln Gln Gln Gln His Lys Gln Gly Thr
 365

245 250 255

Glu Asp Glu His Ser Ser Ser Leu Leu Glu Ser Tyr Glu Leu Leu Ile
 260 265 270

His

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 <221> CDS <222> (32)..(784) <223> G1326

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 52

Met Glu Met Ser Arg Gly Ser
 1 5

aac agt ttt gac aat aag aag cct agt tgc caa aga ggt cac tgg aga
 100

Asn Ser Phe Asp Asn Lys Lys Pro Ser Cys Gln Arg Gly His Trp Arg
 10 15 20

cct gtt gaa gat gac aat ctc cgg caa ctc gtt gaa caa tac ggt ccc
 148

Pro Val Glu Asp Asp Asn Leu Arg Gln Leu Val Glu Gln Tyr Gly Pro
 25 30 35

aag aac tgg aat ttt att gct caa cat ctc tat gga aga tca ggg aaa
 196

Lys Asn Trp Asn Phe Ile Ala Gln His Leu Tyr Gly Arg Ser Gly Lys
 40 45 50 55

agc tgt aga tta aga tgg tac aac caa ctt gat cca aac atc acc aag
 244

Ser Cys Arg Leu Arg Trp Tyr Asn Gln Leu Asp Pro Asn Ile Thr Lys
 60 65 70

aaa ccc ttc acc gag gag gaa gaa gag aga ctg ctt aaa gct cat cgg
 292

Lys Pro Phe Thr Glu Glu Glu Glu Glu Arg Leu Leu Lys Ala His Arg
 75 80 85

atc caa ggg aat cgt tgg gcc tcc ata gcc cga ctg ttc ccc ggg agg
 340

Ile Gln Gly Asn Arg Trp Ala Ser Ile Ala Arg Leu Phe Pro Gly Arg
 90 95 100

acc gac aac gct gtc aaa aac cat ttt cat gtc atc atg gct aga cgc
 388

Thr Asp Asn Ala Val Lys Asn His Phe His Val Ile Met Ala Arg Arg
 105 110 115

aaa cgg gaa aac ttc tct tcc aca gct act tct acg ttc aac caa act
 436

Lys Arg Glu Asn Phe Ser Ser Thr Ala Thr Ser Thr Phe Asn Gln Thr
 120 125 130 135

tgg cat act gtt ttg agc cct agt tct agt ctt aca agg cta aat aga
484

Trp His Thr Val Leu Ser Pro Ser Ser Ser Leu Thr Arg Leu Asn Arg
140 145 150

tcc cat ttc ggg cta tgg agg tat cga aag gat aag agt tgc ggt ctc
532

Ser His Phe Gly Leu Trp Arg Tyr Arg Lys Asp Lys Ser Cys Gly Leu
155 160 165

tgg cct tac tct ttt gtt tca cca cct acg aat ggt caa ttt gga tct
580

Trp Pro Tyr Ser Phe Val Ser Pro Pro Thr Asn Gly Gln Phe Gly Ser
170 175 180

tca tct gtc tct aac gta cac cac gaa att tat ctt gag agg aga aag
628

Ser Ser Val Ser Asn Val His His Glu Ile Tyr Leu Glu Arg Arg Lys
185 190 195

tcg aaa gag ttg gtg gat cct cag aat tac aca ttt cat gca gcc aca
676

Ser Lys Glu Leu Val Asp Pro Gln Asn Tyr Thr Phe His Ala Ala Thr
200 205 210 215

cca gat cat aag atg act tca aat gaa gat gga cca tcc atg gga gat
724

Pro Asp His Lys Met Thr Ser Asn Glu Asp Gly Pro Ser Met Gly Asp
220 225 230

gat ggt gag aag aac gat gtt act ttc att gat ttt ctt ggt gtt gga
772

Asp Gly Glu Lys Asn Asp Val Thr Phe Ile Asp Phe Leu Gly Val Gly
235 240 245

tta gct tct tag gttataacat cacaagtcaa agcttttaag gggttctatc
824

Leu Ala Ser
250

attaggggta ggcacatcttt tcagcctttt gcttccttaa actctcatat ggatct
880

<210> 206 <211> 250 <212> PRT <213> Arabidopsis thaliana <400>
206

Met Glu Met Ser Arg Gly Ser Asn Ser Phe Asp Asn Lys Lys Pro Ser
1 5 10 15

Cys Gln Arg Gly His Trp Arg Pro Val Glu Asp Asp Asn Leu Arg Gln
20 25 30

Leu Val Glu Gln Tyr Gly Pro Lys Asn Trp Asn Phe Ile Ala Gln His
35 40 45

Leu Tyr Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Tyr Asn Gln
50 55 60

Leu Asp Pro Asn Ile Thr Lys Lys Pro Phe Thr Glu Glu Glu Glu Glu
65 70 75 80

Arg Leu Leu Lys Ala His Arg Ile Gln Gly Asn Arg Trp Ala Ser Ile
85 90 95

Ala Arg Leu Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Phe
100 105 110

His Val Ile Met Ala Arg Arg Lys Arg Glu Asn Phe Ser Ser Thr Ala
115 120 125

Thr Ser Thr Phe Asn Gln Thr Trp His Thr Val Leu Ser Pro Ser Ser
130 135 140

Ser Leu Thr Arg Leu Asn Arg Ser His Phe Gly Leu Trp Arg Tyr Arg
145 150 155 160

Lys Asp Lys Ser Cys Gly Leu Trp Pro Tyr Ser Phe Val Ser Pro Pro
165 170 175

Thr Asn Gly Gln Phe Gly Ser Ser Ser Val Ser Asn Val His His Glu
180 185 190

Ile Tyr Leu Glu Arg Arg Lys Ser Lys Glu Leu Val Asp Pro Gln Asn
195 200 205

Tyr Thr Phe His Ala Ala Thr Pro Asp His Lys Met Thr Ser Asn Glu
210 215 220

Asp Gly Pro Ser Met Gly Asp Asp Gly Glu Lys Asn Asp Val Thr Phe
225 230 235 240

Ile Asp Phe Leu Gly Val Gly Leu Ala Ser
245 250

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<221> CDS <222> (36)..(959) <223> G1330

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53

Met Gly Asp Lys Gly Arg
1 5

agc tta aag atc aac aag aac atg gag gaa ttc acg aaa gtg gaa gaa
101

Ser Leu Lys Ile Asn Lys Asn Met Glu Glu Phe Thr Lys Val Glu Glu
 10 15 20
 gaa atg gac gta agg aga ggt cca tgg aca gtt gag gaa gat tta gag
 149
 Glu Met Asp Val Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Glu
 25 30 35
 ctc atc aat tac att gct agt cat ggt gaa ggt cga tgg aac tct ctc
 197
 Leu Ile Asn Tyr Ile Ala Ser His Gly Glu Gly Arg Trp Asn Ser Leu
 40 45 50
 gct cgt tgc gcc gaa ctc aaa agg acc gga aaa agc tgc aga ctt cgg
 245
 Ala Arg Cys Ala Glu Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg
 55 60 65 70
 tgg ctg aac tat ctc cga cca gat gtg cgc cgt gga aac ata acc ctc
 293
 Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu
 75 80 85
 gaa gaa caa ctc ttg att ctt gaa ctt cac aca cgt tgg ggc aat aga
 341
 Glu Glu Gln Leu Leu Ile Leu Glu Leu His Thr Arg Trp Gly Asn Arg
 90 95 100
 tgg tct aag att gca caa tat tta cca gga aga acg gat aac gag atc
 389
 Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile
 105 110 115
 aaa aac tat tgg aga aca cgt gtt caa aag cat gca aaa cag ctt aaa
 437
 Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys
 120 125 130
 tgc gac gtg aac agt caa caa ttt aaa gac acc atg aag tat ctt tgg
 485
 Cys Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp
 135 140 145 150
 atg cct cgg ctc gta gaa agg atc caa gcc gcg tcc atc ggg tct gtt
 533
 Met Pro Arg Leu Val Glu Arg Ile Gln Ala Ala Ser Ile Gly Ser Val
 155 160 165
 tcc atg tca tct tgc gtc acc acc tcc tca gat cag ttc gtg atc aac
 581
 Ser Met Ser Ser Cys Val Thr Thr Ser Ser Asp Gln Phe Val Ile Asn
 170 175 180
 aac aac aac acc aac aac gtg gat aat ttg gct tta atg agt aac cct
 629
 Asn Asn Asn Thr Asn Asn Val Asp Asn Leu Ala Leu Met Ser Asn Pro
 185 190 195
 aat ggt tac atc acg ccg gat aat tcc agc gtg gca gta tct cct gta
 677
 Asn Gly Tyr Ile Thr Pro Asp Asn Ser Ser Val Ala Val Ser Pro Val

200 205 210
 tca gat ttg acg gag tgt caa gtg agt agt gaa gtg tgg aag att ggt
 725
 Ser Asp Leu Thr Glu Cys Gln Val Ser Ser Glu Val Trp Lys Ile Gly
 215 220 225 230
 cag gat gag aat ttg gtg gat cca aaa atg aca tcg ccg aat tat atg
 773
 Gln Asp Glu Asn Leu Val Asp Pro Lys Met Thr Ser Pro Asn Tyr Met
 235 240 245
 gat aat agc agt gga cta tta aac gga gat ttt acg aag atg caa gat
 821
 Asp Asn Ser Ser Gly Leu Leu Asn Gly Asp Phe Thr Lys Met Gln Asp
 250 255 260
 caa agt gac ctt aat tgg ttt gaa aat att aat ggg atg gta cca aat
 869
 Gln Ser Asp Leu Asn Trp Phe Glu Asn Ile Asn Gly Met Val Pro Asn
 265 270 275
 tat tcg gac agt ttt tgg aac att gga aat gat gaa gac ttc tgg ctc
 917
 Tyr Ser Asp Ser Phe Trp Asn Ile Gly Asn Asp Glu Asp Phe Trp Leu
 280 285 290
 tta caa caa cat caa caa gtc cac gac aat gga agc ttc tga
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 Leu Gln Gln His Gln Gln Val His Asp Asn Gly Ser Phe
 295 300 305
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 981

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Phe Thr Lys Val Glu Glu Glu Met Asp Val Arg Arg Gly Pro Trp Thr
 20 25 30

Val Glu Glu Asp Leu Glu Leu Ile Asn Tyr Ile Ala Ser His Gly Glu
 35 40 45

Gly Arg Trp Asn Ser Leu Ala Arg Cys Ala Glu Leu Lys Arg Thr Gly
 50 55 60

Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg
 65 70 75 80

Arg Gly Asn Ile Thr Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His
 85 90 95

Thr Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly
 100 105 110

Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys
 115 120 125

His Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Gln Gln Phe Lys Asp
 130 135 140

Thr Met Lys Tyr Leu Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala
 145 150 155 160

Ala Ser Ile Gly Ser Val Ser Met Ser Ser Cys Val Thr Thr Ser Ser
 165 170 175

Asp Gln Phe Val Ile Asn Asn Asn Asn Thr Asn Asn Val Asp Asn Leu
 180 185 190

Ala Leu Met Ser Asn Pro Asn Gly Tyr Ile Thr Pro Asp Asn Ser Ser
 195 200 205

Val Ala Val Ser Pro Val Ser Asp Leu Thr Glu Cys Gln Val Ser Ser
 210 215 220

Glu Val Trp Lys Ile Gly Gln Asp Glu Asn Leu Val Asp Pro Lys Met
 225 230 235 240

Thr Ser Pro Asn Tyr Met Asp Asn Ser Ser Gly Leu Leu Asn Gly Asp
 245 250 255

Phe Thr Lys Met Gln Asp Gln Ser Asp Leu Asn Trp Phe Glu Asn Ile
 260 265 270

Asn Gly Met Val Pro Asn Tyr Ser Asp Ser Phe Trp Asn Ile Gly Asn
 275 280 285

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Gly Ser Phe
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120

atcctcc atg gat cct tct ctc tct gca acc aat gat cct cat cat cct
169

Met Asp Pro Ser Leu Ser Ala Thr Asn Asp Pro His His Pro
1 5 10

cct cct cct cag ttc aca tct ttc cct cct ttc acc aac acc aac ccc
217

Pro Pro Pro Gln Phe Thr Ser Phe Pro Pro Phe Thr Asn Thr Asn Pro
15 20 25 30

ttc gcc tct cca aac cac ccc ttc ttc acc gga ccc acc gcc gtc gcg
265

Phe Ala Ser Pro Asn His Pro Phe Phe Thr Gly Pro Thr Ala Val Ala
35 40 45

ccg cca aac aac atc cat ctc tat caa gca gct cct ccg cag cag cca
313

Pro Pro Asn Asn Ile His Leu Tyr Gln Ala Ala Pro Pro Gln Gln Pro
50 55 60

caa aca tct cca gtt cct cct cat cca tct att tcc cac cct cct tac
361

Gln Thr Ser Pro Val Pro Pro His Pro Ser Ile Ser His Pro Pro Tyr
65 70 75

tct gac atg att tgc acg gcg att gca gcg tta aac gaa cca gat ggg
409

Ser Asp Met Ile Cys Thr Ala Ile Ala Ala Leu Asn Glu Pro Asp Gly
80 85 90

tca agc aag caa gct att tcg agg tac ata gag aga att tac act ggg
457

Ser Ser Lys Gln Ala Ile Ser Arg Tyr Ile Glu Arg Ile Tyr Thr Gly
95 100 105 110

att cct act gct cat gga gct ttg ttg aca cac cat ctc aag act ttg
505

Ile Pro Thr Ala His Gly Ala Leu Leu Thr His His Leu Lys Thr Leu
115 120 125

aag acc agt ggg att ctt gtc atg gtt aag aaa tct tac aag ctt gct
553

Lys Thr Ser Gly Ile Leu Val Met Val Lys Lys Ser Tyr Lys Leu Ala
130 135 140

tct act cct cct cct cct cct act agt gta gct cct agt ctt gaa
601

Ser Thr Pro Pro Pro Pro Pro Pro Thr Ser Val Ala Pro Ser Leu Glu
145 150 155

cct ccc aga tct gat ttc ata gtc aac gag aac caa cct tta cct gat
649

Pro Pro Arg Ser Asp Phe Ile Val Asn Glu Asn Gln Pro Leu Pro Asp
160 165 170

ccg gtt ttg gct tct tct act cct cag act att aaa cgt ggt cgt ggt
 697
 Pro Val Leu Ala Ser Ser Thr Pro Gln Thr Ile Lys Arg Gly Arg Gly
 175 180 185 190

cga cct cca aaa gct aaa cca gat gtt gtt caa cct caa cct ctg act
 745
 Arg Pro Pro Lys Ala Lys Pro Asp Val Val Gln Pro Gln Pro Leu Thr
 195 200 205

aat gga aaa ctc acc tgg gaa cag agt gaa tta cct gtc tct cga cca
 793
 Asn Gly Lys Leu Thr Trp Glu Gln Ser Glu Leu Pro Val Ser Arg Pro
 210 215 220

gag gag ata cag ata cag ccg cca cag tta ccg tta cag cca cag cag
 841
 Glu Glu Ile Gln Ile Gln Pro Pro Gln Leu Pro Leu Gln Pro Gln Gln
 225 230 235

ccg gtt aag aga ccg ccg ggt cgt cct aga aaa gat gga act tcg ccg
 889
 Pro Val Lys Arg Pro Pro Gly Arg Pro Arg Lys Asp Gly Thr Ser Pro
 240 245 250

acg gtg aag cca gct gct tct gtt tcc ggt ggt gtg gag act gtg aaa
 937
 Thr Val Lys Pro Ala Ala Ser Val Ser Gly Gly Val Glu Thr Val Lys
 255 260 265 270

cga aga ggt aga cct ccg agt gga aga gct gct ggg agg gag aga aag
 985
 Arg Arg Gly Arg Pro Pro Ser Gly Arg Ala Ala Gly Arg Glu Arg Lys
 275 280 285

cct ata gta gtc tca gct cca gct tca gtg ttc ccg tat gtt gct aat
 1033
 Pro Ile Val Val Ser Ala Pro Ala Ser Val Phe Pro Tyr Val Ala Asn
 290 295 300

ggt ggt gtt aga cgc cga ggg aga cca aag aga gtt gac gct ggt ggt
 1081
 Gly Gly Val Arg Arg Arg Gly Arg Pro Lys Arg Val Asp Ala Gly Gly
 305 310 315

gct tcc tct gtt gct cca cca cca cca cca cca act aac gta gag agt
 1129
 Ala Ser Ser Val Ala Pro Pro Pro Pro Pro Pro Thr Asn Val Glu Ser
 320 325 330

gga gga gag gag gtt gca gtc aag aaa cga gga aga gga cgg cct cct
 1177
 Gly Gly Glu Glu Val Ala Val Lys Lys Arg Gly Arg Gly Arg Pro Pro
 335 340 345 350

aag att gga ggt gtt atc agg aag cct atg aag ccg atg aga agc ttt
 1225
 Lys Ile Gly Gly Val Ile Arg Lys Pro Met Lys Pro Met Arg Ser Phe
 355 360 365

gct cgt act gga aaa ccc gta gga aga ccc aga aag aat gcg gtg tca
 1273
 Ala Arg Thr Gly Lys Pro Val Gly Arg Pro Arg Lys Asn Ala Val Ser
 370 375 380

gtg gga gct tct gga cga caa gat ggt gac tat gga gaa ctg aag aag
 1321
 Val Gly Ala Ser Gly Arg Gln Asp Gly Asp Tyr Gly Glu Leu Lys Lys
 385 390 395

aag ttt gag ttg ttt caa gcg aga gct aag gat att gta att gtg ttg
 1369
 Lys Phe Glu Leu Phe Gln Ala Arg Ala Lys Asp Ile Val Ile Val Leu
 400 405 410

aaa tcc gag ata gga gga agt gga aat caa gca gtg gtt caa gcc ata
 1417
 Lys Ser Glu Ile Gly Gly Ser Gly Asn Gln Ala Val Val Gln Ala Ile
 415 420 425 430

cag gac ctg gaa ggg ata gca gag aca aca aac gag cca aag cac atg
 1465
 Gln Asp Leu Glu Gly Ile Ala Glu Thr Thr Asn Glu Pro Lys His Met
 435 440 445

gaa gaa gtg cag ctg cca gac gag gaa cac ctt gaa acc gaa cca gaa
 1513
 Glu Glu Val Gln Leu Pro Asp Glu Glu His Leu Glu Thr Glu Pro Glu
 450 455 460

gca gag ggt caa gga cag aca gaa gca gag gca atg caa gaa gct ctg
 1561
 Ala Glu Gly Gln Gly Gln Thr Glu Ala Glu Ala Met Gln Glu Ala Leu
 465 470 475

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 Phe

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 1677

tgtgatgaac tgatgatgat gattgtgtct ctaaccaaac aacaaggaga ggtagggtaa
 1737

tgtctgtaaa gtgaattagg atgttaccat tgttcatgct tcccatctct ctccatcgtc
 1797

catatctgtg taggcagctt tgttctttgt tccctcgtgt tttttttaga ctgttgtgtc
 1857

tcttattcta ttttgtctcc ttaggctttt taggagttgt tgttgatggt tatcaaaaaa
 1917

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 1964

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 20 25 30
 Ser Pro Asn His Pro Phe Phe Thr Gly Pro Thr Ala Val Ala Pro Pro
 35 40 45
 Asn Asn Ile His Leu Tyr Gln Ala Ala Pro Pro Gln Gln Pro Gln Thr
 50 55 60
 Ser Pro Val Pro Pro His Pro Ser Ile Ser His Pro Pro Tyr Ser Asp
 65 70 75 80
 Met Ile Cys Thr Ala Ile Ala Ala Leu Asn Glu Pro Asp Gly Ser Ser
 85 90 95
 Lys Gln Ala Ile Ser Arg Tyr Ile Glu Arg Ile Tyr Thr Gly Ile Pro
 100 105 110
 Thr Ala His Gly Ala Leu Leu Thr His His Leu Lys Thr Leu Lys Thr
 115 120 125
 Ser Gly Ile Leu Val Met Val Lys Lys Ser Tyr Lys Leu Ala Ser Thr
 130 135 140
 Pro Pro Pro Pro Pro Pro Thr Ser Val Ala Pro Ser Leu Glu Pro Pro
 145 150 155 160
 Arg Ser Asp Phe Ile Val Asn Glu Asn Gln Pro Leu Pro Asp Pro Val
 165 170 175
 Leu Ala Ser Ser Thr Pro Gln Thr Ile Lys Arg Gly Arg Gly Arg Pro
 180 185 190
 Pro Lys Ala Lys Pro Asp Val Val Gln Pro Gln Pro Leu Thr Asn Gly
 195 200 205
 Lys Leu Thr Trp Glu Gln Ser Glu Leu Pro Val Ser Arg Pro Glu Glu
 210 215 220
 Ile Gln Ile Gln Pro Pro Gln Leu Pro Leu Gln Pro Gln Gln Pro Val
 225 230 235 240

Lys Arg Pro Pro Gly Arg Pro Arg Lys Asp Gly Thr Ser Pro Thr Val
245 250 255

Lys Pro Ala Ala Ser Val Ser Gly Gly Val Glu Thr Val Lys Arg Arg
260 265 270

Gly Arg Pro Pro Ser Gly Arg Ala Ala Gly Arg Glu Arg Lys Pro Ile
275 280 285

Val Val Ser Ala Pro Ala Ser Val Phe Pro Tyr Val Ala Asn Gly Gly
290 295 300

Val Arg Arg Arg Gly Arg Pro Lys Arg Val Asp Ala Gly Gly Ala Ser
305 310 315 320

Ser Val Ala Pro Pro Pro Pro Pro Pro Thr Asn Val Glu Ser Gly Gly
325 330 335

Glu Glu Val Ala Val Lys Lys Arg Gly Arg Gly Arg Pro Pro Lys Ile
340 345 350

Gly Gly Val Ile Arg Lys Pro Met Lys Pro Met Arg Ser Phe Ala Arg
355 360 365

Thr Gly Lys Pro Val Gly Arg Pro Arg Lys Asn Ala Val Ser Val Gly
370 375 380

Ala Ser Gly Arg Gln Asp Gly Asp Tyr Gly Glu Leu Lys Lys Lys Phe
385 390 395 400

Glu Leu Phe Gln Ala Arg Ala Lys Asp Ile Val Ile Val Leu Lys Ser
405 410 415

Glu Ile Gly Gly Ser Gly Asn Gln Ala Val Val Gln Ala Ile Gln Asp
420 425 430

Leu Glu Gly Ile Ala Glu Thr Thr Asn Glu Pro Lys His Met Glu Glu
435 440 445

Val Gln Leu Pro Asp Glu Glu His Leu Glu Thr Glu Pro Glu Ala Glu
450 455 460

Gly Gln Gly Gln Thr Glu Ala Glu Ala Met Gln Glu Ala Leu Phe
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 120

aaaactcttt atctctgaat cttgagtttc ttgtagaaga agaagcaatt ttgaatcttt
 180

cgtaatcata aagattcgtg gaggatctct actgatttgt cggaatctct cactacagaa
 240

tcacttgatc ttatgtccgg atg gag gag aga gaa gga acc aac atc aac aac
 293

Met Glu Glu Arg Glu Gly Thr Asn Ile Asn Asn
 1 5 10

.aac atc act agc agt ttc ggc ttg aag cag caa cat gaa gct gct gct
 341

Asn Ile Thr Ser Ser Phe Gly Leu Lys Gln Gln His Glu Ala Ala Ala
 15 20 25

tct gat ggt ggt tac tca atg gac cca cca cca aga ccc gaa aac cct
 389

Ser Asp Gly Gly Tyr Ser Met Asp Pro Pro Pro Arg Pro Glu Asn Pro
 30 35 40

aac ccg ttt tta gtc cca ccc act act gtc ccc gcg gcc gcc acc gta
 437

Asn Pro Phe Leu Val Pro Pro Thr Thr Val Pro Ala Ala Ala Thr Val
 45 50 55

gca gca gct gtt act gag aat gcg gct act ccg ttt agc tta aca atg
 485

Ala Ala Ala Val Thr Glu Asn Ala Ala Thr Pro Phe Ser Leu Thr Met
 60 65 70 75

ccg acg gag aac act tca gct gag cag ctg aaa aag aag aga ggt agg
 533

Pro Thr Glu Asn Thr Ser Ala Glu Gln Leu Lys Lys Lys Arg Gly Arg
 80 85 90

ccg aga aag tat aat ccc gat ggg act ctt gtc gtg act tta tcg ccg
 581

Pro Arg Lys Tyr Asn Pro Asp Gly Thr Leu Val Val Thr Leu Ser Pro
 95 100 105

atg cca atc tcg tcc tct gtt ccg ttg acg tcg gag ttt cct cca agg
 629

Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe Pro Pro Arg
 110 115 120

aaa cga gga aga gga cgt ggc aag tct aat cga tgg ctc aag aag tct
 677

Lys Arg Gly Arg Gly Arg Gly Lys Ser Asn Arg Trp Leu Lys Lys Ser
 125 130 135

caa atg ttc caa ttc gat aga agt cct gtt gat acc aat ttg gca ggt
 725
 Gln Met Phe Gln Phe Asp Arg Ser Pro Val Asp Thr Asn Leu Ala Gly
 140 145 150 155

gta gga act gct gat ttt gtt ggt gcc aac ttt aca cct cat gta ctg
 773
 Val Gly Thr Ala Asp Phe Val Gly Ala Asn Phe Thr Pro His Val Leu
 160 165 170

atc gtc aac gcc gga gag gat gtg acg atg aag ata atg aca ttc tct
 821
 Ile Val Asn Ala Gly Glu Asp Val Thr Met Lys Ile Met Thr Phe Ser
 175 180 185

caa caa gga tct cgt gct atc tgc atc ctt tca gct aat ggt ccc atc
 869
 Gln Gln Gly Ser Arg Ala Ile Cys Ile Leu Ser Ala Asn Gly Pro Ile
 190 195 200

tcc aat gtt acg ctt cgt caa tct atg aca tcc ggt ggt act cta act
 917
 Ser Asn Val Thr Leu Arg Gln Ser Met Thr Ser Gly Gly Thr Leu Thr
 205 210 215

tat gag ggt cgt ttt gag att ctc tct ttg acg ggt tcg ttt atg caa
 965
 Tyr Glu Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ser Phe Met Gln
 220 225 230 235

aat gac tct gga gga act cga agt aga gct ggt ggt atg agt gtt tgc
 1013
 Asn Asp Ser Gly Gly Thr Arg Ser Arg Ala Gly Gly Met Ser Val Cys
 240 245 250

ctt gca gga cca gat ggt cgt gtc ttt ggt gga gga ctc gct ggt ctc
 1061
 Leu Ala Gly Pro Asp Gly Arg Val Phe Gly Gly Gly Leu Ala Gly Leu
 255 260 265

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 1109
 Phe Leu Ala Ala Gly Pro Val Gln Val Met Val Gly Thr Phe Ile Ala
 270 275 280

ggt caa gag cag tca cag ctg gag cta gca aaa gaa aga cgg cta aga
 1157
 Gly Gln Glu Gln Ser Gln Leu Glu Leu Ala Lys Glu Arg Arg Leu Arg
 285 290 295

ttt ggg gct caa cca tct tct atc tcc ttt aac ata tcc gca gaa gaa
 1205
 Phe Gly Ala Gln Pro Ser Ser Ile Ser Phe Asn Ile Ser Ala Glu Glu
 300 305 310 315

cgg aag gcg aga ttc gag agg ctt aac aag tct gtt gct att cct gca
 1253
 Arg Lys Ala Arg Phe Glu Arg Leu Asn Lys Ser Val Ala Ile Pro Ala
 320 325 330

cca acc act tca tac acg cat gta aac aca aca aat gcg gtt cac agt
1301

Pro Thr Thr Ser Tyr Thr His Val Asn Thr Thr Asn Ala Val His Ser
335 340 345

tac tat aca aac tcg gtt aac cat gtc aag gat ccc ttc tcg tct atc
1349

Tyr Tyr Thr Asn Ser Val Asn His Val Lys Asp Pro Phe Ser Ser Ile
350 355 360

cca gta gga gga gga gga ggt gga gag gta gga gaa gaa gag ggt gaa
1397

Pro Val Gly Gly Gly Gly Gly Gly Glu Val Gly Glu Glu Glu Gly Glu
365 370 375

gaa gat gat gat gaa tta gaa ggt gaa gac gaa gaa ttc gga ggc gat
1445

Glu Asp Asp Asp Glu Leu Glu Gly Glu Asp Glu Glu Phe Gly Gly Asp
380 385 390 395

agc caa tct gac aac gag att ccg agc tga tgatgatcat acggtttctt
1495

Ser Gln Ser Asp Asn Glu Ile Pro Ser
400

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1555

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1615

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1674

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20 25 30

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35 40 45

Pro Pro Thr Thr Val Pro Ala Ala Ala Thr Val Ala Ala Ala Val Thr
50 55 60

Glu Asn Ala Ala Thr Pro Phe Ser Leu Thr Met Pro Thr Glu Asn Thr
65 70 75 80

Ser Ala Glu Gln Leu Lys Lys Lys Arg Gly Arg Pro Arg Lys Tyr Asn
85 90 95

Pro Asp Gly Thr Leu Val Val Thr Leu Ser Pro Met Pro Ile Ser Ser
 100 105 110

Ser Val Pro Leu Thr Ser Glu Phe Pro Pro Arg Lys Arg Gly Arg Gly
 115 120 125

Arg Gly Lys Ser Asn Arg Trp Leu Lys Lys Ser Gln Met Phe Gln Phe
 130 135 140

Asp Arg Ser Pro Val Asp Thr Asn Leu Ala Gly Val Gly Thr Ala Asp
 145 150 155 160

Phe Val Gly Ala Asn Phe Thr Pro His Val Leu Ile Val Asn Ala Gly
 165 170 175

Glu Asp Val Thr Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg
 180 185 190

Ala Ile Cys Ile Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu
 195 200 205

Arg Gln Ser Met Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly Arg Phe
 210 215 220

Glu Ile Leu Ser Leu Thr Gly Ser Phe Met Gln Asn Asp Ser Gly Gly
 225 230 235 240

Thr Arg Ser Arg Ala Gly Gly Met Ser Val Cys Leu Ala Gly Pro Asp
 245 250 255

Gly Arg Val Phe Gly Gly Gly Leu Ala Gly Leu Phe Leu Ala Ala Gly
 260 265 270

Pro Val Gln Val Met Val Gly Thr Phe Ile Ala Gly Gln Glu Gln Ser
 275 280 285

Gln Leu Glu Leu Ala Lys Glu Arg Arg Leu Arg Phe Gly Ala Gln Pro
 290 295 300

Ser Ser Ile Ser Phe Asn Ile Ser Ala Glu Glu Arg Lys Ala Arg Phe
 305 310 315 320

Glu Arg Leu Asn Lys Ser Val Ala Ile Pro Ala Pro Thr Thr Ser Tyr
 325 330 335

Thr His Val Asn Thr Thr Asn Ala Val His Ser Tyr Tyr Thr Asn Ser
340 345 350

Val Asn His Val Lys Asp Pro Phe Ser Ser Ile Pro Val Gly Gly Gly
355 360 365

Gly Gly Gly Glu Val Gly Glu Glu Glu Gly Glu Glu Asp Asp Asp Glu
370 375 380

Leu Glu Gly Glu Asp Glu Glu Phe Gly Gly Asp Ser Gln Ser Asp Asn
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Glu Ile Pro Ser

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gaagaaaagg ctatatTTTaa aagaaaatca agcaaaaagta gatcctcgg atg tat ggg
118

Met Tyr Gly
1

aag agg cct ttt gga ggt gat gaa tct gaa gaa agg gaa gaa gat gag
166
Lys Arg Pro Phe Gly Gly Asp Glu Ser Glu Glu Arg Glu Glu Asp Glu
5 10 15

aac ttg ttc ccg gtc ttc tcg gcc cga tct caa cac gac atg cgt gtt
214
Asn Leu Phe Pro Val Phe Ser Ala Arg Ser Gln His Asp Met Arg Val
20 25 30 35

atg gtc tcg gcc ttg act caa gta atc gga aac caa caa agc aaa tct
262
Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Gln Ser Lys Ser
40 45 50

cat gat aac atc agc tct att gat gat aac tat cct tct gtg tat aat
310
His Asp Asn Ile Ser Ser Ile Asp Asp Asn Tyr Pro Ser Val Tyr Asn
55 60 65

cca caa gac cct aat caa caa gtt gcg cct act cat caa gac caa ggg
358
Pro Gln Asp Pro Asn Gln Gln Val Ala Pro Thr His Gln Asp Gln Gly
70 75 80

gac ttg agg agg aga cat tat aga ggt gta agg caa agg cca tgg gga
406
Asp Leu Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly
85 90 95

aag tgg gca gct gaa atc cga gac cca aaa aag gcg gca cgt gtg tgg
454
Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp
100 105 110 115
ctc ggg aca ttt gaa acc gct gaa tct gcg gcc tta gct tat gat gaa
502
Leu Gly Thr Phe Glu Thr Ala Glu Ser Ala Ala Leu Ala Tyr Asp Glu
120 125 130
gca gcc cta aag ttc aaa gga agc aaa gca aaa ctc aat ttc ccg gag
550
Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys Leu Asn Phe Pro Glu
135 140 145
agg gtt cag ctt gga agt aac tct aca tat tac tcc tcc aac caa att
598
Arg Val Gln Leu Gly Ser Asn Ser Thr Tyr Tyr Ser Ser Asn Gln Ile
150 155 160
cca caa atg gaa cca caa agt ata ccg aac tat aat caa tac tat cat
646
Pro Gln Met Glu Pro Gln Ser Ile Pro Asn Tyr Asn Gln Tyr Tyr His
165 170 175
gat gcg agt agt ggt gat atg cta agt ttt aat ttg ggc ggt ggg tat
694
Asp Ala Ser Ser Gly Asp Met Leu Ser Phe Asn Leu Gly Gly Gly Tyr
180 185 190 195
ggg agt ggt acc gga tat tca atg tct cat gat aat agt act acg act
742
Gly Ser Gly Thr Gly Tyr Ser Met Ser His Asp Asn Ser Thr Thr Thr
200 205 210
gct gct aca act tct tcg tct tct ggt ggc tct tct agg caa caa gaa
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Ala Ala Thr Thr Ser Ser Ser Ser Gly Gly Ser Ser Arg Gln Gln Glu
215 220 225
gag caa gat tat gcc aga ttc tgg cgc ttt ggg gat tct tct tcc tct
838
Glu Gln Asp Tyr Ala Arg Phe Trp Arg Phe Gly Asp Ser Ser Ser Ser
230 235 240
cct cat tcg gga tat taa ttaggagatt tgatcagtta cttgtgatga
886
Pro His Ser Gly Tyr
245
agtaatgata catttcccggt caaaattgag atgatcatat gcttctgaa tgtttttgag
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1006
aaaaaaaaa aaaaaaaaaa aaaaaaaaa
1034

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20 25 30

Met Arg Val Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Gln
35 40 45

Ser Lys Ser His Asp Asn Ile Ser Ser Ile Asp Asp Asn Tyr Pro Ser
50 55 60

Val Tyr Asn Pro Gln Asp Pro Asn Gln Gln Val Ala Pro Thr His Gln
65 70 75 80

Asp Gln Gly Asp Leu Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg
85 90 95

Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala
100 105 110

Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ser Ala Ala Leu Ala
115 120 125

Tyr Asp Glu Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys Leu Asn
130 135 140

Phe Pro Glu Arg Val Gln Leu Gly Ser Asn Ser Thr Tyr Tyr Ser Ser
145 150 155 160

Asn Gln Ile Pro Gln Met Glu Pro Gln Ser Ile Pro Asn Tyr Asn Gln
165 170 175

Tyr Tyr His Asp Ala Ser Ser Gly Asp Met Leu Ser Phe Asn Leu Gly
180 185 190

Gly Gly Tyr Gly Ser Gly Thr Gly Tyr Ser Met Ser His Asp Asn Ser
195 200 205

Thr Thr Thr Ala Ala Thr Thr Ser Ser Ser Ser Gly Gly Ser Ser Arg
210 215 220

Gln Gln Glu Glu Gln Asp Tyr Ala Arg Phe Trp Arg Phe Gly Asp Ser
225 230 235 240

Ser Ser Ser Pro His Ser Gly Tyr
245

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53
Met Ala Ser Ser His Gln Gln Gln Gln
1 5

gaa caa gac cag tca gct tta gat ctc ata acc caa cac ctt ctt act
101
Glu Gln Asp Gln Ser Ala Leu Asp Leu Ile Thr Gln His Leu Leu Thr
10 15 20 25

gat ttc cct tcc tta gac acc ttt gcc tcc acc atc cac cac tgc acc
149
Asp Phe Pro Ser Leu Asp Thr Phe Ala Ser Thr Ile His His Cys Thr
30 35 40

acc tca act cta agc caa cgc aaa cca cct ctt gcc act ata gca gtt
197
Thr Ser Thr Leu Ser Gln Arg Lys Pro Pro Leu Ala Thr Ile Ala Val
45 50 55

cct act act gca ccg gtg gtt caa gag aat gat caa agg cat tac aga
245
Pro Thr Thr Ala Pro Val Val Gln Glu Asn Asp Gln Arg His Tyr Arg
60 65 70

ggc gtc agg aga aga cca tgg ggt aag tat gcg gct gag atc aga gac
293
Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp
75 80 85

cca aac aag aaa ggt gtt cgt gtc tgg tta ggc act ttt gac aca gcc
341
Pro Asn Lys Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
90 95 100 105

atg gaa gct gca aga ggt tat gac aag gca gct ttt aaa cta cga gga
389
Met Glu Ala Ala Arg Gly Tyr Asp Lys Ala Ala Phe Lys Leu Arg Gly
110 115 120

agc aaa gct att ctt aac ttc cca ctt gaa gca gga aag cat gag gac
437
Ser Lys Ala Ile Leu Asn Phe Pro Leu Glu Ala Gly Lys His Glu Asp
125 130 135

ttg gga gac aac aag aag act att tct tta aaa gca aag agg aag aga
485
Leu Gly Asp Asn Lys Lys Thr Ile Ser Leu Lys Ala Lys Arg Lys Arg
140 145 150

cag gtg acg gag gat gaa agc cag ctg atc agc cgt aaa gct gtt aag
533

Gln Val Thr Glu Asp Glu Ser Gln Leu Ile Ser Arg Lys Ala Val Lys
155 160 165

agg gaa gaa gct cag gtt cag gct gat gct tgt cca tta acg cca tca
581

Arg Glu Glu Ala Gln Val Gln Ala Asp Ala Cys Pro Leu Thr Pro Ser
170 175 180 185

agt tgg aag ggg ttt tgg gac gga gca gac agt aaa gac atg gga ata
629

Ser Trp Lys Gly Phe Trp Asp Gly Ala Asp Ser Lys Asp Met Gly Ile
190 195 200

ttt tcc gtg cct ctg tta tct cct tgt cca tct ctt gga cac tct caa
677

Phe Ser Val Pro Leu Leu Ser Pro Cys Pro Ser Leu Gly His Ser Gln
205 210 215

ctc gta gtt act taa gcttcagagg gtcaaactgg aaaaaatcaa cattggattg
732

Leu Val Val Thr
220

ttttcaaagc ttctagatta gctgattgta aaaaaatggt ttactatatt cattcattct
792

tcctaaatgc aattctttct acccttcc
820

<210> 216 <211> 221 <212> PRT <213> Arabidopsis thaliana <400>
216

Met Ala Ser Ser His Gln Gln Gln Gln Glu Gln Asp Gln Ser Ala Leu
1 5 10 15

Asp Leu Ile Thr Gln His Leu Leu Thr Asp Phe Pro Ser Leu Asp Thr
20 25 30

Phe Ala Ser Thr Ile His His Cys Thr Thr Ser Thr Leu Ser Gln Arg
35 40 45

Lys Pro Pro Leu Ala Thr Ile Ala Val Pro Thr Thr Ala Pro Val Val
50 55 60

Gln Glu Asn Asp Gln Arg His Tyr Arg Gly Val Arg Arg Arg Pro Trp
65 70 75 80

Gly Lys Tyr Ala Ala Glu Ile Arg Asp Pro Asn Lys Lys Gly Val Arg
85 90 95

Val Trp Leu Gly Thr Phe Asp Thr Ala Met Glu Ala Ala Arg Gly Tyr
100 105 110

385

Asp Lys Ala Ala Phe Lys Leu Arg Gly Ser Lys Ala Ile Leu Asn Phe
 115 120 125

Pro Leu Glu Ala Gly Lys His Glu Asp Leu Gly Asp Asn Lys Lys Thr
 130 135 140

Ile Ser Leu Lys Ala Lys Arg Lys Arg Gln Val Thr Glu Asp Glu Ser
 145 150 155 160

Gln Leu Ile Ser Arg Lys Ala Val Lys Arg Glu Glu Ala Gln Val Gln
 165 170 175

Ala Asp Ala Cys Pro Leu Thr Pro Ser Ser Trp Lys Gly Phe Trp Asp
 180 185 190

Gly Ala Asp Ser Lys Asp Met Gly Ile Phe Ser Val Pro Leu Leu Ser
 195 200 205

Pro Cys Pro Ser Leu Gly His Ser Gln Leu Val Val Thr
 210 215 220

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ctcttgattc cataagcata tattaaaaaa gctctctgct ttcttcaact ttcccgggaa
 120

aatcttcttg ttacaaagca tcaatctctt gttttaccaa ttttctctct ttattccttt
 180

tttgcccttt acttttccta acttttgtct ttatatataa acacacgaca caaagaagaa
 240

cacacataag ttaaaactat tacaacagtt ttaaagagag agatttaaaa a atg gag
 297

Met Glu
 1

aca gag aag aaa gtt tct ctc cca aga atc tta cga atc tct gtt act
 345

Thr Glu Lys Lys Val Ser Leu Pro Arg Ile Leu Arg Ile Ser Val Thr
 5 10 15

gat cct tac gca aca gat tcg tca agc gac gaa gaa gaa gaa gtt gat
 393

Asp Pro Tyr Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Glu Val Asp
 20 25 30

ttt gat gca tta tct aca aaa cga cgt cgt gtt aag aag tac gtg aag
 441
 Phe Asp Ala Leu Ser Thr Lys Arg Arg Arg Val Lys Lys Tyr Val Lys
 35 40 45 50
 gaa gtg gtg ctt gat tcg gtg gtt tct gat aaa gag aag ccg atg aag
 489
 Glu Val Val Leu Asp Ser Val Val Ser Asp Lys Glu Lys Pro Met Lys
 55 60 65
 aag aag aga aag aag cgc gtt gtt act gtt cca gtg gtt gtt acg acg
 537
 Lys Lys Arg Lys Lys Arg Val Val Thr Val Pro Val Val Val Thr Thr
 70 75 80
 gcg acg agg aag ttt cgt gga gtg agg caa aga ccg tgg gga aaa tgg
 585
 Ala Thr Arg Lys Phe Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp
 85 90 95
 gcg gcg gag att aga gat ccg agt aga cgt gtt agg gtt tgg tta ggt
 633
 Ala Ala Glu Ile Arg Asp Pro Ser Arg Arg Val Arg Val Trp Leu Gly
 100 105 110
 act ttt gac acg gcg gag gaa gct gcc att gtt tac gat aac gca gct
 681
 Thr Phe Asp Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn Ala Ala
 115 120 125 130
 att cag cta cgt ggt cct aac gca gag ctt aac ttc cct cct cct ccg
 729
 Ile Gln Leu Arg Gly Pro Asn Ala Glu Leu Asn Phe Pro Pro Pro Pro
 135 140 145
 gtg acg gag aat gtt gaa gaa gct tcg acg gag gtg aaa gga gtt tcg
 777
 Val Thr Glu Asn Val Glu Glu Ala Ser Thr Glu Val Lys Gly Val Ser
 150 155 160
 gat ttt atc att ggc ggt gga gaa tgt ctt cgt tcg ccg gtt tct gtt
 825
 Asp Phe Ile Ile Gly Gly Gly Glu Cys Leu Arg Ser Pro Val Ser Val
 165 170 175
 ctc gaa tct ccg ttc tcc ggc gag tct act gcg gtt aaa gag gag ttt
 873
 Leu Glu Ser Pro Phe Ser Gly Glu Ser Thr Ala Val Lys Glu Glu Phe
 180 185 190
 gtc ggt gta tcg acg gcg gag att gtg gtt aaa aag gag ccg tct ttt
 921
 Val Gly Val Ser Thr Ala Glu Ile Val Val Lys Lys Glu Pro Ser Phe
 195 200 205 210
 aac ggt tca gat ttc tcg gcg ccg ttg ttc tcg gac gac gac gtt ttt
 969
 Asn Gly Ser Asp Phe Ser Ala Pro Leu Phe Ser Asp Asp Asp Val Phe
 215 220 225

ggt ttc tcg acg tcg atg agt gaa agt ttc ggc ggc gat tta ttt gga
1017

Gly Phe Ser Thr Ser Met Ser Glu Ser Phe Gly Gly Asp Leu Phe Gly
230 235 240

gat aat ctt ttt gcg gat atg agt ttt gga tcc ggg ttt gga ttc ggg
1065

Asp Asn Leu Phe Ala Asp Met Ser Phe Gly Ser Gly Phe Gly Phe Gly
245 250 255

tct ggg tct gga ttc tcc agc tgg cac gtt gag gac cat ttt caa gat
1113

Ser Gly Ser Gly Phe Ser Ser Trp His Val Glu Asp His Phe Gln Asp
260 265 270

att ggg gat tta ttc ggg tcg gat cct gtc tta act gtt taa
1155

Ile Gly Asp Leu Phe Gly Ser Asp Pro Val Leu Thr Val
275 280 285

gaaataactg gccgtttaac ggcgttttagt gaagttttgt taccggcgac ggcgaggatt
1215

aaaaaaaaac ggcgatttat tttttgaatg aagatttggt aaata
1260

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218

Met Glu Thr Glu Lys Lys Val Ser Leu Pro Arg Ile Leu Arg Ile Ser
1 5 10 15

Val Thr Asp Pro Tyr Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Glu
20 25 30

Val Asp Phe Asp Ala Leu Ser Thr Lys Arg Arg Arg Val Lys Lys Tyr
35 40 45

Val Lys Glu Val Val Leu Asp Ser Val Val Ser Asp Lys Glu Lys Pro
50 55 60

Met Lys Lys Lys Arg Lys Lys Arg Val Val Thr Val Pro Val Val Val
65 70 75 80

Thr Thr Ala Thr Arg Lys Phe Arg Gly Val Arg Gln Arg Pro Trp Gly
85 90 95

Lys Trp Ala Ala Glu Ile Arg Asp Pro Ser Arg Arg Val Arg Val Trp
100 105 110

Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn
115 120 125

Ala Ala Ile Gln Leu Arg Gly Pro Asn Ala Glu Leu Asn Phe Pro Pro
 130 135 140

Pro Pro Val Thr Glu Asn Val Glu Glu Ala Ser Thr Glu Val Lys Gly
 145 150 155 160

Val Ser Asp Phe Ile Ile Gly Gly Gly Glu Cys Leu Arg Ser Pro Val
 165 170 175

Ser Val Leu Glu Ser Pro Phe Ser Gly Glu Ser Thr Ala Val Lys Glu
 180 185 190

Glu Phe Val Gly Val Ser Thr Ala Glu Ile Val Val Lys Lys Glu Pro
 195 200 205

Ser Phe Asn Gly Ser Asp Phe Ser Ala Pro Leu Phe Ser Asp Asp Asp
 210 215 220

Val Phe Gly Phe Ser Thr Ser Met Ser Glu Ser Phe Gly Gly Asp Leu
 225 230 235 240

Phe Gly Asp Asn Leu Phe Ala Asp Met Ser Phe Gly Ser Gly Phe Gly
 245 250 255

Phe Gly Ser Gly Ser Gly Phe Ser Ser Trp His Val Glu Asp His Phe
 260 265 270

Gln Asp Ile Gly Asp Leu Phe Gly Ser Asp Pro Val Leu Thr Val
 275 280 285

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 49

Met Gly Lys Glu Val Met Val Ser Asp Tyr Gly Asp Asp Asp
 1 5 10

gga gaa gac gcc ggc ggc ggc gat gaa tat agg att ccg gaa tgg gaa
 97

Gly Glu Asp Ala Gly Gly Gly Asp Glu Tyr Arg Ile Pro Glu Trp Glu
 15 20 25 30

att ggt tta ccc aac gga gat gat ttg act ccg tta tct caa tat cta
 145

Ile Gly Leu Pro Asn Gly Asp Asp Leu Thr Pro Leu Ser Gln Tyr Leu
 35 40 45

gtc ccg tcg att ctc gcg tta gct ttc agc atg atc cca gaa cga agc
 193
 Val Pro Ser Ile Leu Ala Leu Ala Phe Ser Met Ile Pro Glu Arg Ser
 50 55 60

cgt aca att cac gac gtc aat cgc gcg tcg caa atc acg ctc tct tcg
 241
 Arg Thr Ile His Asp Val Asn Arg Ala Ser Gln Ile Thr Leu Ser Ser
 65 70 75

ttg aga agc agt acc aat gct tcg tct gtg atg gag gag gtc gtg gat
 289
 Leu Arg Ser Ser Thr Asn Ala Ser Ser Val Met Glu Glu Val Val Asp
 80 85 90

cga gtt gaa tcg agt gtt cca gga tca gat ccg aag aaa cag aag aaa
 337
 Arg Val Glu Ser Ser Val Pro Gly Ser Asp Pro Lys Lys Gln Lys Lys
 95 100 105 110

tcg gat ggt ggt gaa gca gcg gcg gtg gag gat tcc acg gcg gag gaa
 385
 Ser Asp Gly Gly Glu Ala Ala Ala Val Glu Asp Ser Thr Ala Glu Glu
 115 120 125

gga gac tcc ggg cct gaa gac gcg tct ggg aag aca tcg aaa cga ccg
 433
 Gly Asp Ser Gly Pro Glu Asp Ala Ser Gly Lys Thr Ser Lys Arg Pro
 130 135 140

cgt tta gtg tgg aca ccg cag cta cac aag aga ttt gtg gac gtt gtg
 481
 Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val Val
 145 150 155

gct cat cta ggg att aaa aac gca gtg ccg aag acg att atg cag ctg
 529
 Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln Leu
 160 165 170

atg aac gtg gaa gga ctt act cgt gag aac gtt gcg tct cat ttg cag
 577
 Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu Gln
 175 180 185 190

aaa tat agg ctt tac ctt aaa cgg att caa gga ttg acg acg gaa gaa
 625
 Lys Tyr Arg Leu Tyr Leu Lys Arg Ile Gln Gly Leu Thr Thr Glu Glu
 195 200 205

gat cct tat tcg tcg tcg gat cag ctc ttc tct tca acg ccg gtt cct
 673
 Asp Pro Tyr Ser Ser Ser Asp Gln Leu Phe Ser Ser Thr Pro Val Pro
 210 215 220

cca cag agc ttt caa gac ggc gga gga agt aac gga aag ttg ggg gtt
 721
 Pro Gln Ser Phe Gln Asp Gly Gly Gly Ser Asn Gly Lys Leu Gly Val
 225 230 235

ccg gtt ccg gtt ccg tcg atg gtg cct att cca ggc tat ggg aat caa
769

Pro Val Pro Val Pro Ser Met Val Pro Ile Pro Gly Tyr Gly Asn Gln
240 245 250

atg ggt atg caa gga tat tat caa cag tat agt aac cat ggc aat gaa
817

Met Gly Met Gln Gly Tyr Tyr Gln Gln Tyr Ser Asn His Gly Asn Glu
255 260 265 270

tca aac caa tat atg atg cag cag aat aag ttt gga aca atg gtg aca
865

Ser Asn Gln Tyr Met Met Gln Gln Asn Lys Phe Gly Thr Met Val Thr
275 280 285

tat cct tct gtt ggt ggt ggt gac gtg aat gac aag taa atggatctta
914

Tyr Pro Ser Val Gly Gly Gly Asp Val Asn Asp Lys
290 295

aaggctctata atttgctcta cagagagata ctgggtcttg gcttatgggtt tattttccca
974

cttcatgagg ttgtgtgac ttttaattct ccatgttttc cacacaagtc ttattgcct
1034

ttgtatagaa aatgatttcg agaaaatcac tgggaagcct ggtattgttg gaggatgaag
1094

ccttctatga atgatttagt ttctactgt ctccattctt tatgaggtaa taaagccttc
1154

ttttgctcat cgctttagt cttcttaaata tcaagacagc gtcacatgtt tgttcggtta
1214

tgtaattgt ttctttcttt ggataatgaa gatagcatca ggtctcatgt ctctcactt
1274

tgataaa
1281

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220

Met Gly Lys Glu Val Met Val Ser Asp Tyr Gly Asp Asp Asp Gly Glu
1 5 10 15

Asp Ala Gly Gly Gly Asp Glu Tyr Arg Ile Pro Glu Trp Glu Ile Gly
20 25 30

Leu Pro Asn Gly Asp Asp Leu Thr Pro Leu Ser Gln Tyr Leu Val Pro
35 40 45

Ser Ile Leu Ala Leu Ala Phe Ser Met Ile Pro Glu Arg Ser Arg Thr
50 55 60

Ile His Asp Val Asn Arg Ala Ser Gln Ile Thr Leu Ser Ser Leu Arg
 65 70 75 80

Ser Ser Thr Asn Ala Ser Ser Val Met Glu Glu Val Val Asp Arg Val
 85 90 95

Glu Ser Ser Val Pro Gly Ser Asp Pro Lys Lys Gln Lys Lys Ser Asp
 100 105 110

Gly Gly Glu Ala Ala Ala Val Glu Asp Ser Thr Ala Glu Glu Gly Asp
 115 120 125

Ser Gly Pro Glu Asp Ala Ser Gly Lys Thr Ser Lys Arg Pro Arg Leu
 130 135 140

Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val Val Ala His
 145 150 155 160

Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln Leu Met Asn
 165 170 175

Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu Gln Lys Tyr
 180 185 190

Arg Leu Tyr Leu Lys Arg Ile Gln Gly Leu Thr Thr Glu Glu Asp Pro
 195 200 205

Tyr Ser Ser Ser Asp Gln Leu Phe Ser Ser Thr Pro Val Pro Pro Gln
 210 215 220

Ser Phe Gln Asp Gly Gly Gly Ser Asn Gly Lys Leu Gly Val Pro Val
 225 230 235 240

Pro Val Pro Ser Met Val Pro Ile Pro Gly Tyr Gly Asn Gln Met Gly
 245 250 255

Met Gln Gly Tyr Tyr Gln Gln Tyr Ser Asn His Gly Asn Glu Ser Asn
 260 265 270

Gln Tyr Met Met Gln Gln Asn Lys Phe Gly Thr Met Val Thr Tyr Pro
 275 280 285

Ser Val Gly Gly Gly Asp Val Asn Asp Lys
 290 295

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 <221> CDS <222> (105)..(581) <223> G1449

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agaaggaagc atgaagctag ctctgcagct tcaagggtctc atta atg gag gtc tct
 116

Met Glu Val Ser
 1

aac tct tgt tct tca ttt tct tca tcc tct gtc gac agt act aaa cct
 164

Asn Ser Cys Ser Ser Phe Ser Ser Ser Ser Val Asp Ser Thr Lys Pro
 5 10 15 20

tct cct tct gaa tct tct gtt aat ctc tcc ctt agt ctc aca ttt cct
 212

Ser Pro Ser Glu Ser Ser Val Asn Leu Ser Leu Ser Leu Thr Phe Pro
 25 30 35

tct act tct cca caa aga gaa gca aga caa gat tgg cca ccg ata aag
 260

Ser Thr Ser Pro Gln Arg Glu Ala Arg Gln Asp Trp Pro Pro Ile Lys
 40 45 50

tct aga tta aga gat aca cta aag ggt cgt cgt ctt ctt cgt cgt ggt
 308

Ser Arg Leu Arg Asp Thr Leu Lys Gly Arg Arg Leu Leu Arg Arg Gly
 55 60 65

gat gac act tct ctc ttt gtt aag gtt tat atg gaa ggt gtt ccc att
 356

Asp Asp Thr Ser Leu Phe Val Lys Val Tyr Met Glu Gly Val Pro Ile
 70 75 80

gga aga aaa ctc gac ctt tgc gta ttc tca ggc tac gag agt cta tta
 404

Gly Arg Lys Leu Asp Leu Cys Val Phe Ser Gly Tyr Glu Ser Leu Leu
 85 90 95 100

gaa aat ctc tct cac atg ttc gat act tca atc atc tgc ggt aat cga
 452

Glu Asn Leu Ser His Met Phe Asp Thr Ser Ile Ile Cys Gly Asn Arg
 105 110 115

gat cga aaa cat cat gtt ttg aca tat gaa gac aag gat gga gat tgg
 500

Asp Arg Lys His His Val Leu Thr Tyr Glu Asp Lys Asp Gly Asp Trp
 120 125 130

atg atg gtc gga gat att cca tgg gat atg ttt ctt gaa acc gtg aga
 548

Met Met Val Gly Asp Ile Pro Trp Asp Met Phe Leu Glu Thr Val Arg
 135 140 145

aga cta aag atc acg aga ccg gag agg tat taa aacttggatc ggtcaaggct
 601

Arg Leu Lys Ile Thr Arg Pro Glu Arg Tyr
 150 155

gtgattgcgc agttacgaga cgtgtaagat ttaggcattg atgaagagac ttgaggcggg
661

acggagctat tgctgcatat tgcaacaaaag gccttgaaga agttggagaa ttgattgatg
721

catatatatta tttatatgac acctttgagt gtgttttttc ttataaataa atcacaatat
781

ccaagacttc tctttaaa
799

<210> 222 <211> 158 <212> PRT <213> Arabidopsis thaliana <400>
222

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1 5 10 15

Ser Thr Lys Pro Ser Pro Ser Glu Ser Ser Val Asn Leu Ser Leu Ser
20 25 30

Leu Thr Phe Pro Ser Thr Ser Pro Gln Arg Glu Ala Arg Gln Asp Trp
35 40 45

Pro Pro Ile Lys Ser Arg Leu Arg Asp Thr Leu Lys Gly Arg Arg Leu
50 55 60

Leu Arg Arg Gly Asp Asp Thr Ser Leu Phe Val Lys Val Tyr Met Glu
65 70 75 80

Gly Val Pro Ile Gly Arg Lys Leu Asp Leu Cys Val Phe Ser Gly Tyr
85 90 95

Glu Ser Leu Leu Glu Asn Leu Ser His Met Phe Asp Thr Ser Ile Ile
100 105 110

Cys Gly Asn Arg Asp Arg Lys His His Val Leu Thr Tyr Glu Asp Lys
115 120 125

Asp Gly Asp Trp Met Met Val Gly Asp Ile Pro Trp Asp Met Phe Leu
130 135 140

Glu Thr Val Arg Arg Leu Lys Ile Thr Arg Pro Glu Arg Tyr
145 150 155

<210> 223 <211> 1424 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (114)..(1406) <223> G1494

<400> 223

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60

cttctcttcc aacttctgat tcgtccagaa gctttcctaa tctgagatct gac atg
116

Met
1

gaa cac caa ggt tgg agt ttt gag gag aat tat agt ttg tcc act aat
164
Glu His Gln Gly Trp Ser Phe Glu Glu Asn Tyr Ser Leu Ser Thr Asn
5 10 15

aga aga tct atc agg cca caa gat gaa cta gtg gag tta tta tgg cga
212
Arg Arg Ser Ile Arg Pro Gln Asp Glu Leu Val Glu Leu Leu Trp Arg
20 25 30

gat gga caa gtg gtt ctg cag agc caa act cat aga gaa caa acc caa
260
Asp Gly Gln Val Val Leu Gln Ser Gln Thr His Arg Glu Gln Thr Gln
35 40 45

acc cag aaa caa gat cat cat gaa gaa gcc cta aga tcc agc acc ttt
308
Thr Gln Lys Gln Asp His His Glu Glu Ala Leu Arg Ser Ser Thr Phe
50 55 60 65

ctt gaa gat caa gaa act gtc tct tgg atc caa tac cct cca gat gaa
356
Leu Glu Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro Asp Glu
70 75 80

gac cca ttc gaa ccc gac gac ttc tcc tcc cac ttc ttc tca acc atg
404
Asp Pro Phe Glu Pro Asp Asp Phe Ser Ser His Phe Phe Ser Thr Met
85 90 95

gat ccc ctc cag aga cca acc tca gag acg gtt aag cct aag tcc agt
452
Asp Pro Leu Gln Arg Pro Thr Ser Glu Thr Val Lys Pro Lys Ser Ser
100 105 110

cct gaa cct cct caa gtc atg gtt aag cct aag gcc tgt cct gac cct
500
Pro Glu Pro Pro Gln Val Met Val Lys Pro Lys Ala Cys Pro Asp Pro
115 120 125

cct cct caa gtc atg cct cct cca aaa ttt agy tta aca aat tca tca
548
Pro Pro Gln Val Met Pro Pro Pro Lys Phe Arg Leu Thr Asn Ser Ser
130 135 140 145

tcg ggg att agg gaa aca gaa atg gaa cag tac tcg gta acg acc gtt
596
Ser Gly Ile Arg Glu Thr Glu Met Glu Gln Tyr Ser Val Thr Thr Val
150 155 160

gga cct agc cat tgc gga agc aac cca tca cag aac gat ctc gat gtc
644
Gly Pro Ser His Cys Gly Ser Asn Pro Ser Gln Asn Asp Leu Asp Val

165	170	175
tca atg agt cat gat cga agc aaa aac ata gaa gaa aag ctt aat ccg		
692		
Ser Met Ser His Asp Arg Ser Lys Asn Ile Glu Glu Lys Leu Asn Pro		
180	185	190
aac gca agt tcc tca tca ggt ggc tcc tct ggt tgc agc ttt ggc aaa		
740		
Asn Ala Ser Ser Ser Ser Gly Gly Ser Ser Gly Cys Ser Phe Gly Lys		
195	200	205
gat atc aaa gaa atg gct agt gga aga tgc atc aca acc gac cgt aag		
788		
Asp Ile Lys Glu Met Ala Ser Gly Arg Cys Ile Thr Thr Asp Arg Lys		
210	215	220 225
aga aaa cgt ata aat cac act gac gaa tct gta tct cta tca gat gca		
836		
Arg Lys Arg Ile Asn His Thr Asp Glu Ser Val Ser Leu Ser Asp Ala		
	230 235	240
atc ggt aac aag tcg aac caa cga tca gga tca aac cga agg agt cga		
884		
Ile Gly Asn Lys Ser Asn Gln Arg Ser Gly Ser Asn Arg Arg Ser Arg		
	245 250	255
gca gct gaa gtt cat aat ctc tcc gaa agg agg agg aga gat agg atc		
932		
Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg Ile		
	260 265	270
aat gag aga atg aag gct ttg caa gaa cta ata cct cac tgc agt aaa		
980		
Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser Lys		
	275 280	285
act gat aaa gct tcg att tta gac gaa gcc ata gat tat ttg aaa tca		
1028		
Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys Ser		
290	295	300 305
ctt cag tta cag ctt caa gtg atg tgg atg ggg agt gga atg gcg gcg		
1076		
Leu Gln Leu Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala Ala		
	310 315	320
gcg gcg gct tcg gct ccg atg atg ttc ccc gga gtt caa cct cag cag		
1124		
Ala Ala Ala Ser Ala Pro Met Met Phe Pro Gly Val Gln Pro Gln Gln		
	325 330	335
ttc ata cgt cag ata cag agc ccg gta cag tta cct cga ttt ccg gtt		
1172		
Phe Ile Arg Gln Ile Gln Ser Pro Val Gln Leu Pro Arg Phe Pro Val		
	340 345	350
atg gat cag tct gca att cag aac aat ccc ggt tta gtt tgc caa aac		
1220		
Met Asp Gln Ser Ala Ile Gln Asn Asn Pro Gly Leu Val Cys Gln Asn		
	355 360	365

ccg gta caa aac cag atc atc tcc gac cgg ttt gct aga tac atc ggt
1268

Pro Val Gln Asn Gln Ile Ile Ser Asp Arg Phe Ala Arg Tyr Ile Gly
370 375 380 385

ggg ttc cca cac atg cag gcc gcg act cag atg cag ccg atg gag atg
1316

Gly Phe Pro His Met Gln Ala Ala Thr Gln Met Gln Pro Met Glu Met
390 395 400

ttg aga ttt agt tca ccg gcg gga cag caa agt caa caa ccg tcg tct
1364

Leu Arg Phe Ser Ser Pro Ala Gly Gln Gln Ser Gln Gln Pro Ser Ser
405 410 415

gtg ccg acg aag acc acc gac ggt tct cgt ttg gac cac tag
1406

Val Pro Thr Lys Thr Thr Asp Gly Ser Arg Leu Asp His
420 425 430

gttggtgagc cactttgc
1424

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224

Met Glu His Gln Gly Trp Ser Phe Glu Glu Asn Tyr Ser Leu Ser Thr
1 5 10 15

Asn Arg Arg Ser Ile Arg Pro Gln Asp Glu Leu Val Glu Leu Leu Trp
20 25 30

Arg Asp Gly Gln Val Val Leu Gln Ser Gln Thr His Arg Glu Gln Thr
35 40 45

Gln Thr Gln Lys Gln Asp His His Glu Glu Ala Leu Arg Ser Ser Thr
50 55 60

Phe Leu Glu Asp Gln Glu Thr Val Ser Trp Ile Gln Tyr Pro Pro Asp
65 70 75 80

Glu Asp Pro Phe Glu Pro Asp Asp Phe Ser Ser His Phe Phe Ser Thr
85 90 95

Met Asp Pro Leu Gln Arg Pro Thr Ser Glu Thr Val Lys Pro Lys Ser
100 105 110

Ser Pro Glu Pro Pro Gln Val Met Val Lys Pro Lys Ala Cys Pro Asp
115 120 125

Pro Pro Pro Gln Val Met Pro Pro Pro Lys Phe Arg Leu Thr Asn Ser

130 135 140
 Ser Ser Gly Ile Arg Glu Thr Glu Met Glu Gln Tyr Ser Val Thr Thr
 145 150 155 160
 Val Gly Pro Ser His Cys Gly Ser Asn Pro Ser Gln Asn Asp Leu Asp
 165 170 175
 Val Ser Met Ser His Asp Arg Ser Lys Asn Ile Glu Glu Lys Leu Asn
 180 185 190
 Pro Asn Ala Ser Ser Ser Ser Gly Gly Ser Ser Gly Cys Ser Phe Gly
 195 200 205
 Lys Asp Ile Lys Glu Met Ala Ser Gly Arg Cys Ile Thr Thr Asp Arg
 210 215 220
 Lys Arg Lys Arg Ile Asn His Thr Asp Glu Ser Val Ser Leu Ser Asp
 225 230 235 240
 Ala Ile Gly Asn Lys Ser Asn Gln Arg Ser Gly Ser Asn Arg Arg Ser
 245 250 255
 Arg Ala Ala Glu Val His Asn Leu Ser Glu Arg Arg Arg Arg Asp Arg
 260 265 270
 Ile Asn Glu Arg Met Lys Ala Leu Gln Glu Leu Ile Pro His Cys Ser
 275 280 285
 Lys Thr Asp Lys Ala Ser Ile Leu Asp Glu Ala Ile Asp Tyr Leu Lys
 290 295 300
 Ser Leu Gln Leu Gln Leu Gln Val Met Trp Met Gly Ser Gly Met Ala
 305 310 315 320
 Ala Ala Ala Ala Ser Ala Pro Met Met Phe Pro Gly Val Gln Pro Gln
 325 330 335
 Gln Phe Ile Arg Gln Ile Gln Ser Pro Val Gln Leu Pro Arg Phe Pro
 340 345 350
 Val Met Asp Gln Ser Ala Ile Gln Asn Asn Pro Gly Leu Val Cys Gln
 355 360 365
 Asn Pro Val Gln Asn Gln Ile Ile Ser Asp Arg Phe Ala Arg Tyr Ile
 370 375 380

Gly Gly Phe Pro His Met Gln Ala Ala Thr Gln Met Gln Pro Met Glu
385 390 395 400

Met Leu Arg Phe Ser Ser Pro Ala Gly Gln Gln Ser Gln Gln Pro Ser
405 410 415

Ser Val Pro Thr Lys Thr Thr Asp Gly Ser Arg Leu Asp His
420 425 430

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60

actttttggtc tcactttaaa agatcataag ttgaaagatt tctgcagaga acaat atg
118

Met
1

ttg gaa ggt ctt gtc tct caa gaa agc ttg tcc tta aac tct atg gac
166
Leu Glu Gly Leu Val Ser Gln Glu Ser Leu Ser Leu Asn Ser Met Asp
5 10 15

atg tct gta ctt gaa agg ctt aaa tgg gta caa cag caa caa cag caa
214
Met Ser Val Leu Glu Arg Leu Lys Trp Val Gln Gln Gln Gln Gln Gln
20 25 30

ctg caa caa gtt gtg tcc cat agc agt aat aat tca cct gaa ctt ctt
262
Leu Gln Gln Val Val Ser His Ser Ser Asn Asn Ser Pro Glu Leu Leu
35 40 45

cag ata ctt cag ttc cat gga agc aac aat gat gag ttg ttg gag agt
310
Gln Ile Leu Gln Phe His Gly Ser Asn Asn Asp Glu Leu Leu Glu Ser
50 55 60 65

agt ttc agc caa ttt caa atg ctt gga tct ggt ttt gga cca aac tat
358
Ser Phe Ser Gln Phe Gln Met Leu Gly Ser Gly Phe Gly Pro Asn Tyr
70 75 80

aac atg ggt ttt ggt cct cca cat gaa tcc att tca aga aca agt agc
406
Asn Met Gly Phe Gly Pro Pro His Glu Ser Ile Ser Arg Thr Ser Ser
85 90 95

tgc cat atg gaa cct gtg gat aca atg gag gtt ttg ttg aag acc ggt
454
Cys His Met Glu Pro Val Asp Thr Met Glu Val Leu Leu Lys Thr Gly
100 105 110

gaa gaa acc aga gcc gtt gcc ttg aag aac aag aga aaa cca gag gtt
 502
 Glu Glu Thr Arg Ala Val Ala Leu Lys Asn Lys Arg Lys Pro Glu Val
 115 120 125
 aag aca agg gaa gag caa aag aca gag aag aag atc aaa gta gag gct
 550
 Lys Thr Arg Glu Glu Gln Lys Thr Glu Lys Lys Ile Lys Val Glu Ala
 130 135 140 145
 gag aca gag tca agc atg aaa gga aaa tca aac atg gga aac act gaa
 598
 Glu Thr Glu Ser Ser Met Lys Gly Lys Ser Asn Met Gly Asn Thr Glu
 150 155 160
 gca tct tca gac act tca aag gag aca tcg aaa gga gct tca gag aat
 646
 Ala Ser Ser Asp Thr Ser Lys Glu Thr Ser Lys Gly Ala Ser Glu Asn
 165 170 175
 cag aaa tta gat tat atc cac gtg aga gct cgt cga ggc caa gcc act
 694
 Gln Lys Leu Asp Tyr Ile His Val Arg Ala Arg Arg Gly Gln Ala Thr
 180 185 190
 gac aga cac agc tta gca gaa agg gcg aga aga gaa aag atc agc aag
 742
 Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys
 195 200 205
 aaa atg aaa tat ctg caa gat att gtg cct gga tgc aat aag gtc aca
 790
 Lys Met Lys Tyr Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val Thr
 210 215 220 225
 gga aaa gct ggt atg ctt gat gag atc atc aat tat gtt caa tgt ctc
 838
 Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Cys Leu
 230 235 240
 caa aga caa gtc gag ttc ctg tcg atg aaa ctt gct gtc ttg aac ccg
 886
 Gln Arg Gln Val Glu Phe Leu Ser Met Lys Leu Ala Val Leu Asn Pro
 245 250 255
 gaa cta gag ctt gcc gtg gaa gat gta tcc gta aaa cag gct tac ttt
 934
 Glu Leu Glu Leu Ala Val Glu Asp Val Ser Val Lys Gln Ala Tyr Phe
 260 265 270
 aca aat gta gtt gct tca aag caa tca ata atg gtt gat gtg cca ttg
 982
 Thr Asn Val Val Ala Ser Lys Gln Ser Ile Met Val Asp Val Pro Leu
 275 280 285
 ttt ccg tta gac cag caa gga tct cta gat ttg tct gcg ata aac ccg
 1030
 Phe Pro Leu Asp Gln Gln Gly Ser Leu Asp Leu Ser Ala Ile Asn Pro
 290 295 300 305

aac caa acg aca tct atc gaa gct cca tct gga agc tgg gaa act caa
1078

Asn Gln Thr Thr Ser Ile Glu Ala Pro Ser Gly Ser Trp Glu Thr Gln
310 315 320

tca cag agt ctc tac aac aca tct agc ctc ggt ttt cat tac taa
1123

Ser Gln Ser Leu Tyr Asn Thr Ser Ser Leu Gly Phe His Tyr
325 330 335

gcaagattca ttgaaacaac atggttgaca tcaatcaatc atcagaatca gaagcaaatt
1183

ctattacatt tgctcatcaa agtagtaatt tcgaaatttg gttaatgcat taccctttga
1243

tccttggtttt ctgatattta aaccagaaga actggagata gcaatccaat gatcttgtca
1303

cca
1306

<210> 226 <211> 335 <212> PRT <213> Arabidopsis thaliana <400>
226

Met Leu Glu Gly Leu Val Ser Gln Glu Ser Leu Ser Leu Asn Ser Met
1 5 10 15

Asp Met Ser Val Leu Glu Arg Leu Lys Trp Val Gln Gln Gln Gln Gln
20 25 30

Gln Leu Gln Gln Val Val Ser His Ser Ser Asn Asn Ser Pro Glu Leu
35 40 45

Leu Gln Ile Leu Gln Phe His Gly Ser Asn Asn Asp Glu Leu Leu Glu
50 55 60

Ser Ser Phe Ser Gln Phe Gln Met Leu Gly Ser Gly Phe Gly Pro Asn
65 70 75 80

Tyr Asn Met Gly Phe Gly Pro Pro His Glu Ser Ile Ser Arg Thr Ser
85 90 95

Ser Cys His Met Glu Pro Val Asp Thr Met Glu Val Leu Leu Lys Thr
100 105 110

Gly Glu Glu Thr Arg Ala Val Ala Leu Lys Asn Lys Arg Lys Pro Glu
115 120 125

Val Lys Thr Arg Glu Glu Gln Lys Thr Glu Lys Lys Ile Lys Val Glu
130 135 140

Ala Glu Thr Glu Ser Ser Met Lys Gly Lys Ser Asn Met Gly Asn Thr
145 150 155 160

Glu Ala Ser Ser Asp Thr Ser Lys Glu Thr Ser Lys Gly Ala Ser Glu
165 170 175

Asn Gln Lys Leu Asp Tyr Ile His Val Arg Ala Arg Arg Gly Gln Ala
180 185 190

Thr Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser
195 200 205

Lys Lys Met Lys Tyr Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val
210 215 220

Thr Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Cys
225 230 235 240

Leu Gln Arg Gln Val Glu Phe Leu Ser Met Lys Leu Ala Val Leu Asn
245 250 255

Pro Glu Leu Glu Leu Ala Val Glu Asp Val Ser Val Lys Gln Ala Tyr
260 265 270

Phe Thr Asn Val Val Ala Ser Lys Gln Ser Ile Met Val Asp Val Pro
275 280 285

Leu Phe Pro Leu Asp Gln Gln Gly Ser Leu Asp Leu Ser Ala Ile Asn
290 295 300

Pro Asn Gln Thr Thr Ser Ile Glu Ala Pro Ser Gly Ser Trp Glu Thr
305 310 315 320

Gln Ser Gln Ser Leu Tyr Asn Thr Ser Ser Leu Gly Phe His Tyr
325 330 335

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<221> CDS <222> (159)..(833) <223> G1499

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60

cctttaatat atatatatgc tcacacacac acatatatat atacatatataa gcatcgctc
120

aagcattaaa atttttacga accaaacaaa caaaaatt atg aat aat tat aat atg
176

Met Asn Asn Tyr Asn Met
1 5

aac cca tct ctc ttc caa aat tac act tgg aac aac atc atc aac agc
224
Asn Pro Ser Leu Phe Gln Asn Tyr Thr Trp Asn Asn Ile Ile Asn Ser
10 15 20

agc aac aac aac aac aag aat gat gat cat cat cat caa cat aat aat
272
Ser Asn Asn Asn Asn Lys Asn Asp Asp His His His Gln His Asn Asn
25 30 35

gat cca atc ggt atg gcc atg gac cag tac aca cag ctc cat atc ttc
320
Asp Pro Ile Gly Met Ala Met Asp Gln Tyr Thr Gln Leu His Ile Phe
40 45 50

aat cct ttc tct tct tct cat ttc cct cct ctc tct tct tcc ctc aca
368
Asn Pro Phe Ser Ser Ser His Phe Pro Pro Leu Ser Ser Ser Leu Thr
55 60 65 70

acc acc act ctt ctc tcc gga gat caa gaa gac gac gaa gac gaa gaa
416
Thr Thr Thr Leu Leu Ser Gly Asp Gln Glu Asp Asp Glu Asp Glu Glu
75 80 85

gaa cct cta gag gaa ctc ggt gct atg aag gaa atg atg tac aag atc
464
Glu Pro Leu Glu Glu Leu Gly Ala Met Lys Glu Met Met Tyr Lys Ile
90 95 100

gca gcc atg caa tcg gtt gac atc gac cca gca acc gtc aag aaa ccc
512
Ala Ala Met Gln Ser Val Asp Ile Asp Pro Ala Thr Val Lys Lys Pro
105 110 115

aaa cgc cgt aac gtg agg atc tcc gac gac cct cag agt gtg gcg gct
560
Lys Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Ser Val Ala Ala
120 125 130

aga cat cgc cgt gag aga atc agt gag agg atc aga att ctt cag aga
608
Arg His Arg Arg Glu Arg Ile Ser Glu Arg Ile Arg Ile Leu Gln Arg
135 140 145 150

ctc gtg cca ggt ggc act aaa atg gat acg gct tca atg ctc gat gaa
656
Leu Val Pro Gly Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu
155 160 165

gct ata cgc tat gtc aag ttc ttg aaa cgg cag atc cgg cta ctc aat
704
Ala Ile Arg Tyr Val Lys Phe Leu Lys Arg Gln Ile Arg Leu Leu Asn
170 175 180

aat aat acc gga tat act cct ccg ccg ccg caa gat caa gct tct cag
752
Asn Asn Thr Gly Tyr Thr Pro Pro Pro Pro Gln Asp Gln Ala Ser Gln

185 190 195
 gcg gtg acg acg tca tgg gtt tca ccg cca cca ccg cca agt ttc ggc
 800
 Ala Val Thr Thr Ser Trp Val Ser Pro Pro Pro Pro Pro Ser Phe Gly
 200 205 210
 cgt ggg gga aga gga gta gga gaa tta atc tag acaagatgac atttccatta
 853
 Arg Gly Gly Arg Gly Val Gly Glu Leu Ile
 215 220
 gtagtaacta aattatgcta taatgtgtga gtaatggtgc aattatgga
 902

<210> 228 <211> 224 <212> PRT <213> Arabidopsis thaliana <400>
 228

Met Asn Asn Tyr Asn Met Asn Pro Ser Leu Phe Gln Asn Tyr Thr Trp
 1 5 10 15

Asn Asn Ile Ile Asn Ser Ser Asn Asn Asn Asn Lys Asn Asp Asp His
 20 25 30

His His Gln His Asn Asn Asp Pro Ile Gly Met Ala Met Asp Gln Tyr
 35 40 45

Thr Gln Leu His Ile Phe Asn Pro Phe Ser Ser Ser His Phe Pro Pro
 50 55 60

Leu Ser Ser Ser Leu Thr Thr Thr Thr Leu Leu Ser Gly Asp Gln Glu
 65 70 75 80

Asp Asp Glu Asp Glu Glu Glu Pro Leu Glu Glu Leu Gly Ala Met Lys
 85 90 95

Glu Met Met Tyr Lys Ile Ala Ala Met Gln Ser Val Asp Ile Asp Pro
 100 105 110

Ala Thr Val Lys Lys Pro Lys Arg Arg Asn Val Arg Ile Ser Asp Asp
 115 120 125

Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile Ser Glu Arg
 130 135 140

Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys Met Asp Thr
 145 150 155 160

Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Val Lys Phe Leu Lys Arg
 165 170 175

Gln Ile Arg Leu Leu Asn Asn Asn Thr Gly Tyr Thr Pro Pro Pro Pro
 180 185 190

Gln Asp Gln Ala Ser Gln Ala Val Thr Thr Ser Trp Val Ser Pro Pro
 195 200 205

Pro Pro Pro Ser Phe Gly Arg Gly Gly Arg Gly Val Gly Glu Leu Ile
 210 215 220

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 48
 Met Ala Glu Thr Met Lys Asp Ile Thr Met Lys Asn Asp Glu Ser Gln
 1 5 10 15

gaa gaa gaa atc ccc gat caa ttt ctc tgc tgc gtt tgc ctg gaa ctt
 96
 Glu Glu Glu Ile Pro Asp Gln Phe Leu Cys Cys Val Cys Leu Glu Leu
 20 25 30

ctt tac aag cca att gtg tta tct tgt ggt cat cta tca tgt ttt tgg
 144
 Leu Tyr Lys Pro Ile Val Leu Ser Cys Gly His Leu Ser Cys Phe Trp
 35 40 45

tgc gta cat aag tcc atg aat ggc ttt cgt gag tct cat tgt ccg ata
 192
 Cys Val His Lys Ser Met Asn Gly Phe Arg Glu Ser His Cys Pro Ile
 50 55 60

tgt aga gac ccg tat gtt cac ttt ccc tct gtg tgc cag aag ctt tat
 240
 Cys Arg Asp Pro Tyr Val His Phe Pro Ser Val Cys Gln Lys Leu Tyr
 65 70 75 80

ttt ctg tta aag aag atg tac cca ctt gct cat aag aag aga gaa gaa
 288
 Phe Leu Leu Lys Lys Met Tyr Pro Leu Ala His Lys Lys Arg Glu Glu
 85 90 95

caa gtt tta aag gaa gag caa gaa cga gaa tgt ttt tct cct cag att
 336
 Gln Val Leu Lys Glu Glu Gln Glu Arg Glu Cys Phe Ser Pro Gln Ile
 100 105 110

gat ctt gtt ttg gat ttg tct gtg tgt agt gga gat tct ctc aat gtc
 384
 Asp Leu Val Leu Asp Leu Ser Val Cys Ser Gly Asp Ser Leu Asn Val
 115 120 125

tct gat aaa cag aag gtg gaa gag tgt tcg aat gca gcg aac tta tta
 432
 Ser Asp Lys Gln Lys Val Glu Glu Cys Ser Asn Ala Ala Asn Leu Leu

130 135 140
 tct agt tca tca agt aga ggt gac att cca tgt atc ccc aaa aat caa
 480
 Ser Ser Ser Ser Ser Arg Gly Asp Ile Pro Cys Ile Pro Lys Asn Gln
 145 150 155 160
 gaa ccc aca gat gca aaa gct ctt aat gtt cat gaa aat gaa tta ctt
 528
 Glu Pro Thr Asp Ala Lys Ala Leu Asn Val His Glu Asn Glu Leu Leu
 165 170 175
 aag gat aac aaa gtc agt aag cag att tcg aaa gat gat ttg ctc tgt
 576
 Lys Asp Asn Lys Val Ser Lys Gln Ile Ser Lys Asp Asp Leu Leu Cys
 180 185 190
 tca gca tgt aag gag ctg ctt gta cga ccc gta gtt ctc aat tgc gga
 624
 Ser Ala Cys Lys Glu Leu Leu Val Arg Pro Val Val Leu Asn Cys Gly
 195 200 205
 cat gtg tat tgt gaa gga tgt gta gta gat atg gct gaa gaa agc gaa
 672
 His Val Tyr Cys Glu Gly Cys Val Val Asp Met Ala Glu Glu Ser Glu
 210 215 220
 aag atc aaa tgt caa gag tgt aat gtt tgt gac cca aga gga ttt cca
 720
 Lys Ile Lys Cys Gln Glu Cys Asn Val Cys Asp Pro Arg Gly Phe Pro
 225 230 235 240
 aaa gtt tgt ttg att ctt gaa cag ctt ttg gag gaa aac ttt cct gaa
 768
 Lys Val Cys Leu Ile Leu Glu Gln Leu Leu Glu Glu Asn Phe Pro Glu
 245 250 255
 gaa tac aat tca aga agc agt aag gtt cag aaa acg ctc gcc cat aat
 816
 Glu Tyr Asn Ser Arg Ser Ser Lys Val Gln Lys Thr Leu Ala His Asn
 260 265 270
 agc aaa gga aat att caa agc tat ctc aaa gaa ggc ccg tcc tta tca
 864
 Ser Lys Gly Asn Ile Gln Ser Tyr Leu Lys Glu Gly Pro Ser Leu Ser
 275 280 285
 aac gac aat aac aat gat gat ccc tgg ttg gca aac cct gga tca aat
 912
 Asn Asp Asn Asn Asn Asp Asp Pro Trp Leu Ala Asn Pro Gly Ser Asn
 290 295 300
 gtt cac ttt gga gct ggt tgt gat tct tgt ggg gtg tat cca atc ata
 960
 Val His Phe Gly Ala Gly Cys Asp Ser Cys Gly Val Tyr Pro Ile Ile
 305 310 315 320
 ggg gat cga tac aga tgc aaa gac tgc aag gag gaa att ggg tat gac
 1008
 Gly Asp Arg Tyr Arg Cys Lys Asp Cys Lys Glu Glu Ile Gly Tyr Asp
 325 330 335

ctt tgc aaa gac tgt tac gag act cct tcg aaa gtt cca ggg aga ttc
1056

Leu Cys Lys Asp Cys Tyr Glu Thr Pro Ser Lys Val Pro Gly Arg Phe
340 345 350

aac cag caa cac act cct gac cac agg ctt gag ctt gca cgg tct cct
1104

Asn Gln Gln His Thr Pro Asp His Arg Leu Glu Leu Ala Arg Ser Pro
355 360 365

cag gtt ctg atc aat ttc aat tct atc ggt atc ctt ctc gga ccc gtt
1152

Gln Val Leu Ile Asn Phe Asn Ser Ile Gly Ile Leu Leu Gly Pro Val
370 375 380

atc tca aat gaa ggc atg gat aca gat gaa ggc gag gaa ggg cct cct
1200

Ile Ser Asn Glu Gly Met Asp Thr Asp Glu Gly Glu Glu Gly Pro Pro
385 390 395 400

ggt tct tct aat gag tca tca agc aca gaa tga
1233

Gly Ser Ser Asn Glu Ser Ser Ser Thr Glu
405 410

<210> 230 <211> 410 <212> PRT <213> Arabidopsis thaliana <400>
230

Met Ala Glu Thr Met Lys Asp Ile Thr Met Lys Asn Asp Glu Ser Gln
1 5 10 15

Glu Glu Glu Ile Pro Asp Gln Phe Leu Cys Cys Val Cys Leu Glu Leu
20 25 30

Leu Tyr Lys Pro Ile Val Leu Ser Cys Gly His Leu Ser Cys Phe Trp
35 40 45

Cys Val His Lys Ser Met Asn Gly Phe Arg Glu Ser His Cys Pro Ile
50 55 60

Cys Arg Asp Pro Tyr Val His Phe Pro Ser Val Cys Gln Lys Leu Tyr
65 70 75 80

Phe Leu Leu Lys Lys Met Tyr Pro Leu Ala His Lys Lys Arg Glu Glu
85 90 95

Gln Val Leu Lys Glu Glu Gln Glu Arg Glu Cys Phe Ser Pro Gln Ile
100 105 110

Asp Leu Val Leu Asp Leu Ser Val Cys Ser Gly Asp Ser Leu Asn Val
115 120 125

Ser Asp Lys Gln Lys Val Glu Glu Cys Ser Asn Ala Ala Asn Leu Leu
 130 135 140

Ser Ser Ser Ser Ser Arg Gly Asp Ile Pro Cys Ile Pro Lys Asn Gln
 145 150 155 160

Glu Pro Thr Asp Ala Lys Ala Leu Asn Val His Glu Asn Glu Leu Leu
 165 170 175

Lys Asp Asn Lys Val Ser Lys Gln Ile Ser Lys Asp Asp Leu Leu Cys
 180 185 190

Ser Ala Cys Lys Glu Leu Leu Val Arg Pro Val Val Leu Asn Cys Gly
 195 200 205

His Val Tyr Cys Glu Gly Cys Val Val Asp Met Ala Glu Glu Ser Glu
 210 215 220

Lys Ile Lys Cys Gln Glu Cys Asn Val Cys Asp Pro Arg Gly Phe Pro
 225 230 235 240

Lys Val Cys Leu Ile Leu Glu Gln Leu Leu Glu Glu Asn Phe Pro Glu
 245 250 255

Glu Tyr Asn Ser Arg Ser Ser Lys Val Gln Lys Thr Leu Ala His Asn
 260 265 270

Ser Lys Gly Asn Ile Gln Ser Tyr Leu Lys Glu Gly Pro Ser Leu Ser
 275 280 285

Asn Asp Asn Asn Asn Asp Asp Pro Trp Leu Ala Asn Pro Gly Ser Asn
 290 295 300

Val His Phe Gly Ala Gly Cys Asp Ser Cys Gly Val Tyr Pro Ile Ile
 305 310 315 320

Gly Asp Arg Tyr Arg Cys Lys Asp Cys Lys Glu Glu Ile Gly Tyr Asp
 325 330 335

Leu Cys Lys Asp Cys Tyr Glu Thr Pro Ser Lys Val Pro Gly Arg Phe
 340 345 350

Asn Gln Gln His Thr Pro Asp His Arg Leu Glu Leu Ala Arg Ser Pro
 355 360 365

Gln Val Leu Ile Asn Phe Asn Ser Ile Gly Ile Leu Leu Gly Pro Val
 370 375 380

Ile Ser Asn Glu Gly Met Asp Thr Asp Glu Gly Glu Glu Gly Pro Pro
 385 390 395 400

Gly Ser Ser Asn Glu Ser Ser Ser Thr Glu
 405 410

<210> 231 <211> 1146 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(1146) <223> G1519

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 48
 Met Arg Leu Asn Gly Asp Ser Gly Pro Gly Gln Asp Glu Pro Gly Ser
 1 5 10 15
 agc ggg ttt cac ggc gga atc aga cga ttc ccg tta gca gct cag ccg
 96
 Ser Gly Phe His Gly Gly Ile Arg Arg Phe Pro Leu Ala Ala Gln Pro
 20 25 30
 gag att atg aga gct gct gag aaa gac gat caa tac gct tct ttc atc
 144
 Glu Ile Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile
 35 40 45
 cac gaa gct tgc cgc gat gcc ttc cga cac ctt ttc ggt aca aga atc
 192
 His Glu Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile
 50 55 60
 gct ctt gct tac cag aag gag atg aag cta ctt gga cag atg ctt tac
 240
 Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr
 65 70 75 80
 tat gtt ctt acg aca ggt tca ggg caa caa act tta gga gag gaa tat
 288
 Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr
 85 90 95
 tgt gac att ata cag gtt gca ggg cct tat gga ctc tct cct aca cca
 336
 Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro
 100 105 110
 gct aga cgt gct ttg ttc ata ttg tac cag acc gca gtt cca tat atc
 384
 Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile
 115 120 125
 gca gag aga att agc act cga gct gct acg caa gca gtc acc ttt gat
 432
 Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp
 130 135 140

gag tct gat gag ttt ttt ggt gat agt cat atc cac tca cca aga atg
 480
 Glu Ser Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met
 145 150 155 160
 ata gat ctt cca tct tca tct caa gtt gaa act tca act tct gta gta
 528
 Ile Asp Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val
 165 170 175
 tct agg tta aac gat aga ctt atg aga tcg tgg cac cga gct att cag
 576
 Ser Arg Leu Asn Asp Arg Leu Met Arg Ser Trp His Arg Ala Ile Gln
 180 185 190
 cga tgg cct gtg gtt ctt cct gtt gcc cgc gaa gtc tta caa ctg gtt
 624
 Arg Trp Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val
 195 200 205
 ttg cgt gcc aat ctg atg ctc ttc tac ttt gaa ggt ttt tat tat cat
 672
 Leu Arg Ala Asn Leu Met Leu Phe Tyr Phe Glu Gly Phe Tyr Tyr His
 210 215 220
 ata tcg aaa cgt gca tcc ggg gtt cgt tat gtt ttc ata gga aag caa
 720
 Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln
 225 230 235 240
 ctg aat cag aga cct aga tac caa att ctt ggg gtt ttc ctt cta atc
 768
 Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile
 245 250 255
 caa ttg tgc atc ctt gct gct gag ggc ttg cgt cgg agt aat ttg tca
 816
 Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser
 260 265 270
 tct atc act agc tcc att cag cag gct tct ata gga tct tat caa act
 864
 Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr
 275 280 285
 tca gga ggg aga ggt tta cct gtt tta aat gaa gag ggg aat ttg ata
 912
 Ser Gly Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile
 290 295 300
 act tcg gaa gct gaa aag gga aac tgg tct acc tcc gat tca act tca
 960
 Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser
 305 310 315 320
 acg gag gca gta ggg aaa tgc act ctc tgc tta agc acc cgt cag cac
 1008
 Thr Glu Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His
 325 330 335

cca acg gcc act cct tgt ggt cat gtg ttt tgt tgg agc tgc att atg
1056

Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met
340 345 350

gaa tgg tgc aac gag aag caa gaa tgc cct ctt tgt cga acg ccc aat
1104

Glu Trp Cys Asn Glu Lys Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn
355 360 365

acc cat tca agt ttg gtt tgt ttg tat cat tct gat ttt tag
1146

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370 375 380

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20 25 30

Glu Ile Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile
35 40 45

His Glu Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile
50 55 60

Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr
65 70 75 80

Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr
85 90 95

Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro
100 105 110

Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile
115 120 125

Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp
130 135 140

Glu Ser Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met
145 150 155 160

Ile Asp Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val
165 170 175

Ser Arg Leu Asn Asp Arg Leu Met Arg Ser Trp His Arg Ala Ile Gln
180 185 190

Arg Trp Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val
195 200 205

Leu Arg Ala Asn Leu Met Leu Phe Tyr Phe Glu Gly Phe Tyr Tyr His
210 215 220

Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln
225 230 235 240

Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile
245 250 255

Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser
260 265 270

Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr
275 280 285

Ser Gly Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile
290 295 300

Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser
305 310 315 320

Thr Glu Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His
325 330 335

Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met
340 345 350

Glu Trp Cys Asn Glu Lys Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn
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Thr His Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe
370 375 380

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cga tcg ccg gaa agt atc gcg aaa ttt gca ggg aga gca ata ttt cct
96
Arg Ser Pro Glu Ser Ile Ala Lys Phe Ala Gly Arg Ala Ile Phe Pro
20           25           30

gct tta cag ggg aaa tcg tgt ccg ata tgc ctc gaa aat cta acc gag
144
Ala Leu Gln Gly Lys Ser Cys Pro Ile Cys Leu Glu Asn Leu Thr Glu
35           40           45

cga aga tcc gcc gcc gtg atc acg gtg tgc aag cac gga tac tgc ctt
192
Arg Arg Ser Ala Ala Val Ile Thr Val Cys Lys His Gly Tyr Cys Leu
50           55           60

gct tgt att cgg aag tgg agc agc ttc aag agg aat tgt cct ctt tgt
240
Ala Cys Ile Arg Lys Trp Ser Ser Phe Lys Arg Asn Cys Pro Leu Cys
65           70           75           80

aac act cgt ttt gat tcc tgg ttt atc gtt agt gat ttt gct tct aga
288
Asn Thr Arg Phe Asp Ser Trp Phe Ile Val Ser Asp Phe Ala Ser Arg
85           90           95

aaa tac cat aag gag caa tta cca att ctt cgt gat cgt gag act tta
336
Lys Tyr His Lys Glu Gln Leu Pro Ile Leu Arg Asp Arg Glu Thr Leu
100          105          110

act tat cat cgg aat aat cct tcc gat cgc cgg agg ata att caa agg
384
Thr Tyr His Arg Asn Asn Pro Ser Asp Arg Arg Arg Ile Ile Gln Arg
115          120          125

tcg agg gat gtt ttg gaa aac tct agc tca aga tca agg cca ttg cca
432
Ser Arg Asp Val Leu Glu Asn Ser Ser Ser Arg Ser Arg Pro Leu Pro
130          135          140

tgg cgg aga tca ttt gga cga cca ggt tca gtt cct gat tct gtt atc
480
Trp Arg Arg Ser Phe Gly Arg Pro Gly Ser Val Pro Asp Ser Val Ile
145          150          155          160

ttc cag cga aag ctt cag tgg cga gct agc ata tac act aag caa tta
528
Phe Gln Arg Lys Leu Gln Trp Arg Ala Ser Ile Tyr Thr Lys Gln Leu
165          170          175

cga gct gtt cga tta cat tca agg cgc ttg gaa cta agt ttg gcg gtg
576
Arg Ala Val Arg Leu His Ser Arg Arg Leu Glu Leu Ser Leu Ala Val
180          185          190

aat gat tac acc aaa gca aag ata act gaa aga att gag cca tgg att
624
Asn Asp Tyr Thr Lys Ala Lys Ile Thr Glu Arg Ile Glu Pro Trp Ile
195          200          205

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672

Arg Arg Glu Leu Gln Ala Val Leu Gly Asp Pro Asp Pro Ser Val Ile
210 215 220

gtt cat ttt gcg tca gct ctt ttc atc aaa agg ctt gag aga gag aat
720

Val His Phe Ala Ser Ala Leu Phe Ile Lys Arg Leu Glu Arg Glu Asn
225 230 235 240

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768

Asn Arg Gln Thr Gly Gln Thr Gly Met Leu Val Glu Asp Glu Val Ser
245 250 255

tct ctt cga aaa ttc ttg tct gat aag gtg gat ata ttt tgg cat gaa
816

Ser Leu Arg Lys Phe Leu Ser Asp Lys Val Asp Ile Phe Trp His Glu
260 265 270

cta aga tgt ttt gcg gag agt ata ctc.acg atg gag act tat gat gca
864

Leu Arg Cys Phe Ala Glu Ser Ile Leu Thr Met Glu Thr Tyr Asp Ala
275 280 285

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891

Val Val Glu Tyr Asn Glu Val Glu
290 295

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35 40 45

Arg Arg Ser Ala Ala Val Ile Thr Val Cys Lys His Gly Tyr Cys Leu
50 55 60

Ala Cys Ile Arg Lys Trp Ser Ser Phe Lys Arg Asn Cys Pro Leu Cys
65 70 75 80

Asn Thr Arg Phe Asp Ser Trp Phe Ile Val Ser Asp Phe Ala Ser Arg
85 90 95

Lys Tyr His Lys Glu Gln Leu Pro Ile Leu Arg Asp Arg Glu Thr Leu
100 105 110

Thr Tyr His Arg Asn Asn Pro Ser Asp Arg Arg Arg Ile Ile Gln Arg
115 120 125

Ser Arg Asp Val Leu Glu Asn Ser Ser Ser Arg Ser Arg Pro Leu Pro
130 135 140

Trp Arg Arg Ser Phe Gly Arg Pro Gly Ser Val Pro Asp Ser Val Ile
145 150 155 160

Phe Gln Arg Lys Leu Gln Trp Arg Ala Ser Ile Tyr Thr Lys Gln Leu
165 170 175

Arg Ala Val Arg Leu His Ser Arg Arg Leu Glu Leu Ser Leu Ala Val
180 185 190

Asn Asp Tyr Thr Lys Ala Lys Ile Thr Glu Arg Ile Glu Pro Trp Ile
195 200 205

Arg Arg Glu Leu Gln Ala Val Leu Gly Asp Pro Asp Pro Ser Val Ile
210 215 220

Val His Phe Ala Ser Ala Leu Phe Ile Lys Arg Leu Glu Arg Glu Asn
225 230 235 240

Asn Arg Gln Thr Gly Gln Thr Gly Met Leu Val Glu Asp Glu Val Ser
245 250 255

Ser Leu Arg Lys Phe Leu Ser Asp Lys Val Asp Ile Phe Trp His Glu
260 265 270

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Val Val Glu Tyr Asn Glu Val Glu
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gtg ggt tcc gat tac tca gat atg gat ata atc agg gct tta cac atg
96

Val Gly Ser Asp Tyr Ser Asp Met Asp Ile Ile Arg Ala Leu His Met
 20 25 30
 gcg aat cat gat cca acg gct gct atc aat ata atc ttc gac act cca
 144
 Ala Asn His Asp Pro Thr Ala Ala Ile Asn Ile Ile Phe Asp Thr Pro
 35 40 45
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 192
 Ser Phe Ala Lys Pro Asp Val Ala Thr Pro Thr Pro Ser Gly Ser Asn
 50 55 60
 gga ggg aag cga gtt gat agt gga tta aag ggc tgt act ttt ggt gac
 240
 Gly Gly Lys Arg Val Asp Ser Gly Leu Lys Gly Cys Thr Phe Gly Asp
 65 70 75 80
 agc gga agt gtt gga gcg aat cat cgc gtg gag gaa gaa aat gag agt
 288
 Ser Gly Ser Val Gly Ala Asn His Arg Val Glu Glu Glu Asn Glu Ser
 85 90 95
 gtt aat ggt gga gga gaa gag agt gtt tca ggg aat gag tgg tgg ttt
 336
 Val Asn Gly Gly Gly Glu Glu Ser Val Ser Gly Asn Glu Trp Trp Phe
 100 105 110
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 384
 Val Gly Cys Ser Glu Leu Ala Gly Leu Ser Thr Cys Lys Gly Arg Lys
 115 120 125
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 432
 Leu Lys Ser Gly Asp Glu Leu Val Phe Thr Phe Pro His Ser Lys Gly
 130 135 140
 tta aag cct gag act acg cct ggg aag cgc ggt ttt ggg cgg gga agg
 480
 Leu Lys Pro Glu Thr Thr Pro Gly Lys Arg Gly Phe Gly Arg Gly Arg
 145 150 155 160
 cca gct ttg cgt ggt gct tct gat atc gtt agg ttc tct aca aag gat
 528
 Pro Ala Leu Arg Gly Ala Ser Asp Ile Val Arg Phe Ser Thr Lys Asp
 165 170 175
 tca gga gag att ggt aga ata cca aac gag tgg gct cgg tgt ctt cta
 576
 Ser Gly Glu Ile Gly Arg Ile Pro Asn Glu Trp Ala Arg Cys Leu Leu
 180 185 190
 cca ctt gtg aga gac aag aaa att agg ata gaa ggc agt tgc aag tcg
 624
 Pro Leu Val Arg Asp Lys Lys Ile Arg Ile Glu Gly Ser Cys Lys Ser
 195 200 205
 gcg cct gaa gct ttg agc atc atg gat aca att ctt ctg tct gta agc
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210	215	220
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Lys Thr Ala Ser Asn Thr Ala Glu Glu Ser Met Phe His Pro Leu Pro 245 250 255		
aat ctc ttt cgg tta ctc ggt ttg atc ccc ttt aag aag gca gag ttt 816		
Asn Leu Phe Arg Leu Leu Gly Leu Ile Pro Phe Lys Lys Ala Glu Phe 260 265 270		
act cca gag gat ttt tac tct aag aag cga cct ttg agt tcc aag gat 864		
Thr Pro Glu Asp Phe Tyr Ser Lys Lys Arg Pro Leu Ser Ser Lys Asp 275 280 285		
ggt tct gct att cct act tcg ttg ctt caa tta aac aag gtc aag aat 912		
Gly Ser Ala Ile Pro Thr Ser Leu Leu Gln Leu Asn Lys Val Lys Asn 290 295 300		
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ggt gat ctt gat aac att gtt ggt gtt ggg gac agt tct gga tta aag 1008		
Gly Asp Leu Asp Asn Ile Val Gly Val Gly Asp Ser Ser Gly Leu Lys 325 330 335		
gaa atg gaa act cca cat aca ctt ctg tgt gag ctt cgt cca tac caa 1056		
Glu Met Glu Thr Pro His Thr Leu Leu Cys Glu Leu Arg Pro Tyr Gln 340 345 350		
aag cag gca ctt cat tgg atg acc caa ctg gag aaa gga aat tgc act 1104		
Lys Gln Ala Leu His Trp Met Thr Gln Leu Glu Lys Gly Asn Cys Thr 355 360 365		
gat gag gca gca aca atg ctt cac ccg tgt tgg gaa gca tac tgt tta 1152		
Asp Glu Ala Ala Thr Met Leu His Pro Cys Trp Glu Ala Tyr Cys Leu 370 375 380		
gca gac aag agg gaa ctg gtt gtc tac ctg aat tct ttt act ggt gat 1200		
Ala Asp Lys Arg Glu Leu Val Val Tyr Leu Asn Ser Phe Thr Gly Asp 385 390 395 400		
gct aca ata cac ttc cct agc aca ctt caa atg gca aga gga gga ata 1248		
Ala Thr Ile His Phe Pro Ser Thr Leu Gln Met Ala Arg Gly Gly Ile 405 410 415		

tta gca gac gca atg ggt ctt gga aag act gta atg acc ata tcc ctt
 1296
 Leu Ala Asp Ala Met Gly Leu Gly Lys Thr Val Met Thr Ile Ser Leu
 420 425 430

ttg ctt gcc cat tct tgg aaa gct gca tca act ggg ttt cta tgc ccc
 1344
 Leu Leu Ala His Ser Trp Lys Ala Ala Ser Thr Gly Phe Leu Cys Pro
 435 440 445

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 1392
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 450 455 460

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 1440
 Ser Pro Pro Val Lys Ala Thr Lys Phe Leu Gly Phe Asp Lys Arg Leu
 465 470 475 480

ctt gaa caa aaa agt gta ctt caa aat ggt ggt aac ctg att gta tgt
 1488
 Leu Glu Gln Lys Ser Val Leu Gln Asn Gly Gly Asn Leu Ile Val Cys
 485 490 495

ccg atg aca ctt tta gga cag tgg aag aca gag att gaa atg cat gca
 1536
 Pro Met Thr Leu Leu Gly Gln Trp Lys Thr Glu Ile Glu Met His Ala
 500 505 510

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 1584
 Lys Pro Gly Ser Leu Ser Val Tyr Val His Tyr Gly Gln Ser Arg Pro
 515 520 525

aag gat gca aaa ctt ctt tcc cag agt gat gtg gta atc acc aca tat
 1632
 Lys Asp Ala Lys Leu Leu Ser Gln Ser Asp Val Val Ile Thr Thr Tyr
 530 535 540

gga gtt cta aca tcc gaa ttc tcg caa gag aac tca gca gac cat gaa
 1680
 Gly Val Leu Thr Ser Glu Phe Ser Gln Glu Asn Ser Ala Asp His Glu
 545 550 555 560

gga att tat gca gtt cga tgg ttt agg att gtt ctt gac gag gca cat
 1728
 Gly Ile Tyr Ala Val Arg Trp Phe Arg Ile Val Leu Asp Glu Ala His
 565 570 575

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 1776
 Thr Ile Lys Asn Ser Lys Ser Gln Ile Ser Leu Ala Ala Ala Ala Leu
 580 585 590

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 1824
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 595 600 605

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 1872
 Leu Glu Asp Leu Tyr Ser Leu Leu Arg Phe Leu Arg Ile Glu Pro Trp
 610 615 620

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 625 630 635 640

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 1968
 Gly Asp Glu Arg Gly Leu Lys Leu Val Gln Ser Ile Leu Lys Pro Ile
 645 650 655

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 2016
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 660 665 670

ctt gtt cta ccc cct gct gat gca cgg gtc att tac tgt gaa ctt tcg
 2064
 Leu Val Leu Pro Pro Ala Asp Ala Arg Val Ile Tyr Cys Glu Leu Ser
 675 680 685

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 690 695 700

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 2160
 Lys Phe Asp Gln Phe Val Glu Gln Gly Lys Val Leu His Asn Tyr Ala
 705 710 715 720

tcg atc ctg gaa ctg ctt ttg cgt ctt cga caa tgt tgt gat cac cca
 2208
 Ser Ile Leu Glu Leu Leu Leu Arg Leu Arg Gln Cys Cys Asp His Pro
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 740 745 750

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 2304
 Lys Leu Ser Lys Arg Phe Leu Ser Gly Lys Ser Ser Gly Leu Glu Arg
 755 760 765

gaa gga aaa gat gta ccg tca gag gct ttt gtt cag gag gtg gta gag
 2352
 Glu Gly Lys Asp Val Pro Ser Glu Ala Phe Val Gln Glu Val Val Glu
 770 775 780

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 2400
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 785 790 795 800

ctt gag gat gct gta tta acg cca tgt gct cat aga tta tgt cgt gag
 2448
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 805 810 815

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 Cys Leu Leu Ala Ser Trp Arg Asn Ser Thr Ser Gly Leu Cys Pro Val
 820 825 830

tgt agg aac act gta agc aaa caa gaa ctc atc aca gca cca acc gaa
 2544
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 835 840 845

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 850 855 860

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 2832
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 930 935 940

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 945 950 955 960

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 965 970 975

caa act aag gaa gtc aaa atc aga aga ttc atc gtt aag gga acg gtt
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 Gln Thr Lys Glu Val Lys Ile Arg Arg Phe Ile Val Lys Gly Thr Val
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995 1000 1005

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3069

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50 55 60

Gly Gly Lys Arg Val Asp Ser Gly Leu Lys Gly Cys Thr Phe Gly Asp
65 70 75 80

Ser Gly Ser Val Gly Ala Asn His Arg Val Glu Glu Glu Asn Glu Ser
85 90 95

Val Asn Gly Gly Gly Glu Glu Ser Val Ser Gly Asn Glu Trp Trp Phe
100 105 110

Val Gly Cys Ser Glu Leu Ala Gly Leu Ser Thr Cys Lys Gly Arg Lys
115 120 125

Leu Lys Ser Gly Asp Glu Leu Val Phe Thr Phe Pro His Ser Lys Gly
130 135 140

Leu Lys Pro Glu Thr Thr Pro Gly Lys Arg Gly Phe Gly Arg Gly Arg
145 150 155 160

Pro Ala Leu Arg Gly Ala Ser Asp Ile Val Arg Phe Ser Thr Lys Asp
165 170 175

Ser Gly Glu Ile Gly Arg Ile Pro Asn Glu Trp Ala Arg Cys Leu Leu
 180 185 190

Pro Leu Val Arg Asp Lys Lys Ile Arg Ile Glu Gly Ser Cys Lys Ser
 195 200 205

Ala Pro Glu Ala Leu Ser Ile Met Asp Thr Ile Leu Leu Ser Val Ser
 210 215 220

Val Tyr Ile Asn Ser Ser Met Phe Gln Lys His Ser Ala Thr Ser Phe
 225 230 235 240

Lys Thr Ala Ser Asn Thr Ala Glu Glu Ser Met Phe His Pro Leu Pro
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Asn Leu Phe Arg Leu Leu Gly Leu Ile Pro Phe Lys Lys Ala Glu Phe
 260 265 270

Thr Pro Glu Asp Phe Tyr Ser Lys Lys Arg Pro Leu Ser Ser Lys Asp
 275 280 285

Gly Ser Ala Ile Pro Thr Ser Leu Leu Gln Leu Asn Lys Val Lys Asn
 290 295 300

Met Asn Gln Asp Ala Asn Gly Asp Glu Asn Glu Gln Cys Ile Ser Asp
 305 310 315 320

Gly Asp Leu Asp Asn Ile Val Gly Val Gly Asp Ser Ser Gly Leu Lys
 325 330 335

Glu Met Glu Thr Pro His Thr Leu Leu Cys Glu Leu Arg Pro Tyr Gln
 340 345 350

Lys Gln Ala Leu His Trp Met Thr Gln Leu Glu Lys Gly Asn Cys Thr
 355 360 365

Asp Glu Ala Ala Thr Met Leu His Pro Cys Trp Glu Ala Tyr Cys Leu
 370 375 380

Ala Asp Lys Arg Glu Leu Val Val Tyr Leu Asn Ser Phe Thr Gly Asp
 385 390 395 400

Ala Thr Ile His Phe Pro Ser Thr Leu Gln Met Ala Arg Gly Gly Ile
 405 410 415

Leu Ala Asp Ala Met Gly Leu Gly Lys Thr Val Met Thr Ile Ser Leu
 420 425 430

Leu Leu Ala His Ser Trp Lys Ala Ala Ser Thr Gly Phe Leu Cys Pro
 435 440 445

Asn Tyr Glu Gly Asp Lys Val Ile Ser Ser Ser Val Asp Asp Leu Thr
 450 455 460

Ser Pro Pro Val Lys Ala Thr Lys Phe Leu Gly Phe Asp Lys Arg Leu
 465 470 475 480

Leu Glu Gln Lys Ser Val Leu Gln Asn Gly Gly Asn Leu Ile Val Cys
 485 490 495

Pro Met Thr Leu Leu Gly Gln Trp Lys Thr Glu Ile Glu Met His Ala
 500 505 510

Lys Pro Gly Ser Leu Ser Val Tyr Val His Tyr Gly Gln Ser Arg Pro
 515 520 525

Lys Asp Ala Lys Leu Leu Ser Gln Ser Asp Val Val Ile Thr Thr Tyr
 530 535 540

Gly Val Leu Thr Ser Glu Phe Ser Gln Glu Asn Ser Ala Asp His Glu
 545 550 555 560

Gly Ile Tyr Ala Val Arg Trp Phe Arg Ile Val Leu Asp Glu Ala His
 565 570 575

Thr Ile Lys Asn Ser Lys Ser Gln Ile Ser Leu Ala Ala Ala Ala Leu
 580 585 590

Val Ala Asp Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Gln Asn Asn
 595 600 605

Leu Glu Asp Leu Tyr Ser Leu Leu Arg Phe Leu Arg Ile Glu Pro Trp
 610 615 620

Gly Thr Trp Ala Trp Trp Asn Lys Leu Val Gln Lys Pro Phe Glu Glu
 625 630 635 640

Gly Asp Glu Arg Gly Leu Lys Leu Val Gln Ser Ile Leu Lys Pro Ile
 645 650 655

Met Leu Arg Arg Thr Lys Ser Ser Thr Asp Arg Glu Gly Arg Pro Ile
660 665 670

Leu Val Leu Pro Pro Ala Asp Ala Arg Val Ile Tyr Cys Glu Leu Ser
675 680 685

Glu Ser Glu Arg Asp Phe Tyr Asp Ala Leu Phe Lys Arg Ser Lys Val
690 695 700

Lys Phe Asp Gln Phe Val Glu Gln Gly Lys Val Leu His Asn Tyr Ala
705 710 715 720

Ser Ile Leu Glu Leu Leu Leu Arg Leu Arg Gln Cys Cys Asp His Pro
725 730 735

Phe Leu Val Met Ser Arg Gly Asp Thr Ala Glu Tyr Ser Asp Leu Asn
740 745 750

Lys Leu Ser Lys Arg Phe Leu Ser Gly Lys Ser Ser Gly Leu Glu Arg
755 760 765

Glu Gly Lys Asp Val Pro Ser Glu Ala Phe Val Gln Glu Val Val Glu
770 775 780

Glu Leu Arg Lys Gly Glu Gln Gly Glu Cys Pro Ile Cys Leu Glu Ala
785 790 795 800

Leu Glu Asp Ala Val Leu Thr Pro Cys Ala His Arg Leu Cys Arg Glu
805 810 815

Cys Leu Leu Ala Ser Trp Arg Asn Ser Thr Ser Gly Leu Cys Pro Val
820 825 830

Cys Arg Asn Thr Val Ser Lys Gln Glu Leu Ile Thr Ala Pro Thr Glu
835 840 845

Ser Arg Phe Gln Val Asp Val Glu Lys Asn Trp Val Glu Ser Ser Lys
850 855 860

Ile Thr Ala Leu Leu Glu Glu Leu Glu Gly Leu Arg Ser Ser Gly Ser
865 870 875 880

Lys Ser Ile Leu Phe Ser Gln Trp Thr Ala Phe Leu Asp Leu Leu Gln
885 890 895

Ile Pro Leu Ser Arg Asn Asn Phe Ser Phe Val Arg Leu Asp Gly Thr

900 905 910
 Leu Ser Gln Gln Gln Arg Glu Lys Val Leu Lys Glu Phe Ser Glu Asp
 915 920 925
 Gly Ser Ile Leu Val Leu Leu Met Ser Leu Lys Ala Gly Gly Val Gly
 930 935 940
 Ile Asn Leu Thr Ala Ala Ser Asn Ala Phe Val Met Asp Pro Trp Trp
 945 950 955 960
 Asn Pro Ala Val Glu Glu Gln Ala Val Met Arg Ile His Arg Ile Gly
 965 970 975
 Gln Thr Lys Glu Val Lys Ile Arg Arg Phe Ile Val Lys Gly Thr Val
 980 985 990
 Glu Glu Arg Met Glu Ala Val Gln Ala Arg Lys Gln Arg Met Ile Ser
 995 1000 1005
 Gly Ala Leu Thr Asp Gln Glu Val Arg Ser Ala Arg Ile Glu Glu
 1010 1015 1020
 Leu Lys Met Leu Phe Thr
 1025

<210> 237 <211> 783 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(783) <223> G1537

<400> 237
 atg gaa aac gaa gta aac gca gga aca gca agc agt tca aga tgg aac
 48
 Met Glu Asn Glu Val Asn Ala Gly Thr Ala Ser Ser Ser Arg Trp Asn
 1 5 10 15
 cca acg aaa gat cag atc acg cta ctg gaa aat ctt tac aag gaa gga
 96
 Pro Thr Lys Asp Gln Ile Thr Leu Leu Glu Asn Leu Tyr Lys Glu Gly
 20 25 30
 ata cga act ccg agc gcc gat cag att cag cag atc acc ggt agg ctt
 144
 Ile Arg Thr Pro Ser Ala Asp Gln Ile Gln Gln Ile Thr Gly Arg Leu
 35 40 45
 cgt gcg tac ggc cat atc gaa ggt aaa aac gtc ttt tac tgg ttc cag
 192
 Arg Ala Tyr Gly His Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln
 50 55 60
 aac cat aag gct agg caa cgc caa aag cag aaa cag gag cgc atg gct
 240

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Arg Met Ala
 65 70 75 80
 tac ttc aat cgc ctc ctc cac aaa acc tcc cgt ttc ttc tac ccc cct
 288
 Tyr Phe Asn Arg Leu Leu His Lys Thr Ser Arg Phe Phe Tyr Pro Pro
 85 90 95
 cct tgc tca aac gtg ggt tgt gtc agt ccg tac tat tta cag caa gca
 336
 Pro Cys Ser Asn Val Gly Cys Val Ser Pro Tyr Tyr Leu Gln Gln Ala
 100 105 110
 agt gat cat cat atg aat caa cat gga agt gta tac aca aac gat ctt
 384
 Ser Asp His His Met Asn Gln His Gly Ser Val Tyr Thr Asn Asp Leu
 115 120 125
 ctt cac aga aac aat gtg atg att cca agt ggt ggc tac gag aaa cgg
 432
 Leu His Arg Asn Asn Val Met Ile Pro Ser Gly Gly Tyr Glu Lys Arg
 130 135 140
 aca gtc aca caa cat cag aaa caa ctt tca gac ata aga aca aca gca
 480
 Thr Val Thr Gln His Gln Lys Gln Leu Ser Asp Ile Arg Thr Thr Ala
 145 150 155 160
 gcc aca aga atg cca att tct ccg agt tca ctc aga ttt gac aga ttt
 528
 Ala Thr Arg Met Pro Ile Ser Pro Ser Ser Leu Arg Phe Asp Arg Phe
 165 170 175
 gcc ctc cgt gat aac tgt tat gcc ggt gag gac att aac gtc aat tcc
 576
 Ala Leu Arg Asp Asn Cys Tyr Ala Gly Glu Asp Ile Asn Val Asn Ser
 180 185 190
 agt gga cgg aaa aca ctc cct ctt ttt cct ctt cag cct ttg aat gca
 624
 Ser Gly Arg Lys Thr Leu Pro Leu Phe Pro Leu Gln Pro Leu Asn Ala
 195 200 205
 agt aat gct gat ggt atg gga agt tcc agt ttt gcc ctt ggt agt gat
 672
 Ser Asn Ala Asp Gly Met Gly Ser Ser Ser Phe Ala Leu Gly Ser Asp
 210 215 220
 tct ccg gtg gat tgt tct agc gat gga gcc ggc cga gag cag ccg ttt
 720
 Ser Pro Val Asp Cys Ser Ser Asp Gly Ala Gly Arg Glu Gln Pro Phe
 225 230 235 240
 att gat ttc ttt tct ggt ggt tct act tct act cgt ttc gat agt aat
 768
 Ile Asp Phe Phe Ser Gly Gly Ser Thr Ser Thr Arg Phe Asp Ser Asn
 245 250 255
 ggt aat ggg ttg taa
 783
 Gly Asn Gly Leu

260

<210> 238 <211> 260 <212> PRT <213> Arabidopsis thaliana <400>
238

Met Glu Asn Glu Val Asn Ala Gly Thr Ala Ser Ser Ser Arg Trp Asn
1 5 10 15

Pro Thr Lys Asp Gln Ile Thr Leu Leu Glu Asn Leu Tyr Lys Glu Gly
20 25 30

Ile Arg Thr Pro Ser Ala Asp Gln Ile Gln Gln Ile Thr Gly Arg Leu
35 40 45

Arg Ala Tyr Gly His Ile Glu Gly Lys Asn Val Phe Tyr Trp Phe Gln
50 55 60

Asn His Lys Ala Arg Gln Arg Gln Lys Gln Lys Gln Glu Arg Met Ala
65 70 75 80

Tyr Phe Asn Arg Leu Leu His Lys Thr Ser Arg Phe Phe Tyr Pro Pro
85 90 95

Pro Cys Ser Asn Val Gly Cys Val Ser Pro Tyr Tyr Leu Gln Gln Ala
100 105 110

Ser Asp His His Met Asn Gln His Gly Ser Val Tyr Thr Asn Asp Leu
115 120 125

Leu His Arg Asn Asn Val Met Ile Pro Ser Gly Gly Tyr Glu Lys Arg
130 135 140

Thr Val Thr Gln His Gln Lys Gln Leu Ser Asp Ile Arg Thr Thr Ala
145 150 155 160

Ala Thr Arg Met Pro Ile Ser Pro Ser Ser Leu Arg Phe Asp Arg Phe
165 170 175

Ala Leu Arg Asp Asn Cys Tyr Ala Gly Glu Asp Ile Asn Val Asn Ser
180 185 190

Ser Gly Arg Lys Thr Leu Pro Leu Phe Pro Leu Gln Pro Leu Asn Ala
195 200 205

Ser Asn Ala Asp Gly Met Gly Ser Ser Ser Phe Ala Leu Gly Ser Asp
210 215 220

Ser Pro Val Asp Cys Ser Ser Asp Gly Ala Gly Arg Glu Gln Pro Phe
 225 230 235 240

Ile Asp Phe Phe Ser Gly Gly Ser Thr Ser Thr Arg Phe Asp Ser Asn
 245 250 255

Gly Asn Gly Leu
 260

<210> 239 <211> 828 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(828) <223> G1543

<400> 239
 atg ata aaa cta cta ttt acg tac ata tgc aca tac aca tat aaa cta
 48
 Met Ile Lys Leu Leu Phe Thr Tyr Ile Cys Thr Tyr Thr Tyr Lys Leu
 1 5 10 15
 tat gct cta tat cat atg gat tac gca tgc gtg tgt atg tat aaa tat
 96
 Tyr Ala Leu Tyr His Met Asp Tyr Ala Cys Val Cys Met Tyr Lys Tyr
 20 25 30
 aaa ggc atc gtc acg ctt caa gtt tgt ctc ttt tat att aaa ctg aga
 144
 Lys Gly Ile Val Thr Leu Gln Val Cys Leu Phe Tyr Ile Lys Leu Arg
 35 40 45
 gtt ttc ctc tca aac ttt acc ttt tct tct tcg atc cta gct ctt aag
 192
 Val Phe Leu Ser Asn Phe Thr Phe Ser Ser Ser Ile Leu Ala Leu Lys
 50 55 60
 aac cct aat aat tca ttg atc aaa ata atg gcg att ttg ccg gaa aac
 240
 Asn Pro Asn Asn Ser Leu Ile Lys Ile Met Ala Ile Leu Pro Glu Asn
 65 70 75 80
 tct tca aac ttg gat ctt act atc tcc gtt cca ggc ttc tct tca tcc
 288
 Ser Ser Asn Leu Asp Leu Thr Ile Ser Val Pro Gly Phe Ser Ser Ser
 85 90 95
 cct ctc tcc gat gaa gga agt ggc gga gga aga gac cag cta agg cta
 336
 Pro Leu Ser Asp Glu Gly Ser Gly Gly Gly Arg Asp Gln Leu Arg Leu
 100 105 110
 gac atg aat cgg tta ccg tcg tct gaa gac gga gac gat gaa gaa ttc
 384
 Asp Met Asn Arg Leu Pro Ser Ser Glu Asp Gly Asp Asp Glu Glu Phe
 115 120 125
 agt cac gat gat ggc tct gct cct ccg cga aag aaa ctc cgt cta acc
 432
 Ser His Asp Asp Gly Ser Ala Pro Pro Arg Lys Lys Leu Arg Leu Thr
 130 135 140

aga gaa cag tca cgt ctt ctt gaa gat agt ttc aga cag aat cat acc
480

Arg Glu Gln Ser Arg Leu Leu Glu Asp Ser Phe Arg Gln Asn His Thr
145 150 155 160

ctt aat ccc aaa caa aag gaa gta ctt gcc aag cat ttg atg cta cgg
528

Leu Asn Pro Lys Gln Lys Glu Val Leu Ala Lys His Leu Met Leu Arg
165 170 175

cca aga caa att gaa gtt tgg ttt caa aac cgt aga gca agg agc aaa
576

Pro Arg Gln Ile Glu Val Trp Phe Gln Asn Arg Arg Ala Arg Ser Lys
180 185 190

ttg aag caa acc gag atg gaa tgc gag tat ctc aaa agg tgg ttt ggt
624

Leu Lys Gln Thr Glu Met Glu Cys Glu Tyr Leu Lys Arg Trp Phe Gly
195 200 205

tca tta acg gaa gaa aac cac agg ctc cat aga gaa gta gaa gag ctt
672

Ser Leu Thr Glu Glu Asn His Arg Leu His Arg Glu Val Glu Glu Leu
210 215 220

aga gcc ata aag gtt ggc cca aca acg gtg aac tct gcc tcg agc ctt
720

Arg Ala Ile Lys Val Gly Pro Thr Thr Val Asn Ser Ala Ser Ser Leu
225 230 235 240

act atg tgt cct cgc tgc gag cga gtt acc cct gcc gcg agc cct tcg
768

Thr Met Cys Pro Arg Cys Glu Arg Val Thr Pro Ala Ala Ser Pro Ser
245 250 255

agg gcg gtg gtg ccg gtt ccg gct aag aaa acg ttt ccg ccg caa gag
816

Arg Ala Val Val Pro Val Pro Ala Lys Lys Thr Phe Pro Pro Gln Glu
260 265 270

cgt gat cgt tga
828

Arg Asp Arg
275

<210> 240 <211> 275 <212> PRT <213> Arabidopsis thaliana <400>
240

Met Ile Lys Leu Leu Phe Thr Tyr Ile Cys Thr Tyr Thr Tyr Lys Leu
1 5 10 15

Tyr Ala Leu Tyr His Met Asp Tyr Ala Cys Val Cys Met Tyr Lys Tyr
20 25 30

Lys Gly Ile Val Thr Leu Gln Val Cys Leu Phe Tyr Ile Lys Leu Arg
35 40 45

Val Phe Leu Ser Asn Phe Thr Phe Ser Ser Ser Ile Leu Ala Leu Lys
 50 55 60

Asn Pro Asn Asn Ser Leu Ile Lys Ile Met Ala Ile Leu Pro Glu Asn
 65 70 75 80

Ser Ser Asn Leu Asp Leu Thr Ile Ser Val Pro Gly Phe Ser Ser Ser
 85 90 95

Pro Leu Ser Asp Glu Gly Ser Gly Gly Gly Arg Asp Gln Leu Arg Leu
 100 105 110

Asp Met Asn Arg Leu Pro Ser Ser Glu Asp Gly Asp Asp Glu Glu Phe
 115 120 125

Ser His Asp Asp Gly Ser Ala Pro Pro Arg Lys Lys Leu Arg Leu Thr
 130 135 140

Arg Glu Gln Ser Arg Leu Leu Glu Asp Ser Phe Arg Gln Asn His Thr
 145 150 155 160

Leu Asn Pro Lys Gln Lys Glu Val Leu Ala Lys His Leu Met Leu Arg
 165 170 175

Pro Arg Gln Ile Glu Val Trp Phe Gln Asn Arg Arg Ala Arg Ser Lys
 180 185 190

Leu Lys Gln Thr Glu Met Glu Cys Glu Tyr Leu Lys Arg Trp Phe Gly
 195 200 205

Ser Leu Thr Glu Glu Asn His Arg Leu His Arg Glu Val Glu Glu Leu
 210 215 220

Arg Ala Ile Lys Val Gly Pro Thr Thr Val Asn Ser Ala Ser Ser Leu
 225 230 235 240

Thr Met Cys Pro Arg Cys Glu Arg Val Thr Pro Ala Ala Ser Pro Ser
 245 250 255

Arg Ala Val Val Pro Val Pro Ala Lys Lys Thr Phe Pro Pro Gln Glu
 260 265 270

Arg Asp Arg
 275

<210> 241 <211> 1962 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(1962) <223> G1574

<400> 241
 atg gat gat aca atg gac atg agt tca ggt agt gat gaa gaa gta caa
 48
 Met Asp Asp Thr Met Asp Met Ser Ser Gly Ser Asp Glu Glu Val Gln
 1 5 10 15
 gaa gag aag acc act gtt aac gag agg gtc atc tat cag gct gca tta
 96
 Glu Glu Lys Thr Thr Val Asn Glu Arg Val Ile Tyr Gln Ala Ala Leu
 20 25 30
 caa gat ctg aag caa ccc aag acc gaa aag gat cta cct cct ggt gtt
 144
 Gln Asp Leu Lys Gln Pro Lys Thr Glu Lys Asp Leu Pro Pro Gly Val
 35 40 45
 ctt aca gtt cct ctt atg agg cat cag aaa att gca ttg aac tgg atg
 192
 Leu Thr Val Pro Leu Met Arg His Gln Lys Ile Ala Leu Asn Trp Met
 50 55 60
 cgt aag aaa gaa aaa aga agc agg cac tgt ttg gga ggg ata tta gca
 240
 Arg Lys Lys Glu Lys Arg Ser Arg His Cys Leu Gly Gly Ile Leu Ala
 65 70 75 80
 gat gat cag gga ctt ggt aaa acg atc tcg acg atc tct ctt atc ctg
 288
 Asp Asp Gln Gly Leu Gly Lys Thr Ile Ser Thr Ile Ser Leu Ile Leu
 85 90 95
 tta caa aag ttg aag tca caa tca aag cag aga aag cga aaa ggt caa
 336
 Leu Gln Lys Leu Lys Ser Gln Ser Lys Gln Arg Lys Arg Lys Gly Gln
 100 105 110
 aac tct ggt ggt aca ttg att gtt tgt cca gca agt gtt gta aaa caa
 384
 Asn Ser Gly Gly Thr Leu Ile Val Cys Pro Ala Ser Val Val Lys Gln
 115 120 125
 tgg gca aga gaa gtt aaa gag aag gtt tct gat gaa cac aaa ctc tct
 432
 Trp Ala Arg Glu Val Lys Glu Lys Val Ser Asp Glu His Lys Leu Ser
 130 135 140
 gtt tta gtc cac cat gga tct cac aga acc aaa gat cca aca gaa ata
 480
 Val Leu Val His His Gly Ser His Arg Thr Lys Asp Pro Thr Glu Ile
 145 150 155 160
 gca ata tat gat gtg gtc atg aca act tac gcc att gtt aca aat gaa
 528
 Ala Ile Tyr Asp Val Val Met Thr Thr Tyr Ala Ile Val Thr Asn Glu
 165 170 175
 gtt cca caa aac cct atg ctg aat cgt tat gat agt atg aga ggc aga
 576

Val Pro Gln Asn Pro Met Leu Asn Arg Tyr Asp Ser Met Arg Gly Arg
 180 185 190
 gaa agc ctt gac gga tcg agt ttg att cag cct cac gtt ggt gca cta
 624
 Glu Ser Leu Asp Gly Ser Ser Leu Ile Gln Pro His Val Gly Ala Leu
 195 200 205
 gga aga gtt agg tgg ttg aga gta gta tta gat gaa gct cat aca att
 672
 Gly Arg Val Arg Trp Leu Arg Val Val Leu Asp Glu Ala His Thr Ile
 210 215 220
 aaa aac cat aga acc cta att gca aaa gct tgt ttt agc ctt aga gcc
 720
 Lys Asn His Arg Thr Leu Ile Ala Lys Ala Cys Phe Ser Leu Arg Ala
 225 230 235 240
 aaa agg aga tgg tgt ttg act gga acg ccg ata aag aac aaa gta gac
 768
 Lys Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Lys Asn Lys Val Asp
 245 250 255
 gat ctt tat agc tat ttc aga ttt ctt aga tat cat cca tat gcc atg
 816
 Asp Leu Tyr Ser Tyr Phe Arg Phe Leu Arg Tyr His Pro Tyr Ala Met
 260 265 270
 tgc aat tca ttt cac caa aga atc aaa gct cca att gat aaa aag cct
 864
 Cys Asn Ser Phe His Gln Arg Ile Lys Ala Pro Ile Asp Lys Lys Pro
 275 280 285
 ctt cat ggt tac aag aag ctt caa gct att cta agg ggt ata atg ttg
 912
 Leu His Gly Tyr Lys Lys Leu Gln Ala Ile Leu Arg Gly Ile Met Leu
 290 295 300
 cgc cgc acc aaa gaa tgg tct ttc tac agg aag ctt gaa ttg aat tca
 960
 Arg Arg Thr Lys Glu Trp Ser Phe Tyr Arg Lys Leu Glu Leu Asn Ser
 305 310 315 320
 cgt tgg aag ttt gag gaa tat gct gct gat ggg act ttg cat gaa cac
 1008
 Arg Trp Lys Phe Glu Glu Tyr Ala Ala Asp Gly Thr Leu His Glu His
 325 330 335
 atg gct tat ctt ttg gtg atg ctt ttg cga cta cgc caa gct tgt aac
 1056
 Met Ala Tyr Leu Leu Val Met Leu Leu Arg Leu Arg Gln Ala Cys Asn
 340 345 350
 cat cca caa ctt gtt aac gga tat agt cac tca gat act aca aga aaa
 1104
 His Pro Gln Leu Val Asn Gly Tyr Ser His Ser Asp Thr Thr Arg Lys
 355 360 365
 atg tca gat gga gtt cga gta gcc cct aga gag aat cta atc atg ttc
 1152
 Met Ser Asp Gly Val Arg Val Ala Pro Arg Glu Asn Leu Ile Met Phe

370	375	380
ctc gat ctc ttg aaa tta tcc tca acc acc tgc tct gtt tgt agt gat 1200		
Leu Asp Leu Leu Lys Leu Ser Ser Thr Thr Cys Ser Val Cys Ser Asp 385 390 395 400		
cca cca aaa gac cct gtt gtt act ttg tgt ggc cat gtg ttt tgt tat 1248		
Pro Pro Lys Asp Pro Val Val Thr Leu Cys Gly His Val Phe Cys Tyr 405 410 415		
gag tgt gtg tct gta aac att aac ggg gat aac aat acg tgc cct gca 1296		
Glu Cys Val Ser Val Asn Ile Asn Gly Asp Asn Asn Thr Cys Pro Ala 420 425 430		
ctt aat tgc cac agc cag ctt aaa cat gat gtt gtt ttc act gaa tct 1344		
Leu Asn Cys His Ser Gln Leu Lys His Asp Val Val Phe Thr Glu Ser 435 440 445		
gca gtt aga agt tgc atc aac gat tat gat gat cct gaa gat aaa aat 1392		
Ala Val Arg Ser Cys Ile Asn Asp Tyr Asp Asp Pro Glu Asp Lys Asn 450 455 460		
gct tta gtt gca tca agg cga gtt tat ttc atc gaa aat ccg agc tgt 1440		
Ala Leu Val Ala Ser Arg Arg Val Tyr Phe Ile Glu Asn Pro Ser Cys 465 470 475 480		
gat aga gat tct tca gtc gct tgc aga gca agg cag tcc aga cac tcc 1488		
Asp Arg Asp Ser Ser Val Ala Cys Arg Ala Arg Gln Ser Arg His Ser 485 490 495		
acc aat aaa gac aat agt atc agt gga ctg aat ctc att ttt acg ttt 1536		
Thr Asn Lys Asp Asn Ser Ile Ser Gly Leu Asn Leu Ile Phe Thr Phe 500 505 510		
ctc aaa gac aaa tgt aat gat tat gaa aca ggt gcg atg ttg atg tct 1584		
Leu Lys Asp Lys Cys Asn Asp Tyr Glu Thr Gly Ala Met Leu Met Ser 515 520 525		
ctt aaa gct gga aac ctt gga ttg aat atg gta gct gca agt cat gtc 1632		
Leu Lys Ala Gly Asn Leu Gly Leu Asn Met Val Ala Ala Ser His Val 530 535 540		
att cta ctg gac cta tgg tgg aat cca aca aca gag gat caa gct att 1680		
Ile Leu Leu Asp Leu Trp Trp Asn Pro Thr Thr Glu Asp Gln Ala Ile 545 550 555 560		
gat cga gct cat cgt atc gga caa act cga gct gtt acg gtc act cgt 1728		
Asp Arg Ala His Arg Ile Gly Gln Thr Arg Ala Val Thr Val Thr Arg 565 570 575		

att gcc atc aaa aat acc gtt gag gaa cga att ttg act ctt cat gaa
1776

Ile Ala Ile Lys Asn Thr Val Glu Glu Arg Ile Leu Thr Leu His Glu
580 585 590

cgt aaa agg aac att gtt gca tct gca ttg ggt gaa aaa aac tgg caa
1824

Arg Lys Arg Asn Ile Val Ala Ser Ala Leu Gly Glu Lys Asn Trp Gln
595 600 605

aag ttc tgc gat tca act aac act aga aga tct cga ata tct gtt ttt
1872

Lys Phe Cys Asp Ser Thr Asn Thr Arg Arg Ser Arg Ile Ser Val Phe
610 615 620

tgg tgt gta gaa tat ccc aga gtt ttt att gat aag agg aat aaa acc
1920

Trp Cys Val Glu Tyr Pro Arg Val Phe Ile Asp Lys Arg Asn Lys Thr
625 630 635 640

ttt agc tat tta ata agt cac aag tgt gaa tgt aat gaa taa
1962

Phe Ser Tyr Leu Ile Ser His Lys Cys Glu Cys Asn Glu
645 650

<210> 242 <211> 653 <212> PRT <213> Arabidopsis thaliana <400>
242

Met Asp Asp Thr Met Asp Met Ser Ser Gly Ser Asp Glu Glu Val Gln
1 5 10 15

Glu Glu Lys Thr Thr Val Asn Glu Arg Val Ile Tyr Gln Ala Ala Leu
20 25 30

Gln Asp Leu Lys Gln Pro Lys Thr Glu Lys Asp Leu Pro Pro Gly Val
35 40 45

Leu Thr Val Pro Leu Met Arg His Gln Lys Ile Ala Leu Asn Trp Met
50 55 60

Arg Lys Lys Glu Lys Arg Ser Arg His Cys Leu Gly Gly Ile Leu Ala
65 70 75 80

Asp Asp Gln Gly Leu Gly Lys Thr Ile Ser Thr Ile Ser Leu Ile Leu
85 90 95

Leu Gln Lys Leu Lys Ser Gln Ser Lys Gln Arg Lys Arg Lys Gly Gln
100 105 110

Asn Ser Gly Gly Thr Leu Ile Val Cys Pro Ala Ser Val Val Lys Gln
115 120 125

Trp Ala Arg Glu Val Lys Glu Lys Val Ser Asp Glu His Lys Leu Ser
 130 135 140
 Val Leu Val His His Gly Ser His Arg Thr Lys Asp Pro Thr Glu Ile
 145 150 155 160
 Ala Ile Tyr Asp Val Val Met Thr Thr Tyr Ala Ile Val Thr Asn Glu
 165 170 175
 Val Pro Gln Asn Pro Met Leu Asn Arg Tyr Asp Ser Met Arg Gly Arg
 180 185 190
 Glu Ser Leu Asp Gly Ser Ser Leu Ile Gln Pro His Val Gly Ala Leu
 195 200 205
 Gly Arg Val Arg Trp Leu Arg Val Val Leu Asp Glu Ala His Thr Ile
 210 215 220
 Lys Asn His Arg Thr Leu Ile Ala Lys Ala Cys Phe Ser Leu Arg Ala
 225 230 235 240
 Lys Arg Arg Trp Cys Leu Thr Gly Thr Pro Ile Lys Asn Lys Val Asp
 245 250 255
 Asp Leu Tyr Ser Tyr Phe Arg Phe Leu Arg Tyr His Pro Tyr Ala Met
 260 265 270
 Cys Asn Ser Phe His Gln Arg Ile Lys Ala Pro Ile Asp Lys Lys Pro
 275 280 285
 Leu His Gly Tyr Lys Lys Leu Gln Ala Ile Leu Arg Gly Ile Met Leu
 290 295 300
 Arg Arg Thr Lys Glu Trp Ser Phe Tyr Arg Lys Leu Glu Leu Asn Ser
 305 310 315 320
 Arg Trp Lys Phe Glu Glu Tyr Ala Ala Asp Gly Thr Leu His Glu His
 325 330 335
 Met Ala Tyr Leu Leu Val Met Leu Leu Arg Leu Arg Gln Ala Cys Asn
 340 345 350
 His Pro Gln Leu Val Asn Gly Tyr Ser His Ser Asp Thr Thr Arg Lys
 355 360 365

Met Ser Asp Gly Val Arg Val Ala Pro Arg Glu Asn Leu Ile Met Phe
370 375 380

Leu Asp Leu Leu Lys Leu Ser Ser Thr Thr Cys Ser Val Cys Ser Asp
385 390 395 400

Pro Pro Lys Asp Pro Val Val Thr Leu Cys Gly His Val Phe Cys Tyr
405 410 415

Glu Cys Val Ser Val Asn Ile Asn Gly Asp Asn Asn Thr Cys Pro Ala
420 425 430

Leu Asn Cys His Ser Gln Leu Lys His Asp Val Val Phe Thr Glu Ser
435 440 445

Ala Val Arg Ser Cys Ile Asn Asp Tyr Asp Asp Pro Glu Asp Lys Asn
450 455 460

Ala Leu Val Ala Ser Arg Arg Val Tyr Phe Ile Glu Asn Pro Ser Cys
465 470 475 480

Asp Arg Asp Ser Ser Val Ala Cys Arg Ala Arg Gln Ser Arg His Ser
485 490 495

Thr Asn Lys Asp Asn Ser Ile Ser Gly Leu Asn Leu Ile Phe Thr Phe
500 505 510

Leu Lys Asp Lys Cys Asn Asp Tyr Glu Thr Gly Ala Met Leu Met Ser
515 520 525

Leu Lys Ala Gly Asn Leu Gly Leu Asn Met Val Ala Ala Ser His Val
530 535 540

Ile Leu Leu Asp Leu Trp Trp Asn Pro Thr Thr Glu Asp Gln Ala Ile
545 550 555 560

Asp Arg Ala His Arg Ile Gly Gln Thr Arg Ala Val Thr Val Thr Arg
565 570 575

Ile Ala Ile Lys Asn Thr Val Glu Glu Arg Ile Leu Thr Leu His Glu
580 585 590

Arg Lys Arg Asn Ile Val Ala Ser Ala Leu Gly Glu Lys Asn Trp Gln
595 600 605

Lys Phe Cys Asp Ser Thr Asn Thr Arg Arg Ser Arg Ile Ser Val Phe

610 615 620

Trp Cys Val Glu Tyr Pro Arg Val Phe Ile Asp Lys Arg Asn Lys Thr
 625 630 635 640

Phe Ser Tyr Leu Ile Ser His Lys Cys Glu Cys Asn Glu
 645 650

<210> 243 <211> 807 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(807) <223> G1586

<400> 243

atg aat caa gaa ggt gct tca cat agc cca tcc tcc act tcc acc gaa
 48
 Met Asn Gln Glu Gly Ala Ser His Ser Pro Ser Ser Thr Ser Thr Glu
 1 5 10 15

cca gtc cgg gca cgt tgg tca cct aaa ccg gag caa atc ttg ata ctc
 96
 Pro Val Arg Ala Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu
 20 25 30

gaa tcc atc ttc aac agt ggt act gtt aac cca cca aaa gat gaa acg
 144
 Glu Ser Ile Phe Asn Ser Gly Thr Val Asn Pro Pro Lys Asp Glu Thr
 35 40 45

gtg agg ata aga aag atg ctt gag aaa ttc ggt gct gtg gga gac gca
 192
 Val Arg Ile Arg Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala
 50 55 60

aac gtc ttc tac tgg ttt caa aac cga cgg tca aga tct cgc cgg aga
 240
 Asn Val Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg
 65 70 75 80

cac cgg cag ctt tta gca gcc acc acc gca gcc gcc acc tcc ata gga
 288
 His Arg Gln Leu Leu Ala Ala Thr Thr Ala Ala Ala Thr Ser Ile Gly
 85 90 95

gct gaa gac cac cag cac atg acg gcc atg agc atg cat caa tat cct
 336
 Ala Glu Asp His Gln His Met Thr Ala Met Ser Met His Gln Tyr Pro
 100 105 110

tgc agc aac aac gag att gat ttg ggg ttt gga agt tgt agc aac tta
 384
 Cys Ser Asn Asn Glu Ile Asp Leu Gly Phe Gly Ser Cys Ser Asn Leu
 115 120 125

tca gct aat tac ttc ctt aat gga tgc tgc tca tct caa atc cct tcc
 432
 Ser Ala Asn Tyr Phe Leu Asn Gly Ser Ser Ser Ser Gln Ile Pro Ser
 130 135 140

ttt ttc ctc ggc ctc tct tct tca agt ggt ggg tgt gag aac aac aat
480

Phe Phe Leu Gly Leu Ser Ser Ser Ser Gly Gly Cys Glu Asn Asn Asn
145 150 155 160

ggt atg gag aat ctc ttc aaa atg tat ggc cat gaa tct gat cat aat
528

Gly Met Glu Asn Leu Phe Lys Met Tyr Gly His Glu Ser Asp His Asn
165 170 175

cat cag cag cag cat cat agc tca aat gct gca tca gtt tta aac cca
576

His Gln Gln Gln His His Ser Ser Asn Ala Ala Ser Val Leu Asn Pro
180 185 190

tct gat caa aac tcc aac tcc caa tac gaa caa gaa ggg ttt atg acg
624

Ser Asp Gln Asn Ser Asn Ser Gln Tyr Glu Gln Glu Gly Phe Met Thr
195 200 205

gtg ttt ata aac gga gtt cct atg gaa gta aca aaa gga gca ata gac
672

Val Phe Ile Asn Gly Val Pro Met Glu Val Thr Lys Gly Ala Ile Asp
210 215 220

atg aaa aca atg ttc ggt gat gat tcg gtg tta ctt cat tcc tct ggt
720

Met Lys Thr Met Phe Gly Asp Asp Ser Val Leu Leu His Ser Ser Gly
225 230 235 240

ctt cct ctt ccc act gat gag ttt ggt ttc ttg atg cat tct tta caa
768

Leu Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln
245 250 255

cat gga caa act tat ttc ctg gta ccg aga cag aca tga
807

His Gly Gln Thr Tyr Phe Leu Val Pro Arg Gln Thr
260 265

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244

Met Asn Gln Glu Gly Ala Ser His Ser Pro Ser Ser Thr Ser Thr Glu
1 5 10 15

Pro Val Arg Ala Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu
20 25 30

Glu Ser Ile Phe Asn Ser Gly Thr Val Asn Pro Pro Lys Asp Glu Thr
35 40 45

Val Arg Ile Arg Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala
50 55 60

Asn Val Phe Tyr Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg

439

gtg cca act tct gac cac cgg ttt gta gtt caa gag atg atg tgc ttg
 99
 Val Pro Thr Ser Asp His Arg Phe Val Val Gln Glu Met Met Cys Leu
 15 20 25

caa agc tcg agc tgg act aaa gaa gag aac aag aag ttt gag cga gct
 147
 Gln Ser Ser Ser Trp Thr Lys Glu Glu Asn Lys Lys Phe Glu Arg Ala
 30 35 40

ctt gct gtc tac gct gat gac acg cct gat cgc tgg ttc aaa gtt gct
 195
 Leu Ala Val Tyr Ala Asp Asp Thr Pro Asp Arg Trp Phe Lys Val Ala
 45 50 55

gct atg atc cct gga aag acc ata tca gat gtc atg agg caa tac tct
 243
 Ala Met Ile Pro Gly Lys Thr Ile Ser Asp Val Met Arg Gln Tyr Ser
 60 65 70

aag ctt gaa gaa gac ctc ttc gat atc gaa gca gga ctt gtc ccg atc
 291
 Lys Leu Glu Glu Asp Leu Phe Asp Ile Glu Ala Gly Leu Val Pro Ile
 75 80 85 90

ccg ggt tac cgt tca gtt act cct tgt gga ttt gat cag gtt gtg agt
 339
 Pro Gly Tyr Arg Ser Val Thr Pro Cys Gly Phe Asp Gln Val Val Ser
 95 100 105

cca cgt gac ttt gat gcg tat cgt aaa ctt cct aat gga gcc aga gga
 387
 Pro Arg Asp Phe Asp Ala Tyr Arg Lys Leu Pro Asn Gly Ala Arg Gly
 110 115 120

ttt gat caa gac cgt agg aaa gga gtt cca tgg acg gag gaa gaa cac
 435
 Phe Asp Gln Asp Arg Arg Lys Gly Val Pro Trp Thr Glu Glu Glu His
 125 130 135

agg aga ttc ttg tta ggg ctt ctc aag tat ggg aaa gga gat tgg aga
 483
 Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly Lys Gly Asp Trp Arg
 140 145 150

aac ata tcg agg aac ttt gtg gga tca aaa aca cca act cag gtt gca
 531
 Asn Ile Ser Arg Asn Phe Val Gly Ser Lys Thr Pro Thr Gln Val Ala
 155 160 165 170

agt cat gcc caa aag tac tac caa aga cag ctt tcc ggt gcg aaa gac
 579
 Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu Ser Gly Ala Lys Asp
 175 180 185

aaa cga cgg cct agc att cac gac atc acc acc gtc aat ctt ctc aat
 627
 Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr Val Asn Leu Leu Asn
 190 195 200

gcc aat ctt agc cgt cca tcg tct gat cac ggt tgc tta gtc tca aaa
675
Ala Asn Leu Ser Arg Pro Ser Ser Asp His Gly Cys Leu Val Ser Lys
205 210 215

cag gcc gag ccg aaa cta ggg ttc acc gac agg gat aat gca gag gag
723
Gln Ala Glu Pro Lys Leu Gly Phe Thr Asp Arg Asp Asn Ala Glu Glu
220 225 230

gga gtt atg ttt ctt ggt cag aat cta tcc tcg gtc ttc tct tcc tac
771
Gly Val Met Phe Leu Gly Gln Asn Leu Ser Ser Val Phe Ser Ser Tyr
235 240 245 250

gat cct gcc att aag ttt tcc gga gca aat gtt tac ggt gaa gga ggt
819
Asp Pro Ala Ile Lys Phe Ser Gly Ala Asn Val Tyr Gly Glu Gly Gly
255 260 265

tac tgt atc tca caa gat ctt gaa acg aga aaa tga gaattttgaa
865
Tyr Cys Ile Ser Gln Asp Leu Glu Thr Arg Lys
270 275

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896

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Met Glu Thr Leu His Pro Leu Leu Ser His Val Pro Thr Ser Asp His
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20 25 30

Lys Glu Glu Asn Lys Lys Phe Glu Arg Ala Leu Ala Val Tyr Ala Asp
35 40 45

Asp Thr Pro Asp Arg Trp Phe Lys Val Ala Ala Met Ile Pro Gly Lys
50 55 60

Thr Ile Ser Asp Val Met Arg Gln Tyr Ser Lys Leu Glu Glu Asp Leu
65 70 75 80

Phe Asp Ile Glu Ala Gly Leu Val Pro Ile Pro Gly Tyr Arg Ser Val
85 90 95

Thr Pro Cys Gly Phe Asp Gln Val Val Ser Pro Arg Asp Phe Asp Ala
100 105 110

Tyr Arg Lys Leu Pro Asn Gly Ala Arg Gly Phe Asp Gln Asp Arg Arg

115 120 125
 Lys Gly Val Pro Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly
 130 135 140
 Leu Leu Lys Tyr Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe
 145 150 155 160
 Val Gly Ser Lys Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr
 165 170 175
 Tyr Gln Arg Gln Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile
 180 185 190
 His Asp Ile Thr Thr Val Asn Leu Leu Asn Ala Asn Leu Ser Arg Pro
 195 200 205
 Ser Ser Asp His Gly Cys Leu Val Ser Lys Gln Ala Glu Pro Lys Leu
 210 215 220
 Gly Phe Thr Asp Arg Asp Asn Ala Glu Glu Gly Val Met Phe Leu Gly
 225 230 235 240
 Gln Asn Leu Ser Ser Val Phe Ser Ser Tyr Asp Pro Ala Ile Lys Phe
 245 250 255
 Ser Gly Ala Asn Val Tyr Gly Glu Gly Gly Tyr Cys Ile Ser Gln Asp
 260 265 270
 Leu Glu Thr Arg Lys
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 ttg agg aat aga gat gaa gaa act gca gac aag cag ata caa ttc aat
 96
 Leu Arg Asn Arg Asp Glu Glu Thr Ala Asp Lys Gln Ile Gln Phe Asn
 20 25 30
 gac caa agt ttt ggg gga aat gac tat gca ccc aag gta cgg aag cca
 144
 Asp Gln Ser Phe Gly Gly Asn Asp Tyr Ala Pro Lys Val Arg Lys Pro
 35 40 45

tac acg ata aca aaa gag aga gag aga tgg aca gat gaa gag cac aag
 192
 Tyr Thr Ile Thr Lys Glu Arg Glu Arg Trp Thr Asp Glu Glu His Lys
 50 55 60

aag ttt gtt gaa gcc ttg aaa tta tac ggg cga gct tgg aga cga ata
 240
 Lys Phe Val Glu Ala Leu Lys Leu Tyr Gly Arg Ala Trp Arg Arg Ile
 65 70 75 80

gaa gaa cat gtg ggc tca aag acc gca gtt cag att cga agc cat gct
 288
 Glu Glu His Val Gly Ser Lys Thr Ala Val Gln Ile Arg Ser His Ala
 85 90 95

cag aag ttt ttc tct aag gtt gct cga gaa gca act gga ggt gat ggg
 336
 Gln Lys Phe Phe Ser Lys Val Ala Arg Glu Ala Thr Gly Gly Asp Gly
 100 105 110

agc tca gta gag ccg att gta ata cct cct cct cgt ccc aag aga aag
 384
 Ser Ser Val Glu Pro Ile Val Ile Pro Pro Pro Arg Pro Lys Arg Lys
 115 120 125

cca gcg cat ccg tac cct cgt aag ttt ggg aac gag gca gat caa aca
 432
 Pro Ala His Pro Tyr Pro Arg Lys Phe Gly Asn Glu Ala Asp Gln Thr
 130 135 140

agt aga tcg gtt tct ccc tca gaa cgt gat act caa tct cca acc tct
 480
 Ser Arg Ser Val Ser Pro Ser Glu Arg Asp Thr Gln Ser Pro Thr Ser
 145 150 155 160

gtg ttg tcc act gtt gga tca gaa gca ttg tgt tcc ctt gat tcg agt
 528
 Val Leu Ser Thr Val Gly Ser Glu Ala Leu Cys Ser Leu Asp Ser Ser
 165 170 175

tca ccc aat cga agc ttg tcc cca gtt tct tct gca tca cca cca gct
 576
 Ser Pro Asn Arg Ser Leu Ser Pro Val Ser Ser Ala Ser Pro Pro Ala
 180 185 190

gct ctt aca acc act gca aat gca cct gaa gag ctt gag act ctg aag
 624
 Ala Leu Thr Thr Thr Ala Asn Ala Pro Glu Glu Leu Glu Thr Leu Lys
 195 200 205

ctg gag ttg ttt cct agt gag aga ctc tta aac agg gag agc tcg atc
 672
 Leu Glu Leu Phe Pro Ser Glu Arg Leu Leu Asn Arg Glu Ser Ser Ile
 210 215 220

aag gaa cca acg aag caa agt ctt aaa ctc ttt ggg aag aca gtt ttg
 720
 Lys Glu Pro Thr Lys Gln Ser Leu Lys Leu Phe Gly Lys Thr Val Leu
 225 230 235 240

gta tct gat tca ggc atg tcc tct tct cta aca act tca aca tat tgt
768

Val Ser Asp Ser Gly Met Ser Ser Ser Leu Thr Thr Ser Thr Tyr Cys
245 250 255

aaa tcc cca att cag cca tta cca cgg aaa ctc tca tca tcc aag aca
816

Lys Ser Pro Ile Gln Pro Leu Pro Arg Lys Leu Ser Ser Ser Lys Thr
260 265 270

cta ccc ata ata aga aac tca caa gaa gaa ctc ttg agc tgc tgg ata
864

Leu Pro Ile Ile Arg Asn Ser Gln Glu Glu Leu Leu Ser Cys Trp Ile
275 280 285

caa gtc cct ctt aag caa gaa gat gtg gaa aat aga tgt ttg gat tca
912

Gln Val Pro Leu Lys Gln Glu Asp Val Glu Asn Arg Cys Leu Asp Ser
290 295 300

gga aag gct gtc caa aac gaa gga tca tcg act gga tca aac act ggt
960

Gly Lys Ala Val Gln Asn Glu Gly Ser Ser Thr Gly Ser Asn Thr Gly
305 310 315 320

tcg gtg gat gat acg gga cac acg gaa aag acc aca gaa ccc gaa aca
1008

Ser Val Asp Asp Thr Gly His Thr Glu Lys Thr Thr Glu Pro Glu Thr
325 330 335

atg cta tgt caa tgg gag ttt aaa cca agt gag agg tct gca ttt tct
1056

Met Leu Cys Gln Trp Glu Phe Lys Pro Ser Glu Arg Ser Ala Phe Ser
340 345 350

gag ctc aga aga aca aac tcc gag tca aat tca aga gga ttt ggt cca
1104

Glu Leu Arg Arg Thr Asn Ser Glu Ser Asn Ser Arg Gly Phe Gly Pro
355 360 365

tac aag aag aga aag atg gta aca gaa gaa gaa gag cat gag att cat
1152

Tyr Lys Lys Arg Lys Met Val Thr Glu Glu Glu Glu His Glu Ile His
370 375 380

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1164

Leu His Leu

385

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Leu Arg Asn Arg Asp Glu Glu Thr Ala Asp Lys Gln Ile Gln Phe Asn
20 25 30

Asp Gln Ser Phe Gly Gly Asn Asp Tyr Ala Pro Lys Val Arg Lys Pro
 35 40 45
 Tyr Thr Ile Thr Lys Glu Arg Glu Arg Trp Thr Asp Glu Glu His Lys
 50 55 60
 Lys Phe Val Glu Ala Leu Lys Leu Tyr Gly Arg Ala Trp Arg Arg Ile
 65 70 75 80
 Glu Glu His Val Gly Ser Lys Thr Ala Val Gln Ile Arg Ser His Ala
 85 90 95
 Gln Lys Phe Phe Ser Lys Val Ala Arg Glu Ala Thr Gly Gly Asp Gly
 100 105 110
 Ser Ser Val Glu Pro Ile Val Ile Pro Pro Pro Arg Pro Lys Arg Lys
 115 120 125
 Pro Ala His Pro Tyr Pro Arg Lys Phe Gly Asn Glu Ala Asp Gln Thr
 130 135 140
 Ser Arg Ser Val Ser Pro Ser Glu Arg Asp Thr Gln Ser Pro Thr Ser
 145 150 155 160
 Val Leu Ser Thr Val Gly Ser Glu Ala Leu Cys Ser Leu Asp Ser Ser
 165 170 175
 Ser Pro Asn Arg Ser Leu Ser Pro Val Ser Ser Ala Ser Pro Pro Ala
 180 185 190
 Ala Leu Thr Thr Thr Ala Asn Ala Pro Glu Glu Leu Glu Thr Leu Lys
 195 200 205
 Leu Glu Leu Phe Pro Ser Glu Arg Leu Leu Asn Arg Glu Ser Ser Ile
 210 215 220
 Lys Glu Pro Thr Lys Gln Ser Leu Lys Leu Phe Gly Lys Thr Val Leu
 225 230 235 240
 Val Ser Asp Ser Gly Met Ser Ser Ser Leu Thr Thr Ser Thr Tyr Cys
 245 250 255
 Lys Ser Pro Ile Gln Pro Leu Pro Arg Lys Leu Ser Ser Ser Lys Thr
 260 265 270

Leu Pro Ile Ile Arg Asn Ser Gln Glu Glu Leu Leu Ser Cys Trp Ile
 275 280 285

Gln Val Pro Leu Lys Gln Glu Asp Val Glu Asn Arg Cys Leu Asp Ser
 290 295 300

Gly Lys Ala Val Gln Asn Glu Gly Ser Ser Thr Gly Ser Asn Thr Gly
 305 310 315 320

Ser Val Asp Asp Thr Gly His Thr Glu Lys Thr Thr Glu Pro Glu Thr
 325 330 335

Met Leu Cys Gln Trp Glu Phe Lys Pro Ser Glu Arg Ser Ala Phe Ser
 340 345 350

Glu Leu Arg Arg Thr Asn Ser Glu Ser Asn Ser Arg Gly Phe Gly Pro
 355 360 365

Tyr Lys Lys Arg Lys Met Val Thr Glu Glu Glu Glu His Glu Ile His
 370 375 380

Leu His Leu
 385

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aag atg ttt gag caa gct ttg gtt ctt ttt cct gaa gga tct cct aat
 99

Lys Met Phe Glu Gln Ala Leu Val Leu Phe Pro Glu Gly Ser Pro Asn
 15 20 25

cgg tgg gag aga atc gct gat cag ctt cat aaa tct gct ggt gaa gtt
 147

Arg Trp Glu Arg Ile Ala Asp Gln Leu His Lys Ser Ala Gly Glu Val
 30 35 40

agg gag cat tac gag gtc ttg gtt cat gat gtt ttc gag att gat tct
 195

Arg Glu His Tyr Glu Val Leu Val His Asp Val Phe Glu Ile Asp Ser
 45 50 55

ggt cga gtt gat gtc cct gat tac atg gat gac tcg gcg gct gcg gcg
 243

Gly Arg Val Asp Val Pro Asp Tyr Met Asp Asp Ser Ala Ala Ala Ala
 60 65 70 75

gcg ggt tgg gat tcc gct ggt cag atc tct ttt ggg tct aaa cat ggc
291

Ala Gly Trp Asp Ser Ala Gly Gln Ile Ser Phe Gly Ser Lys His Gly
80 85 90

gag agt gaa cgc aaa aga gga act cct tgg aca gag aac gaa cac aaa
339

Glu Ser Glu Arg Lys Arg Gly Thr Pro Trp Thr Glu Asn Glu His Lys
95 100 105

ttg ttt ctg atc gga tta aag aga tat ggt aag gga gat tgg agg agt
387

Leu Phe Leu Ile Gly Leu Lys Arg Tyr Gly Lys Gly Asp Trp Arg Ser
110 115 120

atc tcg aga aac gtt gtg gtg acg agg aca ccg acg caa gtc gcg agt
435

Ile Ser Arg Asn Val Val Val Thr Arg Thr Pro Thr Gln Val Ala Ser
125 130 135

cac gct cag aag tat ttt ctg aga cag aac tcg gtg aag aag gag agg
483

His Ala Gln Lys Tyr Phe Leu Arg Gln Asn Ser Val Lys Lys Glu Arg
140 145 150 155

aaa agg tcg agc atc cat gat ata act acg gtt gat gct act ttg gct
531

Lys Arg Ser Ser Ile His Asp Ile Thr Thr Val Asp Ala Thr Leu Ala
160 165 170

atg cct ggg tct aac atg gac tgg act ggc caa cac ggg agt cct gtt
579

Met Pro Gly Ser Asn Met Asp Trp Thr Gly Gln His Gly Ser Pro Val
175 180 185

cag gcg ccg cag cag caa cag att atg tct gag ttc ggt cag caa ttg
627

Gln Ala Pro Gln Gln Gln Gln Ile Met Ser Glu Phe Gly Gln Gln Leu
190 195 200

aat cct ggt cat ttc gag gat ttt ggg ttt cgg atg tga tg
668

Asn Pro Gly His Phe Glu Asp Phe Gly Phe Arg Met
205 210 215

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Met Ala Ser Ser Gln Trp Thr Arg Ser Glu Asp Lys Met Phe Glu Gln
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20 25 30

Ala Asp Gln Leu His Lys Ser Ala Gly Glu Val Arg Glu His Tyr Glu
35 40 45

Val Leu Val His Asp Val Phe Glu Ile Asp Ser Gly Arg Val Asp Val
50 55 60

Pro Asp Tyr Met Asp Asp Ser Ala Ala Ala Ala Gly Trp Asp Ser
65 70 75 80

Ala Gly Gln Ile Ser Phe Gly Ser Lys His Gly Glu Ser Glu Arg Lys
85 90 95

Arg Gly Thr Pro Trp Thr Glu Asn Glu His Lys Leu Phe Leu Ile Gly
100 105 110

Leu Lys Arg Tyr Gly Lys Gly Asp Trp Arg Ser Ile Ser Arg Asn Val
115 120 125

Val Val Thr Arg Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr
130 135 140

Phe Leu Arg Gln Asn Ser Val Lys Lys Glu Arg Lys Arg Ser Ser Ile
145 150 155 160

His Asp Ile Thr Thr Val Asp Ala Thr Leu Ala Met Pro Gly Ser Asn
165 170 175

Met Asp Trp Thr Gly Gln His Gly Ser Pro Val Gln Ala Pro Gln Gln
180 185 190

Gln Gln Ile Met Ser Glu Phe Gly Gln Gln Leu Asn Pro Gly His Phe
195 200 205

Glu Asp Phe Gly Phe Arg Met
210 215

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120

ctttttcagt ttctctttct ctttttgaca gaagagaccg agaagca atg gga agg
176

Met Gly Arg
1

gct ccg tgt tgt gag aaa atc ggg ttg aag aga ggg aga tgg aca gcc
224

Ala Pro Cys Cys Glu Lys Ile Gly Leu Lys Arg Gly Arg Trp Thr Ala
 5 10 15
 gag gaa gat gag atc ctc acc aag tat att cag acc aat ggt gaa ggt
 272
 Glu Glu Asp Glu Ile Leu Thr Lys Tyr Ile Gln Thr Asn Gly Glu Gly
 20 25 30 35
 tct tgg cga tct ttg cct aag aaa gct gga ttg ttg aga tgt gga aag
 320
 Ser Trp Arg Ser Leu Pro Lys Lys Ala Gly Leu Leu Arg Cys Gly Lys
 40 45 50
 agc tgt aga cta agg tgg ata aac tac tta aga aga gac tta aaa aga
 368
 Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Arg Asp Leu Lys Arg
 55 60 65
 gga aat att act tcc gac gaa gaa gaa ata atc gtc aag ttg cat tcc
 416
 Gly Asn Ile Thr Ser Asp Glu Glu Glu Ile Ile Val Lys Leu His Ser
 70 75 80
 ctt ctc ggc aac aga tgg tca ctt att gca aca cat cta cca gga aga
 464
 Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Thr His Leu Pro Gly Arg
 85 90 95
 aca gac aac gaa att aaa aac tat tgg aac tca cat ctc agc cgc aaa
 512
 Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys
 100 105 110 115
 atc tat gcc ttc act gcc gtt tcc gga gat gga cac aat cta ctc gtc
 560
 Ile Tyr Ala Phe Thr Ala Val Ser Gly Asp Gly His Asn Leu Leu Val
 120 125 130
 aac gat gta gtc ttg aag aaa tct tgt tca tgc tct tct gga gcc aag
 608
 Asn Asp Val Val Leu Lys Lys Ser Cys Ser Ser Ser Ser Gly Ala Lys
 135 140 145
 aac aat aac aag acc aag aag aag aag gga agg act agt agg tca
 656
 Asn Asn Asn Lys Thr Lys Lys Lys Lys Lys Gly Arg Thr Ser Arg Ser
 150 155 160
 tcc atg aag aaa cac aag caa atg gtg acg gcc tca caa tgt ttc tca
 704
 Ser Met Lys Lys His Lys Gln Met Val Thr Ala Ser Gln Cys Phe Ser
 165 170 175
 caa cct aag gag cta gag agt gat ttc agt gag gga ggg caa aat ggt
 752
 Gln Pro Lys Glu Leu Glu Ser Asp Phe Ser Glu Gly Gly Gln Asn Gly
 180 185 190 195
 aat ttt gaa gga gag tct ttg ggg cct tat gag tgg ttg gat ggt gag
 800
 Asn Phe Glu Gly Glu Ser Leu Gly Pro Tyr Glu Trp Leu Asp Gly Glu

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848			
Leu Glu Arg Leu Leu Ser Ser Cys Val Trp Glu Cys Thr Ser Glu Glu			
215	220	225	
gct gtg att gga gta aat gat gaa aag gtg tgt gag agt ggg gac aat			
896			
Ala Val Ile Gly Val Asn Asp Glu Lys Val Cys Glu Ser Gly Asp Asn			
230	235	240	
agt agt tgt tgt gtt aat ttg ttt gaa gaa gaa caa gga agc gag aca			
944			
Ser Ser Cys Cys Val Asn Leu Phe Glu Glu Glu Gln Gly Ser Glu Thr			
245	250	255	
aag att ggt cac gta gga atc aca gag gtt gat cat gat atg acg gtg			
992			
Lys Ile Gly His Val Gly Ile Thr Glu Val Asp His Asp Met Thr Val			
260	265	270	275
gaa aga gaa aga gag gga agt ttt tta agt tgc aat tca aat gaa aat			
1040			
Glu Arg Glu Arg Glu Gly Ser Phe Leu Ser Ser Asn Ser Asn Glu Asn			
280	285	290	
aat gat aaa gat tgg tgg gtt ggt cta tgt aat tct tca gaa gtt ggg			
1088			
Asn Asp Lys Asp Trp Trp Val Gly Leu Cys Asn Ser Ser Glu Val Gly			
295	300	305	
ttt ggg gtt gat gag gag ttg ctt gat tgg gag ttt caa ggt aat gtc			
1136			
Phe Gly Val Asp Glu Glu Leu Leu Asp Trp Glu Phe Gln Gly Asn Val			
310	315	320	
act tgt caa agt gat gat cta tgg gat ctc tca gat att gga gag ata			
1184			
Thr Cys Gln Ser Asp Asp Leu Trp Asp Leu Ser Asp Ile Gly Glu Ile			
325	330	335	
aca ttg gag tga ttgtaccgag caagtggatt ggcggccgct ctagacaggc			
1236			
Thr Leu Glu			
340			
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1296			
aagt			
1300			
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 20 25 30

Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Lys Ala Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Arg Asp
 50 55 60

Leu Lys Arg Gly Asn Ile Thr Ser Asp Glu Glu Glu Ile Ile Val Lys
 65 70 75 80

Leu His Ser Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Thr His Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
 100 105 110

Ser Arg Lys Ile Tyr Ala Phe Thr Ala Val Ser Gly Asp Gly His Asn
 115 120 125

Leu Leu Val Asn Asp Val Val Leu Lys Lys Ser Cys Ser Ser Ser Ser
 130 135 140

Gly Ala Lys Asn Asn Asn Lys Thr Lys Lys Lys Lys Lys Gly Arg Thr
 145 150 155 160

Ser Arg Ser Ser Met Lys Lys His Lys Gln Met Val Thr Ala Ser Gln
 165 170 175

Cys Phe Ser Gln Pro Lys Glu Leu Glu Ser Asp Phe Ser Glu Gly Gly
 180 185 190

Gln Asn Gly Asn Phe Glu Gly Glu Ser Leu Gly Pro Tyr Glu Trp Leu
 195 200 205

Asp Gly Glu Leu Glu Arg Leu Leu Ser Ser Cys Val Trp Glu Cys Thr
 210 215 220

Ser Glu Glu Ala Val Ile Gly Val Asn Asp Glu Lys Val Cys Glu Ser
 225 230 235 240

Gly Asp Asn Ser Ser Cys Cys Val Asn Leu Phe Glu Glu Glu Gln Gly
 245 250 255

Ser Glu Thr Lys Ile Gly His Val Gly Ile Thr Glu Val Asp His Asp

260 265 270

Met Thr Val Glu Arg Glu Arg Glu Gly Ser Phe Leu Ser Ser Asn Ser
275 280 285

Asn Glu Asn Asn Asp Lys Asp Trp Trp Val Gly Leu Cys Asn Ser Ser
290 295 300

Glu Val Gly Phe Gly Val Asp Glu Glu Leu Leu Asp Trp Glu Phe Gln
305 310 315 320

Gly Asn Val Thr Cys Gln Ser Asp Asp Leu Trp Asp Leu Ser Asp Ile
325 330 335

Gly Glu Ile Thr Leu Glu
340

<210> 253 <211> 867 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(867) <223> G1641

<400> 253
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48
Met Glu Val Met Arg Pro Ser Thr Ser His Val Ser Gly Gly Asn Trp
1 5 10 15
ctc atg gag gaa act aag agc ggc gtc gca gct tct ggt gaa ggt gcc
96
Leu Met Glu Glu Thr Lys Ser Gly Val Ala Ala Ser Gly Glu Gly Ala
20 25 30
acg tgg acg gcg gca gag aac aag gca ttc gag aat gct ttg gcg gtt
144
Thr Trp Thr Ala Ala Glu Asn Lys Ala Phe Glu Asn Ala Leu Ala Val
35 40 45
tac gac gac aac act cct gat cgg tgg cag aag gtg gct gcg gtg att
192
Tyr Asp Asp Asn Thr Pro Asp Arg Trp Gln Lys Val Ala Ala Val Ile
50 55 60
ccg ggg aag aca gtg agt gac gta att aga cag tat aac gat ttg gaa
240
Pro Gly Lys Thr Val Ser Asp Val Ile Arg Gln Tyr Asn Asp Leu Glu
65 70 75 80
gct gat gtc agc agc atc gag gcc ggt tta atc ccg gtc ccc ggt tac
288
Ala Asp Val Ser Ser Ile Glu Ala Gly Leu Ile Pro Val Pro Gly Tyr
85 90 95
atc acc tcg ccg cct ttc act cta gat tgg gcc ggc ggc ggt ggc gga
336
Ile Thr Ser Pro Pro Phe Thr Leu Asp Trp Ala Gly Gly Gly Gly Gly
100 105 110

tgt aac ggg ttt aaa ccg ggt cat cag gtt tgt aat aaa cgg tcg cag
 384
 Cys Asn Gly Phe Lys Pro Gly His Gln Val Cys Asn Lys Arg Ser Gln
 115 120 125

 gcc ggt aga tcg ccg gag ctg gag cgg aag aaa ggc gtt cct tgg acg
 432
 Ala Gly Arg Ser Pro Glu Leu Glu Arg Lys Lys Gly Val Pro Trp Thr
 130 135 140

 gag gaa gaa cac aag cta ttt cta atg ggt ttg aag aaa tat ggg aaa
 480
 Glu Glu Glu His Lys Leu Phe Leu Met Gly Leu Lys Lys Tyr Gly Lys
 145 150 155 160

 gga gat tgg aga aac ata tct cgg aac ttt gtg ata acg cga acg cca
 528
 Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Ile Thr Arg Thr Pro
 165 170 175

 aca caa gta gct agc cac gcc caa aag tac ttc atc cgg caa ctt tcc
 576
 Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile Arg Gln Leu Ser
 180 185 190

 ggc ggc aag gac aag aga cga gca agc att cac gac ata acc acc gta
 624
 Gly Gly Lys Asp Lys Arg Arg Ala Ser Ile His Asp Ile Thr Thr Val
 195 200 205

 aat ctc gaa gag gag gct tct ttg gag acc aat aag agc tcc att gtt
 672
 Asn Leu Glu Glu Glu Ala Ser Leu Glu Thr Asn Lys Ser Ser Ile Val
 210 215 220

 gtt gga gat cag cgt tca agg cta acc gcg ttt cct tgg aac caa acg
 720
 Val Gly Asp Gln Arg Ser Arg Leu Thr Ala Phe Pro Trp Asn Gln Thr
 225 230 235 240

 gac aac aat gga aca cag gca gac gct ttc aat ata acg att gga aac
 768
 Asp Asn Asn Gly Thr Gln Ala Asp Ala Phe Asn Ile Thr Ile Gly Asn
 245 250 255

 gct att agt ggc gtt cat tca tac ggc cag gtt atg att gga ggg tat
 816
 Ala Ile Ser Gly Val His Ser Tyr Gly Gln Val Met Ile Gly Gly Tyr
 260 265 270

 aac aat gca gat tct tgc tat gac gcc caa aac aca atg ttt caa cta
 864
 Asn Asn Ala Asp Ser Cys Tyr Asp Ala Gln Asn Thr Met Phe Gln Leu
 275 280 285

 tag
 867

<210> 254 <211> 288 <212> PRT <213> Arabidopsis thaliana <400>
254

Met Glu Val Met Arg Pro Ser Thr Ser His Val Ser Gly Gly Asn Trp
1 5 10 15

Leu Met Glu Glu Thr Lys Ser Gly Val Ala Ala Ser Gly Glu Gly Ala
20 25 30

Thr Trp Thr Ala Ala Glu Asn Lys Ala Phe Glu Asn Ala Leu Ala Val
35 40 45

Tyr Asp Asp Asn Thr Pro Asp Arg Trp Gln Lys Val Ala Ala Val Ile
50 55 60

Pro Gly Lys Thr Val Ser Asp Val Ile Arg Gln Tyr Asn Asp Leu Glu
65 70 75 80

Ala Asp Val Ser Ser Ile Glu Ala Gly Leu Ile Pro Val Pro Gly Tyr
85 90 95

Ile Thr Ser Pro Pro Phe Thr Leu Asp Trp Ala Gly Gly Gly Gly Gly
100 105 110

Cys Asn Gly Phe Lys Pro Gly His Gln Val Cys Asn Lys Arg Ser Gln
115 120 125

Ala Gly Arg Ser Pro Glu Leu Glu Arg Lys Lys Gly Val Pro Trp Thr
130 135 140

Glu Glu Glu His Lys Leu Phe Leu Met Gly Leu Lys Lys Tyr Gly Lys
145 150 155 160

Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Ile Thr Arg Thr Pro
165 170 175

Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile Arg Gln Leu Ser
180 185 190

Gly Gly Lys Asp Lys Arg Arg Ala Ser Ile His Asp Ile Thr Thr Val
195 200 205

Asn Leu Glu Glu Glu Ala Ser Leu Glu Thr Asn Lys Ser Ser Ile Val
210 215 220

Val Gly Asp Gln Arg Ser Arg Leu Thr Ala Phe Pro Trp Asn Gln Thr
225 230 235 240

Asp Asn Asn Gly Thr Gln Ala Asp Ala Phe Asn Ile Thr Ile Gly Asn
245 250 255

Ala Ile Ser Gly Val His Ser Tyr Gly Gln Val Met Ile Gly Gly Tyr
260 265 270

Asn Asn Ala Asp Ser Cys Tyr Asp Ala Gln Asn Thr Met Phe Gln Leu
275 280 285

<210> 255 <211> 800 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (34)..(786) <223> G1646

<400> 255
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54

Met Asp Asn Asn Asn Asn Asn
1 5

aac aac cag caa cca cca cca acc tcc gtc tat cca cct ggc tcc gcc
102

Asn Asn Gln Gln Pro Pro Pro Thr Ser Val Tyr Pro Pro Gly Ser Ala
10 15 20

gtc aca acc gta atc cct cct cca cca tct gga tct gca tca ata gtc
150

Val Thr Thr Val Ile Pro Pro Pro Pro Ser Gly Ser Ala Ser Ile Val
25 30 35

acc gga gga gga gcg aca tac cac cac ctc ctc cag caa caa cag caa
198

Thr Gly Gly Gly Ala Thr Tyr His His Leu Leu Gln Gln Gln Gln Gln
40 45 50 55

cag ctt caa atg ttc tgg aca tac cag aga caa gag atc gaa cag gta
246

Gln Leu Gln Met Phe Trp Thr Tyr Gln Arg Gln Glu Ile Glu Gln Val
60 65 70

aac gat ttc aaa aac cat cag ctc cct cta gct cgt atc aaa aaa atc
294

Asn Asp Phe Lys Asn His Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile
75 80 85

atg aaa gct gat gaa gat gtg cgt atg atc tcc gcc gaa gca ccg att
342

Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Ile
90 95 100

ctc ttc gcg aaa gct tgt gag ctt ttc att ctc gaa ctt acg att aga
390

Leu Phe Ala Lys Ala Cys Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg
105 110 115

tct tgg ctt cac gct gaa gag aac aaa cgt cgt acg ctt cag aaa aac
438

Ser Trp Leu His Ala Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn

120 125 130 135
 gat atc gct gct gcg att act aga acc gat atc ttc gat ttc ctt gtt
 486
 Asp Ile Ala Ala Ala Ile Thr Arg Thr Asp Ile Phe Asp Phe Leu Val
 140 145 150

 gat att gtt cct agg gaa gag atc aag gaa gag gaa gat gca gca tcg
 534
 Asp Ile Val Pro Arg Glu Glu Ile Lys Glu Glu Glu Asp Ala Ala Ser
 155 160 165

 gct ctt ggt gga gga ggt atg gtt gct ccc gcc gcg agc ggt gtt cct
 582
 Ala Leu Gly Gly Gly Gly Met Val Ala Pro Ala Ala Ser Gly Val Pro
 170 175 180

 tat tat tat cca ccg atg gga caa ccg gcg gtt cct gga ggg atg atg
 630
 Tyr Tyr Tyr Pro Pro Met Gly Gln Pro Ala Val Pro Gly Gly Met Met
 185 190 195

 att gga aga ccg gcg atg gat cct agc ggt gtt tat gct cag cct cct
 678
 Ile Gly Arg Pro Ala Met Asp Pro Ser Gly Val Tyr Ala Gln Pro Pro
 200 205 210 215

 tct cag gca tgg caa agc gtt tgg cag aat tca gct ggt ggt ggt gat
 726
 Ser Gln Ala Trp Gln Ser Val Trp Gln Asn Ser Ala Gly Gly Gly Asp
 220 225 230

 gat gtg tct tat gga agt gga gga agt agc ggc cat ggt aat ctc gat
 774
 Asp Val Ser Tyr Gly Ser Gly Gly Ser Ser Gly His Gly Asn Leu Asp
 235 240 245

 agc caa ggg taa gtgaattcta gtag
 800
 Ser Gln Gly
 250

 <210> 256 <211> 250 <212> PRT <213> Arabidopsis thaliana <400>
 256

 Met Asp Asn Asn Asn Asn Asn Asn Asn Gln Gln Pro Pro Pro Thr Ser
 1 5 10 15

 Val Tyr Pro Pro Gly Ser Ala Val Thr Thr Val Ile Pro Pro Pro Pro
 20 25 30

 Ser Gly Ser Ala Ser Ile Val Thr Gly Gly Gly Ala Thr Tyr His His
 35 40 45

 Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Met Phe Trp Thr Tyr Gln
 50 55 60

Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn His Gln Leu Pro
65 70 75 80

Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met
85 90 95

Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys Ala Cys Glu Leu Phe
100 105 110

Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala Glu Glu Asn Lys
115 120 125

Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Ile Thr Arg Thr
130 135 140

Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Glu Glu Ile Lys
145 150 155 160

Glu Glu Glu Asp Ala Ala Ser Ala Leu Gly Gly Gly Gly Met Val Ala
165 170 175

Pro Ala Ala Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro
180 185 190

Ala Val Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Ser
195 200 205

Gly Val Tyr Ala Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln
210 215 220

Asn Ser Ala Gly Gly Gly Asp Asp Val Ser Tyr Gly Ser Gly Gly Ser
225 230 235 240

Ser Gly His Gly Asn Leu Asp Ser Gln Gly
245 250

<210> 257 <211> 938 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (142)..(903) <223> G1667

<400> 257
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60

caaaatctcc ttacttaaac tcacaaactc ctcacaaatt ttctgaatct ttcagttgaa
120

catataacaa cattcataac a atg gct gga ggt aca gct cta act cca acc
171

458

190 195 200
 gat gat gat gaa gct gcc tct atg cag aac cag cag tac tac cag aat
 795
 Asp Asp Asp Glu Ala Ala Ser Met Gln Asn Gln Gln Tyr Tyr Gln Asn
 205 210 215
 gga aga tcc cgt cct tta gat gac att cat gga ctg cct caa aat ctg
 843
 Gly Arg Ser Arg Pro Leu Asp Asp Ile His Gly Leu Pro Gln Asn Leu
 220 225 230
 ctc act aat gga aac tcg gct tct gat atc tac tct tgg ggg cct tgg
 891
 Leu Thr Asn Gly Asn Ser Ala Ser Asp Ile Tyr Ser Trp Gly Pro Trp
 235 240 245 250
 aat caa aga taa atgtgtctgt aggttgagag agaaccgtaa gtctg
 938
 Asn Gln Arg

<210> 258 <211> 253 <212> PRT <213> Arabidopsis thaliana <400>
 258

Met Ala Gly Gly Thr Ala Leu Thr Pro Thr Ser Val Gly Ser Lys Ser
 1 5 10 15

Val Pro Met Arg Asn His Glu Ala Thr Glu Arg Gly Asn Thr Asn Asn
 20 25 30

Asn Leu Arg Ala Leu Pro Lys Ala Val Gln Pro Val Ser Ser Ile Glu
 35 40 45

Gly Glu Met Ala Lys Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn
 50 55 60

Lys Pro Lys Pro Pro Ile Ile Val Thr His Asp Ser Pro Asn Ser Leu
 65 70 75 80

Arg Ala Asn Ala Val Glu Ile Ser Ser Gly Cys Asp Ile Cys Glu Thr
 85 90 95

Leu Ser Asp Phe Ala Arg Arg Lys Gln Arg Gly Leu Cys Ile Leu Ser
 100 105 110

Ala Asn Gly Cys Val Thr Asn Val Thr Leu Arg Gln Pro Ala Ser Ser
 115 120 125

Gly Ala Ile Val Thr Leu His Gly Arg Tyr Glu Ile Leu Ser Leu Leu
 130 135 140

Gly Ser Ile Leu Pro Pro Pro Ala Pro Leu Gly Ile Thr Gly Leu Thr
145 150 155 160

Ile Tyr Leu Ala Gly Pro Gln Gly Gln Val Val Gly Gly Gly Val Val
165 170 175

Gly Gly Leu Ile Ala Ser Gly Pro Val Val Leu Met Ala Ala Ser Phe
180 185 190

Met Asn Ala Val Phe Asp Arg Leu Pro Met Asp Asp Asp Glu Ala Ala
195 200 205

Ser Met Gln Asn Gln Gln Tyr Tyr Gln Asn Gly Arg Ser Arg Pro Leu
210 215 220

Asp Asp Ile His Gly Leu Pro Gln Asn Leu Leu Thr Asn Gly Asn Ser
225 230 235 240

Ala Ser Asp Ile Tyr Ser Trp Gly Pro Trp Asn Gln Arg
245 250

<210> 259 <211> 1221 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1221) <223> G1706

<400> 259

atg aaa aat aaa acc caa aaa tat ata gat aag aag acg tgg aac tat
48

Met Lys Asn Lys Thr Gln Lys Tyr Ile Asp Lys Lys Thr Trp Asn Tyr
1 5 10 15

ata aat atg gac cac cat cac gcc ttt gca tca cat tca tac aac tca
96

Ile Asn Met Asp His His His Ala Phe Ala Ser His Ser Tyr Asn Ser
20 25 30

gtt ttc ata agc aaa aag gca atg gaa gag tca cga tcc tac aga aag
144

Val Phe Ile Ser Lys Lys Ala Met Glu Glu Ser Arg Ser Tyr Arg Lys
35 40 45

gag agg aag cag aca aag aag aaa acg ggt cgt ggg tca gga tcc agg
192

Glu Arg Lys Gln Thr Lys Lys Lys Thr Gly Arg Gly Ser Gly Ser Arg
50 55 60

tcg atc cat ata aag atg agg aag ctt cga gtg ctt ata ccg ggt gga
240

Ser Ile His Ile Lys Met Arg Lys Leu Arg Val Leu Ile Pro Gly Gly
65 70 75 80

cga aga ttg aac caa ccg gat ctg ctt cta tca aag act gct gat tat
288

Arg Arg Leu Asn Gln Pro Asp Leu Leu Leu Ser Lys Thr Ala Asp Tyr

	85	90	95
att atg cat ttg gag ttg agg att agc att cta cat ttg ttg gtc aga			
336			
Ile Met His Leu Glu Leu Arg Ile Ser Ile Leu His Leu Leu Val Arg			
	100	105	110
tat tac tta aag aag aaa aga tca aac ctt tcg tca tca cca aac gaa			
384			
Tyr Tyr Leu Lys Lys Lys Arg Ser Asn Leu Ser Ser Ser Pro Asn Glu			
	115	120	125
tct aat caa aac cca gaa ttt tcc gac tcc gat act tac caa aga cag			
432			
Ser Asn Gln Asn Pro Glu Phe Ser Asp Ser Asp Thr Tyr Gln Arg Gln			
	130	135	140
ctt caa cag ctc ttt cat ctc cat gat tca ggt cta gat caa gct tta			
480			
Leu Gln Gln Leu Phe His Leu His Asp Ser Gly Leu Asp Gln Ala Leu			
	145	150	155
atc gat gct ctt cct gtg ttt ctt tac aaa gag atc aaa ggt acg aaa			
528			
Ile Asp Ala Leu Pro Val Phe Leu Tyr Lys Glu Ile Lys Gly Thr Lys			
	165	170	175
gag cct ttt gat tgt gca gtg tgt ctc tgt gaa ttc tcg gaa gat gat			
576			
Glu Pro Phe Asp Cys Ala Val Cys Leu Cys Glu Phe Ser Glu Asp Asp			
	180	185	190
aag ctt aga ttg ctt ccg aat tgt agt cac gct ttt cac ata gat tgt			
624			
Lys Leu Arg Leu Leu Pro Asn Cys Ser His Ala Phe His Ile Asp Cys			
	195	200	205
atc gat act tgg ctt ctc tcg aat tcg act tgt cca ctt tgt aga gga			
672			
Ile Asp Thr Trp Leu Leu Ser Asn Ser Thr Cys Pro Leu Cys Arg Gly			
	210	215	220
acc ctt ttc tct tta ggt cat caa ttt gaa tac cct gat ttc aat ttc			
720			
Thr Leu Phe Ser Leu Gly His Gln Phe Glu Tyr Pro Asp Phe Asn Phe			
	225	230	235
ggg ttt ttc gcc gga gat gat gga gga gga gga gtt agg gtt tct ccg			
768			
Gly Phe Phe Ala Gly Asp Asp Gly Gly Gly Gly Val Arg Val Ser Pro			
	245	250	255
gtt cag aaa cca gct gag aat gag att ggg aag aga gtg ttt tca gtg			
816			
Val Gln Lys Pro Ala Glu Asn Glu Ile Gly Lys Arg Val Phe Ser Val			
	260	265	270
agg ctt ggt aag ttt agg agc agt aat att gtc aac aat ggt gaa gta			
864			
Arg Leu Gly Lys Phe Arg Ser Ser Asn Ile Val Asn Asn Gly Glu Val			
	275	280	285

gta gta gga gga gga gga gag aca agt agt agt agt ctt gat aat aga
912

Val Val Gly Gly Gly Gly Glu Thr Ser Ser Ser Ser Leu Asp Asn Arg
290 295 300

aga tgt ttc tca atg ggg tct tat cag tac ata gtg gct gaa tca gat
960

Arg Cys Phe Ser Met Gly Ser Tyr Gln Tyr Ile Val Ala Glu Ser Asp
305 310 315 320

ctg gtt gtt gct ttg tgt cct aat aat gaa gga ttg aag aat aat aag
1008

Leu Val Val Ala Leu Cys Pro Asn Asn Glu Gly Leu Lys Asn Asn Lys
325 330 335

gat gtt gaa ggg aag aag att aat atg aga agt aaa ggt gag agc ttt
1056

Asp Val Glu Gly Lys Lys Ile Asn Met Arg Ser Lys Gly Glu Ser Phe
340 345 350

tct gtg tca aag att tgg caa tgg tct aat aag aga tca aag ttt cct
1104

Ser Val Ser Lys Ile Trp Gln Trp Ser Asn Lys Arg Ser Lys Phe Pro
355 360 365

aat aat cat cca tca gag act aat ctt gtg gtt ggt ggt tct tct tct
1152

Asn Asn His Pro Ser Glu Thr Asn Leu Val Val Gly Gly Ser Ser Ser
370 375 380

tct tct tct tat gtt tgt tct gga tct gat ggg tta tca ttg aat gga
1200

Ser Ser Ser Tyr Val Cys Ser Gly Ser Asp Gly Leu Ser Leu Asn Gly
385 390 395 400

agg aga ttt cag ggt cca tga
1221

Arg Arg Phe Gln Gly Pro
405

<210> 260 <211> 406 <212> PRT <213> Arabidopsis thaliana <400>
260

Met Lys Asn Lys Thr Gln Lys Tyr Ile Asp Lys Lys Thr Trp Asn Tyr
1 5 10 15

Ile Asn Met Asp His His His Ala Phe Ala Ser His Ser Tyr Asn Ser
20 25 30

Val Phe Ile Ser Lys Lys Ala Met Glu Glu Ser Arg Ser Tyr Arg Lys
35 40 45

Glu Arg Lys Gln Thr Lys Lys Lys Thr Gly Arg Gly Ser Gly Ser Arg
50 55 60

Ser Ile His Ile Lys Met Arg Lys Leu Arg Val Leu Ile Pro Gly Gly
 65 70 75 80
 Arg Arg Leu Asn Gln Pro Asp Leu Leu Leu Ser Lys Thr Ala Asp Tyr
 85 90 95
 Ile Met His Leu Glu Leu Arg Ile Ser Ile Leu His Leu Leu Val Arg
 100 105 110
 Tyr Tyr Leu Lys Lys Lys Arg Ser Asn Leu Ser Ser Ser Pro Asn Glu
 115 120 125
 Ser Asn Gln Asn Pro Glu Phe Ser Asp Ser Asp Thr Tyr Gln Arg Gln
 130 135 140
 Leu Gln Gln Leu Phe His Leu His Asp Ser Gly Leu Asp Gln Ala Leu
 145 150 155 160
 Ile Asp Ala Leu Pro Val Phe Leu Tyr Lys Glu Ile Lys Gly Thr Lys
 165 170 175
 Glu Pro Phe Asp Cys Ala Val Cys Leu Cys Glu Phe Ser Glu Asp Asp
 180 185 190
 Lys Leu Arg Leu Leu Pro Asn Cys Ser His Ala Phe His Ile Asp Cys
 195 200 205
 Ile Asp Thr Trp Leu Leu Ser Asn Ser Thr Cys Pro Leu Cys Arg Gly
 210 215 220
 Thr Leu Phe Ser Leu Gly His Gln Phe Glu Tyr Pro Asp Phe Asn Phe
 225 230 235 240
 Gly Phe Phe Ala Gly Asp Asp Gly Gly Gly Gly Val Arg Val Ser Pro
 245 250 255
 Val Gln Lys Pro Ala Glu Asn Glu Ile Gly Lys Arg Val Phe Ser Val
 260 265 270
 Arg Leu Gly Lys Phe Arg Ser Ser Asn Ile Val Asn Asn Gly Glu Val
 275 280 285
 Val Val Gly Gly Gly Gly Glu Thr Ser Ser Ser Ser Leu Asp Asn Arg
 290 295 300
 Arg Cys Phe Ser Met Gly Ser Tyr Gln Tyr Ile Val Ala Glu Ser Asp

305 310 315 320
 Leu Val Val Ala Leu Cys Pro Asn Asn Glu Gly Leu Lys Asn Asn Lys
 325 330 335
 Asp Val Glu Gly Lys Lys Ile Asn Met Arg Ser Lys Gly Glu Ser Phe
 340 345 350
 Ser Val Ser Lys Ile Trp Gln Trp Ser Asn Lys Arg Ser Lys Phe Pro
 355 360 365
 Asn Asn His Pro Ser Glu Thr Asn Leu Val Val Gly Gly Ser Ser Ser
 370 375 380
 Ser Ser Ser Tyr Val Cys Ser Gly Ser Asp Gly Leu Ser Leu Asn Gly
 385 390 395 400
 Arg Arg Phe Gln Gly Pro
 405

<210> 261 <211> 1410 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (32)..(1216) <223> G1766

<400> 261

aggctattct cggaataaaca aagaataaag a atg aat tcg ttt tca caa gta
 52

Met Asn Ser Phe Ser Gln Val
 1 5

cct cct ggc ttc aga ttt cat cct act gat gaa gaa ctt gta gac tac
 100

Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Asp Tyr
 10 15 20

tac ttg agg aaa aaa gtt gca tca aag aga ata gaa atc gat atc atc
 148

Tyr Leu Arg Lys Lys Val Ala Ser Lys Arg Ile Glu Ile Asp Ile Ile
 25 30 35

aag gat gtt gat ctt tac aag att gag cca tgt gat ctt caa gag tta
 196

Lys Asp Val Asp Leu Tyr Lys Ile Glu Pro Cys Asp Leu Gln Glu Leu
 40 45 50 55

tgc aag ata gga aac gaa gag cag agc gaa tgg tac ttc ttt agt cat
 244

Cys Lys Ile Gly Asn Glu Glu Gln Ser Glu Trp Tyr Phe Phe Ser His
 60 65 70

aaa gac aag aag tat ccc acg gga act cga acc aat aga gcc acg aaa
 292

Lys Asp Lys Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala Thr Lys
 75 80 85

gca gga ttt tgg aaa gcc act gga aga gac aag gct ata tat ata aga
 340
 Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ala Ile Tyr Ile Arg
 90 95 100

cat agt ctt atc ggt atg agg aaa aca ctt gtg ttt tac aaa gga aga
 388
 His Ser Leu Ile Gly Met Arg Lys Thr Leu Val Phe Tyr Lys Gly Arg
 105 110 115

gcc cca aat ggt cag aaa tcc gat tgg atc atg cac gaa tat cgc tta
 436
 Ala Pro Asn Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr Arg Leu
 120 125 130 135

gaa aca agt gaa aat gga acc cct cag gaa gaa gga tgg gta gta tgt
 484
 Glu Thr Ser Glu Asn Gly Thr Pro Gln Glu Glu Gly Trp Val Val Cys
 140 145 150

agg gta ttc aag aag aaa ttg gca gcg aca gtg agg aaa atg gga gat
 532
 Arg Val Phe Lys Lys Lys Leu Ala Ala Thr Val Arg Lys Met Gly Asp
 155 160 165

tac cat tca tca cca tcg cag cat tgg tac gat gat cag ctc tct ttt
 580
 Tyr His Ser Ser Pro Ser Gln His Trp Tyr Asp Asp Gln Leu Ser Phe
 170 175 180

atg gcc tcc gag atc att tct agt tct cca cga cag ttt ctt ccc aat
 628
 Met Ala Ser Glu Ile Ile Ser Ser Ser Pro Arg Gln Phe Leu Pro Asn
 185 190 195

cat cat tat aac cgc cac cat cac cag cag aca ttg cct tgt ggc ctc
 676
 His His Tyr Asn Arg His His His Gln Gln Thr Leu Pro Cys Gly Leu
 200 205 210 215

aat gca ttc aac aac aac aat cct aac ttg caa tgc aag caa gag ctc
 724
 Asn Ala Phe Asn Asn Asn Asn Pro Asn Leu Gln Cys Lys Gln Glu Leu
 220 225 230

gag tta cat tac aat caa atg gta caa cat caa caa caa aac cat cat
 772
 Glu Leu His Tyr Asn Gln Met Val Gln His Gln Gln Gln Asn His His
 235 240 245

ctt cgt gaa tct atg ttt ctc cag ctt cct cag ctc gaa agc cct acc
 820
 Leu Arg Glu Ser Met Phe Leu Gln Leu Pro Gln Leu Glu Ser Pro Thr
 250 255 260

agt aat tgc aat tct gac aac aac aat aac aca aga aat att agt aac
 868
 Ser Asn Cys Asn Ser Asp Asn Asn Asn Asn Thr Arg Asn Ile Ser Asn
 265 270 275

ttg cag aaa tca tca aat ata tct cat gag gaa caa ttg caa caa ggg
916

Leu Gln Lys Ser Ser Asn Ile Ser His Glu Glu Gln Leu Gln Gln Gly
280 285 290 295

aat caa agt ttc agc tct ctg tat tac gat caa gga gta gag caa atg
964

Asn Gln Ser Phe Ser Ser Leu Tyr Tyr Asp Gln Gly Val Glu Gln Met
300 305 310

act act gac tgg aga gtt ctc gat aaa ttt gtt gct tca cag ctt agc
1012

Thr Thr Asp Trp Arg Val Leu Asp Lys Phe Val Ala Ser Gln Leu Ser
315 320 325

aat gat gaa gag gct gca gcc gtg gtt tct tct tct tct cat caa aac
1060

Asn Asp Glu Glu Ala Ala Ala Val Val Ser Ser Ser Ser His Gln Asn
330 335 340

aac gtc aag att gac acg aga aac acg ggt tat cat gtg ata gat gag
1108

Asn Val Lys Ile Asp Thr Arg Asn Thr Gly Tyr His Val Ile Asp Glu
345 350 355

gga ata aat ttg ccg gag aat gat tct gaa agg gtt gtt gaa atg gga
1156

Gly Ile Asn Leu Pro Glu Asn Asp Ser Glu Arg Val Val Glu Met Gly
360 365 370 375

gaa gag tat tca aat gct cat gct gct tct act tct tca agt tgt cag
1204

Glu Glu Tyr Ser Asn Ala His Ala Ala Ser Thr Ser Ser Ser Cys Gln
380 385 390

att gat ctc tag aaatagtgat agagagatga aaaagatgca aggtgaatat
1256

Ile Asp Leu

atatgaaaat acatgcacac tagtggttatt tatacttaaa gatggaaggg gaaaaacaag
1316

gagttatttc ctggatttat ggaggttttg tacataataa aaacctacaa ccatatggta
1376

ttttcttttg aaaaaaaaaa aaaaaaaaaa aaaa
1410

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262

Met Asn Ser Phe Ser Gln Val Pro Pro Gly Phe Arg Phe His Pro Thr
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Asp Glu Glu Leu Val Asp Tyr Tyr Leu Arg Lys Lys Val Ala Ser Lys
20 25 30

Arg Ile Glu Ile Asp Ile Ile Lys Asp Val Asp Leu Tyr Lys Ile Glu
 35 40 45

Pro Cys Asp Leu Gln Glu Leu Cys Lys Ile Gly Asn Glu Glu Gln Ser
 50 55 60

Glu Trp Tyr Phe Phe Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr
 65 70 75 80

Arg Thr Asn Arg Ala Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg
 85 90 95

Asp Lys Ala Ile Tyr Ile Arg His Ser Leu Ile Gly Met Arg Lys Thr
 100 105 110

Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp
 115 120 125

Ile Met His Glu Tyr Arg Leu Glu Thr Ser Glu Asn Gly Thr Pro Gln
 130 135 140

Glu Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Lys Leu Ala Ala
 145 150 155 160

Thr Val Arg Lys Met Gly Asp Tyr His Ser Ser Pro Ser Gln His Trp
 165 170 175

Tyr Asp Asp Gln Leu Ser Phe Met Ala Ser Glu Ile Ile Ser Ser Ser
 180 185 190

Pro Arg Gln Phe Leu Pro Asn His His Tyr Asn Arg His His His Gln
 195 200 205

Gln Thr Leu Pro Cys Gly Leu Asn Ala Phe Asn Asn Asn Asn Pro Asn
 210 215 220

Leu Gln Cys Lys Gln Glu Leu Glu Leu His Tyr Asn Gln Met Val Gln
 225 230 235 240

His Gln Gln Gln Asn His His Leu Arg Glu Ser Met Phe Leu Gln Leu
 245 250 255

Pro Gln Leu Glu Ser Pro Thr Ser Asn Cys Asn Ser Asp Asn Asn Asn
 260 265 270

Asn Thr Arg Asn Ile Ser Asn Leu Gln Lys Ser Ser Asn Ile Ser His

275 280 285
 Glu Glu Gln Leu Gln Gln Gly Asn Gln Ser Phe Ser Ser Leu Tyr Tyr
 290 295 300
 Asp Gln Gly Val Glu Gln Met Thr Thr Asp Trp Arg Val Leu Asp Lys
 305 310 315 320
 Phe Val Ala Ser Gln Leu Ser Asn Asp Glu Glu Ala Ala Ala Val Val
 325 330 335
 Ser Ser Ser Ser His Gln Asn Asn Val Lys Ile Asp Thr Arg Asn Thr
 340 345 350
 Gly Tyr His Val Ile Asp Glu Gly Ile Asn Leu Pro Glu Asn Asp Ser
 355 360 365
 Glu Arg Val Val Glu Met Gly Glu Glu Tyr Ser Asn Ala His Ala Ala
 370 375 380
 Ser Thr Ser Ser Ser Cys Gln Ile Asp Leu
 385 390
 <210> 263 <211> 927 <212> DNA <213> Arabidopsis thaliana <220>
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 48
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 1 5 10 15
 cct aca aca aat tca aat att caa gga tct gaa tct ttc agc ttg act
 96
 Pro Thr Thr Asn Ser Asn Ile Gln Gly Ser Glu Ser Phe Ser Leu Thr
 20 25 30
 aag gat atg ata atg tct aca aca caa tta ccc gcg atg aaa cat tcg
 144
 Lys Asp Met Ile Met Ser Thr Thr Gln Leu Pro Ala Met Lys His Ser
 35 40 45
 ggt ttg cag ctg caa aat caa gat tca acc tca tca caa tct act gaa
 192
 Gly Leu Gln Leu Gln Asn Gln Asp Ser Thr Ser Ser Gln Ser Thr Glu
 50 55 60
 gaa gaa tca ggc ggc ggt gaa gtt gca agc ttt gga gaa tat aag cgt
 240
 Glu Glu Ser Gly Gly Gly Glu Val Ala Ser Phe Gly Glu Tyr Lys Arg
 65 70 75 80

tat gga tgc agc att gtt aat aac aat ctc tca ggt tac atc gaa aac
 288
 Tyr Gly Cys Ser Ile Val Asn Asn Asn Leu Ser Gly Tyr Ile Glu Asn
 85 90 95

ttg gga aag cct att gaa aat tat act aag tca att act acc tcg tcg
 336
 Leu Gly Lys Pro Ile Glu Asn Tyr Thr Lys Ser Ile Thr Thr Ser Ser
 100 105 110

atg gtg tct caa gac tct gtg ttt cct gct cct act tct ggt caa ata
 384
 Met Val Ser Gln Asp Ser Val Phe Pro Ala Pro Thr Ser Gly Gln Ile
 115 120 125

tct tgg tct ctt caa tgt gct gaa acg tca cat ttc aat ggt ttc ttg
 432
 Ser Trp Ser Leu Gln Cys Ala Glu Thr Ser His Phe Asn Gly Phe Leu
 130 135 140

gct cct gaa tat gca tca aca cca acg gcg ctg cca cat tta gag atg
 480
 Ala Pro Glu Tyr Ala Ser Thr Pro Thr Ala Leu Pro His Leu Glu Met
 145 150 155 160

atg ggt ttg gtt tct tca aga gtg cca ttg cct cat cac att caa gag
 528
 Met Gly Leu Val Ser Ser Arg Val Pro Leu Pro His His Ile Gln Glu
 165 170 175

aat gaa cca ata ttt gtc aat gcg aaa cag tat cat gcg att ctc cgt
 576
 Asn Glu Pro Ile Phe Val Asn Ala Lys Gln Tyr His Ala Ile Leu Arg
 180 185 190

cgc agg aag cac cgt gct aaa ctc gaa gct cag aac aaa ctc atc aaa
 624
 Arg Arg Lys His Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Ile Lys
 195 200 205

tgc cgt aaa ccg tac ctt cat gag tct cgc cat ctt cat gct tta aag
 672
 Cys Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His Ala Leu Lys
 210 215 220

aga gct aga ggc tcc ggt gga cgt ttc ctc aat aca aag aag ctt caa
 720
 Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Lys Leu Gln
 225 230 235 240

gaa tca tca aac tca ctg tgt tct tct caa atg gca aat gga caa aat
 768
 Glu Ser Ser Asn Ser Leu Cys Ser Ser Gln Met Ala Asn Gly Gln Asn
 245 250 255

ttc tct atg agc cct cac ggt ggt gga agc gga atc ggg tct agt tcg
 816
 Phe Ser Met Ser Pro His Gly Gly Gly Ser Gly Ile Gly Ser Ser Ser
 260 265 270

atc tca ccg agc tcc aat tca aac tgt atc aac atg ttc caa aac ccg
864

Ile Ser Pro Ser Ser Asn Ser Asn Cys Ile Asn Met Phe Gln Asn Pro
275 280 285

cag ttg aga ttc tca ggt tat ccg tca aca cac cat gcc tca gct ctg
912

Gln Phe Arg Phe Ser Gly Tyr Pro Ser Thr His His Ala Ser Ala Leu
290 295 300

atg tca ggg act tga
927

Met Ser Gly Thr
305

<210> 264 <211> 308 <212> PRT <213> Arabidopsis thaliana <400>
264

Met Gln Val Phe Gln Arg Lys Glu Asp Ser Ser Trp Gly Asn Ser Met
1 5 10 15

Pro Thr Thr Asn Ser Asn Ile Gln Gly Ser Glu Ser Phe Ser Leu Thr
20 25 30

Lys Asp Met Ile Met Ser Thr Thr Gln Leu Pro Ala Met Lys His Ser
35 40 45

Gly Leu Gln Leu Gln Asn Gln Asp Ser Thr Ser Ser Gln Ser Thr Glu
50 55 60

Glu Glu Ser Gly Gly Gly Glu Val Ala Ser Phe Gly Glu Tyr Lys Arg
65 70 75 80

Tyr Gly Cys Ser Ile Val Asn Asn Asn Leu Ser Gly Tyr Ile Glu Asn
85 90 95

Leu Gly Lys Pro Ile Glu Asn Tyr Thr Lys Ser Ile Thr Thr Ser Ser
100 105 110

Met Val Ser Gln Asp Ser Val Phe Pro Ala Pro Thr Ser Gly Gln Ile
115 120 125

Ser Trp Ser Leu Gln Cys Ala Glu Thr Ser His Phe Asn Gly Phe Leu
130 135 140

Ala Pro Glu Tyr Ala Ser Thr Pro Thr Ala Leu Pro His Leu Glu Met
145 150 155 160

Met Gly Leu Val Ser Ser Arg Val Pro Leu Pro His His Ile Gln Glu
165 170 175

Asn Glu Pro Ile Phe Val Asn Ala Lys Gln Tyr His Ala Ile Leu Arg
180 185 190

Arg Arg Lys His Arg Ala Lys Leu Glu Ala Gln Asn Lys Leu Ile Lys
195 200 205

Cys Arg Lys Pro Tyr Leu His Glu Ser Arg His Leu His Ala Leu Lys
210 215 220

Arg Ala Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Lys Leu Gln
225 230 235 240

Glu Ser Ser Asn Ser Leu Cys Ser Ser Gln Met Ala Asn Gly Gln Asn
245 250 255

Phe Ser Met Ser Pro His Gly Gly Gly Ser Gly Ile Gly Ser Ser Ser
260 265 270

Ile Ser Pro Ser Ser Asn Ser Asn Cys Ile Asn Met Phe Gln Asn Pro
275 280 285

Gln Phe Arg Phe Ser Gly Tyr Pro Ser Thr His His Ala Ser Ala Leu
290 295 300

Met Ser Gly Thr
305

<210> 265 <211> 450 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (27)..(422) <223> G1795

<400> 265
acaaacacgc aaaaagtcac taatat atg gat caa gga ggt cga ggt gtc ggt
53

Met Asp Gln Gly Gly Arg Gly Val Gly
1 5

gcc gag cat gga aag tac cgg gga gtt cgg aga cga cct tgg gga aaa
101

Ala Glu His Gly Lys Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys
10 15 20 25

tat gca gca gag ata cga gat tcg agg aag cac ggt gaa cgt gtg tgg
149

Tyr Ala Ala Glu Ile Arg Asp Ser Arg Lys His Gly Glu Arg Val Trp
30 35 40

ctt gga acg ttc gat acg gca gag gaa gcg gct aga gcc tat gac caa
197

Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Gln
45 50 55

gct gct tac tcc atg aga ggc caa gca gca atc ctt aac ttc cct cat
 245
 Ala Ala Tyr Ser Met Arg Gly Gln Ala Ala Ile Leu Asn Phe Pro His
 60 65 70

gag tat aac atg ggg agt ggt gtc tct tct tcc acc gcc atg gct gga
 293
 Glu Tyr Asn Met Gly Ser Gly Val Ser Ser Ser Thr Ala Met Ala Gly
 75 80 85

tct tcc tcc gcc tcc gcc tcc gct tct tct tct tct agg caa gtt ttt
 341
 Ser Ser Ser Ala Ser Ala Ser Ala Ser Ser Ser Ser Arg Gln Val Phe
 90 95 100 105

gaa ttt gag tac ttg gat gat agt gtt ttg gag gag ctc ctt gag gaa
 389
 Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Glu Glu Leu Leu Glu Glu
 110 115 120

gga gag aaa cct aac aag ggc aag aag aaa tga gcgagatata attcatgatt
 442
 Gly Glu Lys Pro Asn Lys Gly Lys Lys Lys
 125 130

atttctaa
 450

<210> 266 <211> 131 <212> PRT <213> Arabidopsis thaliana <400>
 266

Met Asp Gln Gly Gly Arg Gly Val Gly Ala Glu His Gly Lys Tyr Arg
 1 5 10 15

Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp
 20 25 30

Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
 35 40 45

Glu Glu Ala Ala Arg Ala Tyr Asp Gln Ala Ala Tyr Ser Met Arg Gly
 50 55 60

Gln Ala Ala Ile Leu Asn Phe Pro His Glu Tyr Asn Met Gly Ser Gly
 65 70 75 80

Val Ser Ser Ser Thr Ala Met Ala Gly Ser Ser Ser Ala Ser Ala Ser
 85 90 95

Ala Ser Ser Ser Ser Arg Gln Val Phe Glu Phe Glu Tyr Leu Asp Asp
 100 105 110

Ser Val Leu Glu Glu Leu Leu Glu Glu Gly Glu Lys Pro Asn Lys Gly
 115 120 125

Lys Lys Lys
 130

<210> 267 <211> 1716 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (169)..(1497) <223> G1804

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aaggaggaga acctccataa caagaagcgg attctctcag ttttccggcg gcggaggaac
 120

acaaagccac cggttttttag acacacagat ttcattttca gttgttaa atg gta act
 177

Met Val Thr
 1

aga gaa acg aag ttg acg tca gag cga gaa gta gag tcg tcc atg gcg
 225
 Arg Glu Thr Lys Leu Thr Ser Glu Arg Glu Val Glu Ser Ser Met Ala
 5 10 15

caa gcg aga cat aat gga gga ggt ggt ggt gag aat cat ccg ttt act
 273
 Gln Ala Arg His Asn Gly Gly Gly Gly Glu Asn His Pro Phe Thr
 20 25 30 35

tct ttg gga aga caa tcc tct atc tac tca ttg acc ctt gac gag ttc
 321
 Ser Leu Gly Arg Gln Ser Ser Ile Tyr Ser Leu Thr Leu Asp Glu Phe
 40 45 50

caa cat gct tta tgt gag aac ggc aag aac ttt ggg tcc atg aac atg
 369
 Gln His Ala Leu Cys Glu Asn Gly Lys Asn Phe Gly Ser Met Asn Met
 55 60 65

gac gag ttt ctt gtc tct att tgg aac gca gag gag aat aat aac aat
 417
 Asp Glu Phe Leu Val Ser Ile Trp Asn Ala Glu Glu Asn Asn Asn Asn
 70 75 80

caa caa caa gca gca gca gct gca ggt tca cat tct gtt ccg gct aat
 465
 Gln Gln Gln Ala Ala Ala Ala Ala Gly Ser His Ser Val Pro Ala Asn
 85 90 95

cac aat ggt ttc aac aac aac aat aac aat gga ggc gag ggt ggt gtt
 513
 His Asn Gly Phe Asn Asn Asn Asn Asn Asn Gly Gly Glu Gly Gly Val
 100 105 110 115

ggt gtc ttt agt ggt ggt tct aga ggc aac gaa gat gct aac aat aag
 561
 Gly Val Phe Ser Gly Gly Ser Arg Gly Asn Glu Asp Ala Asn Asn Lys

	120	125	130
aga ggg ata gcg aac gag tct agt ctt cct cga caa ggc tct ttg aca			
609			
Arg Gly Ile Ala Asn Glu Ser Ser Leu Pro Arg Gln Gly Ser Leu Thr			
	135	140	145
ctt cca gct ccg ctt tgt agg aag act gtt gat gag gtt tgg tct gag			
657			
Leu Pro Ala Pro Leu Cys Arg Lys Thr Val Asp Glu Val Trp Ser Glu			
	150	155	160
ata cat aga ggt ggt ggt agc ggt aat gga gga gac agc aat gga cgt .			
705			
Ile His Arg Gly Gly Gly Ser Gly Asn Gly Gly Asp Ser Asn Gly Arg			
	165	170	175
agt agt agt agt aat gga cag aac aat gct cag aac ggc ggt gag act			
753			
Ser Ser Ser Ser Asn Gly Gln Asn Asn Ala Gln Asn Gly Gly Glu Thr			
	180	185	190
gcg gct aga caa ccg act ttt gga gag atg aca ctt gag gat ttc ttg			
801			
Ala Ala Arg Gln Pro Thr Phe Gly Glu Met Thr Leu Glu Asp Phe Leu			
	200	205	210
gtg aag gct ggt gtg gtt aga gaa cat ccc act aat cct aaa cct aat			
849			
Val Lys Ala Gly Val Val Arg Glu His Pro Thr Asn Pro Lys Pro Asn			
	215	220	225
cca aac ccg aac caa aac caa aac ccg tct agt gta ata ccc gca gct			
897			
Pro Asn Pro Asn Gln Asn Gln Asn Pro Ser Ser Val Ile Pro Ala Ala			
	230	235	240
gca cag caa cag ctt tat ggt gtg ttt caa gga acc ggt gat cct tca			
945			
Ala Gln Gln Gln Leu Tyr Gly Val Phe Gln Gly Thr Gly Asp Pro Ser			
	245	250	255
ttc ccg ggt caa gct atg ggt gtg ggt gac cca tca ggt tat gct aaa			
993			
Phe Pro Gly Gln Ala Met Gly Val Gly Asp Pro Ser Gly Tyr Ala Lys			
	260	265	270
agg aca gga gga gga ggg tat cag cag gcg cca cca gtt cag gca ggt			
1041			
Arg Thr Gly Gly Gly Gly Tyr Gln Gln Ala Pro Pro Val Gln Ala Gly			
	280	285	290
gtt tgc tat gga ggt ggc gtt ggg ttt gga gcg ggt gga cag caa atg			
1089			
Val Cys Tyr Gly Gly Gly Val Gly Phe Gly Ala Gly Gly Gln Gln Met			
	295	300	305
gga atg gtt gga ccg tta agc ccg gtg tct tca gat gga tta gga cat			
1137			
Gly Met Val Gly Pro Leu Ser Pro Val Ser Ser Asp Gly Leu Gly His			
	310	315	320

gga caa gtg gat aac ata gga ggt cag tat gga gta gat atg gga ggg
1185

Gly Gln Val Asp Asn Ile Gly Gly Gln Tyr Gly Val Asp Met Gly Gly
325 330 335

cta agg gga agg aaa aga gta gtg gat ggt cca gtg gag aaa gta gtg
1233

Leu Arg Gly Arg Lys Arg Val Val Asp Gly Pro Val Glu Lys Val Val
340 345 350 355

gag aga aga cag agg agg atg atc aag aac cgc gag tct gct gct aga
1281

Glu Arg Arg Gln Arg Arg Met Ile Lys Asn Arg Glu Ser Ala Ala Arg
360 365 370

tct aga gca aga aaa caa gca tat aca gtg gaa ttg gaa gct gaa ctt
1329

Ser Arg Ala Arg Lys Gln Ala Tyr Thr Val Glu Leu Glu Ala Glu Leu
375 380 385

aac cag ttg aaa gaa gag aat gcg cag cta aaa cat gca ttg gcg gag
1377

Asn Gln Leu Lys Glu Glu Asn Ala Gln Leu Lys His Ala Leu Ala Glu
390 395 400

ttg gag agg aag agg aag caa cag tat ttt gag agt ttg aag tca agg
1425

Leu Glu Arg Lys Arg Lys Gln Gln Tyr Phe Glu Ser Leu Lys Ser Arg
405 410 415

gca caa ccg aaa ttg ccg aaa tcg aac ggg aga ttg cgg aca ttg atg
1473

Ala Gln Pro Lys Leu Pro Lys Ser Asn Gly Arg Leu Arg Thr Leu Met
420 425 430 435

agg aac ccg agt tgt cca ctc taa acaacaata ggaagatgga gaagaagtcg
1527

Arg Asn Pro Ser Cys Pro Leu
440

gagacagaac gagggaaaaa ctgatgattt tctacgttgt tgttttgtct ttgaggaatg
1587

aggttataga atctttatac ttgatgttt tctgtgttg taggaggaac accatctgat
1647

ctgctttact agtgttcct gtgaacaaag aaagtgttc tgtgtttcaa catcatcaat
1707

ctttggaaa
1716

<210> 268 <211> 442 <212> PRT <213> Arabidopsis thaliana <400>
268

Met Val Thr Arg Glu Thr Lys Leu Thr Ser Glu Arg Glu Val Glu Ser
1 5 10 15

Ser Met Ala Gln Ala Arg His Asn Gly Gly Gly Gly Glu Asn His
20 25 30

Pro Phe Thr Ser Leu Gly Arg Gln Ser Ser Ile Tyr Ser Leu Thr Leu
35 40 45

Asp Glu Phe Gln His Ala Leu Cys Glu Asn Gly Lys Asn Phe Gly Ser
50 55 60

Met Asn Met Asp Glu Phe Leu Val Ser Ile Trp Asn Ala Glu Glu Asn
65 70 75 80

Asn Asn Asn Gln Gln Gln Ala Ala Ala Ala Gly Ser His Ser Val
85 90 95

Pro Ala Asn His Asn Gly Phe Asn Asn Asn Asn Asn Gly Gly Glu
100 105 110

Gly Gly Val Gly Val Phe Ser Gly Gly Ser Arg Gly Asn Glu Asp Ala
115 120 125

Asn Asn Lys Arg Gly Ile Ala Asn Glu Ser Ser Leu Pro Arg Gln Gly
130 135 140

Ser Leu Thr Leu Pro Ala Pro Leu Cys Arg Lys Thr Val Asp Glu Val
145 150 155 160

Trp Ser Glu Ile His Arg Gly Gly Gly Ser Gly Asn Gly Gly Asp Ser
165 170 175

Asn Gly Arg Ser Ser Ser Ser Asn Gly Gln Asn Asn Ala Gln Asn Gly
180 185 190

Gly Glu Thr Ala Ala Arg Gln Pro Thr Phe Gly Glu Met Thr Leu Glu
195 200 205

Asp Phe Leu Val Lys Ala Gly Val Val Arg Glu His Pro Thr Asn Pro
210 215 220

Lys Pro Asn Pro Asn Pro Asn Gln Asn Gln Asn Pro Ser Ser Val Ile
225 230 235 240

Pro Ala Ala Ala Gln Gln Gln Leu Tyr Gly Val Phe Gln Gly Thr Gly
245 250 255

Asp Pro Ser Phe Pro Gly Gln Ala Met Gly Val Gly Asp Pro Ser Gly

260 265 270
 Tyr Ala Lys Arg Thr Gly Gly Gly Gly Tyr Gln Gln Ala Pro Pro Val
 275 280 285
 Gln Ala Gly Val Cys Tyr Gly Gly Gly Val Gly Phe Gly Ala Gly Gly
 290 295 300
 Gln Gln Met Gly Met Val Gly Pro Leu Ser Pro Val Ser Ser Asp Gly
 305 310 315 320
 Leu Gly His Gly Gln Val Asp Asn Ile Gly Gly Gln Tyr Gly Val Asp
 325 330 335
 Met Gly Gly Leu Arg Gly Arg Lys Arg Val Val Asp Gly Pro Val Glu
 340 345 350
 Lys Val Val Glu Arg Arg Gln Arg Arg Met Ile Lys Asn Arg Glu Ser
 355 360 365
 Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Val Glu Leu Glu
 370 375 380
 Ala Glu Leu Asn Gln Leu Lys Glu Glu Asn Ala Gln Leu Lys His Ala
 385 390 395 400
 Leu Ala Glu Leu Glu Arg Lys Arg Lys Gln Gln Tyr Phe Glu Ser Leu
 405 410 415
 Lys Ser Arg Ala Gln Pro Lys Leu Pro Lys Ser Asn Gly Arg Leu Arg
 420 425 430
 Thr Leu Met Arg Asn Pro Ser Cys Pro Leu
 435 440

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 <221> CDS <222> (1)..(1662) <223> G1807

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 48
 Met Gly Asp Thr Glu Lys Cys Asn Ser Asp Met Ile Gln Arg Leu His
 1 5 10 15
 tca tct ttc ggc act act tct tct tcc att ccc aaa aat ccc att tct
 96
 Ser Ser Phe Gly Thr Thr Ser Ser Ser Ile Pro Lys Asn Pro Ile Ser
 20 25 30

cag ctc gat tta aac cct aat ttc atc cgc tca tca gct cct caa ttc
 144
 Gln Leu Asp Leu Asn Pro Asn Phe Ile Arg Ser Ser Ala Pro Gln Phe
 35 40 45

tcc aag cct ttc agt gac agt ggc aaa cga atc ggt gtt cct ccg tcg
 192
 Ser Lys Pro Phe Ser Asp Ser Gly Lys Arg Ile Gly Val Pro Pro Ser
 50 55 60

cac ccc aac tta atc cca ccg act tct ccg ttt tct cag atc ccg acc
 240
 His Pro Asn Leu Ile Pro Pro Thr Ser Pro Phe Ser Gln Ile Pro Thr
 65 70 75 80

acc cga caa ccc ggt tcg cat aat ttt aac ccg gga gga gct aat cat
 288
 Thr Arg Gln Pro Gly Ser His Asn Phe Asn Pro Gly Gly Ala Asn His
 85 90 95

tca cgg tca atg tca cag ccc aac tct ttc ttc tct ttt gac tcc tta
 336
 Ser Arg Ser Met Ser Gln Pro Asn Ser Phe Phe Ser Phe Asp Ser Leu
 100 105 110

cct ccg tta agc cct tct ccg ttt cga gat cac gat gtt tca atg gag
 384
 Pro Pro Leu Ser Pro Ser Pro Phe Arg Asp His Asp Val Ser Met Glu
 115 120 125

gat aga gat tcc ggc gtg ttt aac agc aac cat tcg ttg cct cca tcg
 432
 Asp Arg Asp Ser Gly Val Phe Asn Ser Asn His Ser Leu Pro Pro Ser
 130 135 140

ccg ttc acg agg tgt aat tcg acc tct tct agc tcc ttg aga gtc ggt
 480
 Pro Phe Thr Arg Cys Asn Ser Thr Ser Ser Ser Ser Leu Arg Val Gly
 145 150 155 160

gag agt tta cct ccg aga aag tct cat aga cgc tcc aac agt gat atc
 528
 Glu Ser Leu Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Ile
 165 170 175

ccc agt ggg ttt aat tcg atg cct ttg atc cct ccg aga cca ttg gag
 576
 Pro Ser Gly Phe Asn Ser Met Pro Leu Ile Pro Pro Arg Pro Leu Glu
 180 185 190

agg tct ttt tct ggt ggg gag tgt gct gat tgg tca aag tct aat cct
 624
 Arg Ser Phe Ser Gly Gly Glu Cys Ala Asp Trp Ser Lys Ser Asn Pro
 195 200 205

ttt gtg aag aag gaa tcg agc tgc gaa agg gaa ggt gtc gga gag aga
 672
 Phe Val Lys Lys Glu Ser Ser Cys Glu Arg Glu Gly Val Gly Glu Arg
 210 215 220

gaa gct atg gat gat ctc ttc tca gca tat atg aat ctt gaa aac att
 720
 Glu Ala Met Asp Asp Leu Phe Ser Ala Tyr Met Asn Leu Glu Asn Ile
 225 230 235 240
 gat gtg ttg aac tcc tct gaa gct gat gat agc aag aac ggt aat gag
 768
 Asp Val Leu Asn Ser Ser Glu Ala Asp Asp Ser Lys Asn Gly Asn Glu
 245 250 255
 aat agg gat gat atg gag agc agc aga gca agc ggg acc aag act aac
 816
 Asn Arg Asp Asp Met Glu Ser Ser Arg Ala Ser Gly Thr Lys Thr Asn
 260 265 270
 ggt agt gat acg gaa gga gag agc agc agt gtc aat gag agt gcc aat
 864
 Gly Ser Asp Thr Glu Gly Glu Ser Ser Ser Val Asn Glu Ser Ala Asn
 275 280 285
 aat aat atg aat tct tct ggt gaa aag aga gag agc gtg aag aga aga
 912
 Asn Asn Met Asn Ser Ser Gly Glu Lys Arg Glu Ser Val Lys Arg Arg
 290 295 300
 gcg gct gga gga gat att gct cct acc acc aga cat tac agg agt gtt
 960
 Ala Ala Gly Gly Asp Ile Ala Pro Thr Thr Arg His Tyr Arg Ser Val
 305 310 315 320
 tca gtg gac agt tgt ttc atg gag aag ttg tct ttt ggt gat gaa tct
 1008
 Ser Val Asp Ser Cys Phe Met Glu Lys Leu Ser Phe Gly Asp Glu Ser
 325 330 335
 cta aag ccg cct cct tct cct gga tct atg tca agg aaa gtt tcc cct
 1056
 Leu Lys Pro Pro Pro Ser Pro Gly Ser Met Ser Arg Lys Val Ser Pro
 340 345 350
 acc aat tcg gtt gat ggg aac tcg ggt gct gct ttt agc atc gag ttc
 1104
 Thr Asn Ser Val Asp Gly Asn Ser Gly Ala Ala Phe Ser Ile Glu Phe
 355 360 365
 aat aac ggt gag ttt act gca gcg gaa atg aag aag atc atg gca aat
 1152
 Asn Asn Gly Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Met Ala Asn
 370 375 380
 gat aaa cta gca gag atg gcc atg tct gac cct aaa cgt gtc aaa agg
 1200
 Asp Lys Leu Ala Glu Met Ala Met Ser Asp Pro Lys Arg Val Lys Arg
 385 390 395 400
 aat gat cct ctt ttc aga atc tta gcg aac cgt caa tcc gca gca cgg
 1248
 Asn Asp Pro Leu Phe Arg Ile Leu Ala Asn Arg Gln Ser Ala Ala Arg
 405 410 415

tca aag gag agg aag atg cgg tac ata gta gaa ttg gaa cac aaa gtg
1296

Ser Lys Glu Arg Lys Met Arg Tyr Ile Val Glu Leu Glu His Lys Val
420 425 430

cag act ctt cag acc gag gct acc aca ttg tct gct cag ctc aca ctt
1344

Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Thr Leu
435 440 445

ttg cag cgc gat atg atg ggg ttg aca aat cag aac aat gag ctt aag
1392

Leu Gln Arg Asp Met Met Gly Leu Thr Asn Gln Asn Asn Glu Leu Lys
450 455 460

ttc cgg ctt caa gca atg gag caa caa gcg cgt ctt cgc gat gct ctg
1440

Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Arg Leu Arg Asp Ala Leu
465 470 475 480

aac gaa gca ctg aat gga gaa gtc cag cga ctg aaa ctg gca atc ggt
1488

Asn Glu Ala Leu Asn Gly Glu Val Gln Arg Leu Lys Leu Ala Ile Gly
485 490 495

gag agc agt cag aac gaa tca gag aga tca aag atg caa tca ctc aac
1536

Glu Ser Ser Gln Asn Glu Ser Glu Arg Ser Lys Met Gln Ser Leu Asn
500 505 510

gct gag atg ttc cag caa ctc aac atc agc cag tta aga cag cag cca
1584

Ala Glu Met Phe Gln Gln Leu Asn Ile Ser Gln Leu Arg Gln Gln Pro
515 520 525

caa cag atg cag caa cag tct cat cag cag aac cac cag aat gga acc
1632

Gln Gln Met Gln Gln Gln Ser His Gln Gln Asn His Gln Asn Gly Thr
530 535 540

atg gca aca aaa tct gaa tca aat gaa tag
1662

Met Ala Thr Lys Ser Glu Ser Asn Glu
545 550

<210> 270 <211> 553 <212> PRT <213> Arabidopsis thaliana <400>
270

Met Gly Asp Thr Glu Lys Cys Asn Ser Asp Met Ile Gln Arg Leu His
1 5 10 15

Ser Ser Phe Gly Thr Thr Ser Ser Ser Ile Pro Lys Asn Pro Ile Ser
20 25 30

Gln Leu Asp Leu Asn Pro Asn Phe Ile Arg Ser Ser Ala Pro Gln Phe
35 40 45

Ser Lys Pro Phe Ser Asp Ser Gly Lys Arg Ile Gly Val Pro Pro Ser
 50 55 60

His Pro Asn Leu Ile Pro Pro Thr Ser Pro Phe Ser Gln Ile Pro Thr
 65 70 75 80

Thr Arg Gln Pro Gly Ser His Asn Phe Asn Pro Gly Gly Ala Asn His
 85 90 95

Ser Arg Ser Met Ser Gln Pro Asn Ser Phe Phe Ser Phe Asp Ser Leu
 100 105 110

Pro Pro Leu Ser Pro Ser Pro Phe Arg Asp His Asp Val Ser Met Glu
 115 120 125

Asp Arg Asp Ser Gly Val Phe Asn Ser Asn His Ser Leu Pro Pro Ser
 130 135 140

Pro Phe Thr Arg Cys Asn Ser Thr Ser Ser Ser Ser Leu Arg Val Gly
 145 150 155 160

Glu Ser Leu Pro Pro Arg Lys Ser His Arg Arg Ser Asn Ser Asp Ile
 165 170 175

Pro Ser Gly Phe Asn Ser Met Pro Leu Ile Pro Pro Arg Pro Leu Glu
 180 185 190

Arg Ser Phe Ser Gly Gly Glu Cys Ala Asp Trp Ser Lys Ser Asn Pro
 195 200 205

Phe Val Lys Lys Glu Ser Ser Cys Glu Arg Glu Gly Val Gly Glu Arg
 210 215 220

Glu Ala Met Asp Asp Leu Phe Ser Ala Tyr Met Asn Leu Glu Asn Ile
 225 230 235 240

Asp Val Leu Asn Ser Ser Glu Ala Asp Asp Ser Lys Asn Gly Asn Glu
 245 250 255

Asn Arg Asp Asp Met Glu Ser Ser Arg Ala Ser Gly Thr Lys Thr Asn
 260 265 270

Gly Ser Asp Thr Glu Gly Glu Ser Ser Ser Val Asn Glu Ser Ala Asn
 275 280 285

Asn Asn Met Asn Ser Ser Gly Glu Lys Arg Glu Ser Val Lys Arg Arg

290 295 300
 Ala Ala Gly Gly Asp Ile Ala Pro Thr Thr Arg His Tyr Arg Ser Val
 305 310 315 320
 Ser Val Asp Ser Cys Phe Met Glu Lys Leu Ser Phe Gly Asp Glu Ser
 325 330 335
 Leu Lys Pro Pro Pro Ser Pro Gly Ser Met Ser Arg Lys Val Ser Pro
 340 345 350
 Thr Asn Ser Val Asp Gly Asn Ser Gly Ala Ala Phe Ser Ile Glu Phe
 355 360 365
 Asn Asn Gly Glu Phe Thr Ala Ala Glu Met Lys Lys Ile Met Ala Asn
 370 375 380
 Asp Lys Leu Ala Glu Met Ala Met Ser Asp Pro Lys Arg Val Lys Arg
 385 390 395 400
 Asn Asp Pro Leu Phe Arg Ile Leu Ala Asn Arg Gln Ser Ala Ala Arg
 405 410 415
 Ser Lys Glu Arg Lys Met Arg Tyr Ile Val Glu Leu Glu His Lys Val
 420 425 430
 Gln Thr Leu Gln Thr Glu Ala Thr Thr Leu Ser Ala Gln Leu Thr Leu
 435 440 445
 Leu Gln Arg Asp Met Met Gly Leu Thr Asn Gln Asn Asn Glu Leu Lys
 450 455 460
 Phe Arg Leu Gln Ala Met Glu Gln Gln Ala Arg Leu Arg Asp Ala Leu
 465 470 475 480
 Asn Glu Ala Leu Asn Gly Glu Val Gln Arg Leu Lys Leu Ala Ile Gly
 485 490 495
 Glu Ser Ser Gln Asn Glu Ser Glu Arg Ser Lys Met Gln Ser Leu Asn
 500 505 510
 Ala Glu Met Phe Gln Gln Leu Asn Ile Ser Gln Leu Arg Gln Gln Pro
 515 520 525
 Gln Gln Met Gln Gln Gln Ser His Gln Gln Asn His Gln Asn Gly Thr
 530 535 540

Met Ala Thr Lys Ser Glu Ser Asn Glu
545 550

<210> 271 <211> 969 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(969) <223> G1835

<400> 271
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48
Met Ile Gly Thr Ser Phe Pro Glu Asp Leu Asp Cys Gly Asn Phe Phe
1 5 10 15
gac aac atg gat gat ctc atg gac ttt ccc ggt gga gat atc gat gtc
96
Asp Asn Met Asp Asp Leu Met Asp Phe Pro Gly Gly Asp Ile Asp Val
20 25 30
ggt ttc ggc ata ggt gac tcc gac tct ttc cct acc atc tgg acc act
144
Gly Phe Gly Ile Gly Asp Ser Asp Ser Phe Pro Thr Ile Trp Thr Thr
35 40 45
cat cac gac acg tgg cct gcc gct tct gat cct ctc ttc tct tcc aac
192
His His Asp Thr Trp Pro Ala Ala Ser Asp Pro Leu Phe Ser Ser Asn
50 55 60
acc aac tct gat tca tca cct gag ctc tat gtt ccg ttt gag gac att
240
Thr Asn Ser Asp Ser Ser Pro Glu Leu Tyr Val Pro Phe Glu Asp Ile
65 70 75 80
gtt aag gtg gaa aga cct cca agc ttt gta gag gaa aca ttg gtt gag
288
Val Lys Val Glu Arg Pro Pro Ser Phe Val Glu Glu Thr Leu Val Glu
85 90 95
aag aag gaa gat tcg ttt tcg aca aac act gat tca tca tct tct cat
336
Lys Lys Glu Asp Ser Phe Ser Thr Asn Thr Asp Ser Ser Ser Ser His
100 105 110
agc caa ttc agg agc tca agt cca gtg tcg gtt ctc gag agc agc tcc
384
Ser Gln Phe Arg Ser Ser Ser Pro Val Ser Val Leu Glu Ser Ser Ser
115 120 125
tcc tcg tct caa acc acc aac aca acc tcc ctt gtt ctc cct gga aag
432
Ser Ser Ser Gln Thr Thr Asn Thr Thr Ser Leu Val Leu Pro Gly Lys
130 135 140
cac ggt cgt cca cgc aca aaa cgc cct cgt cca cct gtc cag gat aaa
480
His Gly Arg Pro Arg Thr Lys Arg Pro Arg Pro Pro Val Gln Asp Lys
145 150 155 160

gat aga gtc aaa gac aat gtg tgc ggt ggt gac tcg cgc ctc atc att
528
Asp Arg Val Lys Asp Asn Val Cys Gly Gly Asp Ser Arg Leu Ile Ile
165 170 175

aga ata ccg aaa cag ttt ctc tct gat cac aac aag atg atc aac aag
576
Arg Ile Pro Lys Gln Phe Leu Ser Asp His Asn Lys Met Ile Asn Lys
180 185 190

aag aag aag aag aag gcc aag att act tct tcc tct tct tcg tcc ggg
624
Lys Lys Lys Lys Lys Ala Lys Ile Thr Ser Ser Ser Ser Ser Ser Gly
195 200 205

att gat ctt gaa gtc aat gga aac aac gtc gat tcg tat tct tca gag
672
Ile Asp Leu Glu Val Asn Gly Asn Asn Val Asp Ser Tyr Ser Ser Glu
210 215 220

caa tat ccg ctt agg aaa tgt atg cac tgt gag gtc acc aag act cca
720
Gln Tyr Pro Leu Arg Lys Cys Met His Cys Glu Val Thr Lys Thr Pro
225 230 235 240

cag tgg agg ctt ggt cca atg ggt cca aag aca ctt tgc aat gcg tgc
768
Gln Trp Arg Leu Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys
245 250 255

ggt gta cgt tac aaa tca ggg agg ctt ttc ccg gag tac cgt cca gct
816
Gly Val Arg Tyr Lys Ser Gly Arg Leu Phe Pro Glu Tyr Arg Pro Ala
260 265 270

gct agt cca aca ttt act cca gct ctt cac tca aac tca cac aag aaa
864
Ala Ser Pro Thr Phe Thr Pro Ala Leu His Ser Asn Ser His Lys Lys
275 280 285

gtg gct gaa atg aga aac aag aga tgc agt gat ggt agc tac ata acc
912
Val Ala Glu Met Arg Asn Lys Arg Cys Ser Asp Gly Ser Tyr Ile Thr
290 295 300

gaa gag aat gat ctg caa ggg ctg att ccg aac aat gcc tac att ggc
960
Glu Glu Asn Asp Leu Gln Gly Leu Ile Pro Asn Asn Ala Tyr Ile Gly
305 310 315 320

gta gac taa
969
Val Asp

<210> 272 <211> 322 <212> PRT <213> Arabidopsis thaliana <400>
272

Met Ile Gly Thr Ser Phe Pro Glu Asp Leu Asp Cys Gly Asn Phe Phe
1 5 10 15

Asp Asn Met Asp Asp Leu Met Asp Phe Pro Gly Gly Asp Ile Asp Val
 20 25 30
 Gly Phe Gly Ile Gly Asp Ser Asp Ser Phe Pro Thr Ile Trp Thr Thr
 35 40 45
 His His Asp Thr Trp Pro Ala Ala Ser Asp Pro Leu Phe Ser Ser Asn
 50 55 60
 Thr Asn Ser Asp Ser Ser Pro Glu Leu Tyr Val Pro Phe Glu Asp Ile
 65 70 75 80
 Val Lys Val Glu Arg Pro Pro Ser Phe Val Glu Glu Thr Leu Val Glu
 85 90 95
 Lys Lys Glu Asp Ser Phe Ser Thr Asn Thr Asp Ser Ser Ser Ser His
 100 105 110
 Ser Gln Phe Arg Ser Ser Ser Pro Val Ser Val Leu Glu Ser Ser Ser
 115 120 125
 Ser Ser Ser Gln Thr Thr Asn Thr Thr Ser Leu Val Leu Pro Gly Lys
 130 135 140
 His Gly Arg Pro Arg Thr Lys Arg Pro Arg Pro Pro Val Gln Asp Lys
 145 150 155 160
 Asp Arg Val Lys Asp Asn Val Cys Gly Gly Asp Ser Arg Leu Ile Ile
 165 170 175
 Arg Ile Pro Lys Gln Phe Leu Ser Asp His Asn Lys Met Ile Asn Lys
 180 185 190
 Lys Lys Lys Lys Lys Ala Lys Ile Thr Ser Ser Ser Ser Ser Ser Gly
 195 200 205
 Ile Asp Leu Glu Val Asn Gly Asn Asn Val Asp Ser Tyr Ser Ser Glu
 210 215 220
 Gln Tyr Pro Leu Arg Lys Cys Met His Cys Glu Val Thr Lys Thr Pro
 225 230 235 240
 Gln Trp Arg Leu Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys
 245 250 255

Gly Val Arg Tyr Lys Ser Gly Arg Leu Phe Pro Glu Tyr Arg Pro Ala
260 265 270

Ala Ser Pro Thr Phe Thr Pro Ala Leu His Ser Asn Ser His Lys Lys
275 280 285

Val Ala Glu Met Arg Asn Lys Arg Cys Ser Asp Gly Ser Tyr Ile Thr
290 295 300

Glu Glu Asn Asp Leu Gln Gly Leu Ile Pro Asn Asn Ala Tyr Ile Gly
305 310 315 320

Val Asp

<210> 273 <211> 668 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (47)..(610) <223> G1836

<400> 273
ataacaagcc tagaacacta gaaacttcaa aaaagaaaa aatctt atg gag aac
55

Met Glu Asn
1

aac aac ggc aac aac cag ctg cca ccg aaa ggt aac gag caa ctg aag
103

Asn Asn Gly Asn Asn Gln Leu Pro Pro Lys Gly Asn Glu Gln Leu Lys
5 10 15

agt ttc tgg tca aaa gag atg gaa ggt aac tta gat ttc aaa aat cac
151

Ser Phe Trp Ser Lys Glu Met Glu Gly Asn Leu Asp Phe Lys Asn His
20 25 30 35

gac ctt cct ata act cgt atc aag aag att atg aag tat gat ccg gat
199

Asp Leu Pro Ile Thr Arg Ile Lys Lys Ile Met Lys Tyr Asp Pro Asp
40 45 50

gtg act atg ata gct agt gag gct cca atc ctc ctc tcg aaa gca tgt
247

Val Thr Met Ile Ala Ser Glu Ala Pro Ile Leu Leu Ser Lys Ala Cys
55 60 65

gag atg ttt atc atg gat ctc acg atg cgt tcg tgg ctc cat gct cag
295

Glu Met Phe Ile Met Asp Leu Thr Met Arg Ser Trp Leu His Ala Gln
70 75 80

gaa agc aaa cga gtc acg cta cag aaa tct aat gtc gat gcc gca gtg
343

Glu Ser Lys Arg Val Thr Leu Gln Lys Ser Asn Val Asp Ala Ala Val
85 90 95

gct caa act gtt atc ttt gat ttc ttg ctt gat gat gac att gag gta
 391
 Ala Gln Thr Val Ile Phe Asp Phe Leu Leu Asp Asp Asp Ile Glu Val
 100 105 110 115

aag aga gag tct gtt gcc gcc gct gct gat cct gtg gcc atg cca cct
 439
 Lys Arg Glu Ser Val Ala Ala Ala Ala Asp Pro Val Ala Met Pro Pro
 120 125 130

att gac gat gga gag ctg cct cca gga atg gta att gga act cct gtt
 487
 Ile Asp Asp Gly Glu Leu Pro Pro Gly Met Val Ile Gly Thr Pro Val
 135 140 145

tgt tgt agt ctt gga atc cac caa cca caa cca atg cag gca tgg
 535
 Cys Cys Ser Leu Gly Ile His Gln Pro Gln Pro Gln Met Gln Ala Trp
 150 155 160

cct gga gct tgg acc tcg gtg tct ggt gag gag gaa gaa gcg cgt ggg
 583
 Pro Gly Ala Trp Thr Ser Val Ser Gly Glu Glu Glu Glu Ala Arg Gly
 165 170 175

aaa aaa gga ggt gac gac gga aac taa taagtggaat acgttttagg
 630
 Lys Lys Gly Gly Asp Asp Gly Asn
 180 185

gtattttcaa gggaatatgt agtaaatagt catggatc
 668

<210> 274 <211> 187 <212> PRT <213> Arabidopsis thaliana <400>
 274

Met Glu Asn Asn Asn Gly Asn Asn Gln Leu Pro Pro Lys Gly Asn Glu
 1 5 10 15

Gln Leu Lys Ser Phe Trp Ser Lys Glu Met Glu Gly Asn Leu Asp Phe
 20 25 30

Lys Asn His Asp Leu Pro Ile Thr Arg Ile Lys Lys Ile Met Lys Tyr
 35 40 45

Asp Pro Asp Val Thr Met Ile Ala Ser Glu Ala Pro Ile Leu Leu Ser
 50 55 60

Lys Ala Cys Glu Met Phe Ile Met Asp Leu Thr Met Arg Ser Trp Leu
 65 70 75 80

His Ala Gln Glu Ser Lys Arg Val Thr Leu Gln Lys Ser Asn Val Asp
 85 90 95

Ala Ala Val Ala Gln Thr Val Ile Phe Asp Phe Leu Leu Asp Asp Asp
100 105 110

Ile Glu Val Lys Arg Glu Ser Val Ala Ala Ala Asp Pro Val Ala
115 120 125

Met Pro Pro Ile Asp Asp Gly Glu Leu Pro Pro Gly Met Val Ile Gly
130 135 140

Thr Pro Val Cys Cys Ser Leu Gly Ile His Gln Pro Gln Pro Gln Met
145 150 155 160

Gln Ala Trp Pro Gly Ala Trp Thr Ser Val Ser Gly Glu Glu Glu Glu
165 170 175

Ala Arg Gly Lys Lys Gly Gly Asp Asp Gly Asn
180 185

<210> 275 <211> 897 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(897) <223> G1900

<400> 275
atg ctg gaa act aaa gat cct gcg ata aag ctc ttt ggt atg aaa att
48
Met Leu Glu Thr Lys Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile
1 5 10 15

cct ttc ccg acg gtt tta gag gtt gct gat gaa gaa gaa gaa aag aac
96
Pro Phe Pro Thr Val Leu Glu Val Ala Asp Glu Glu Glu Glu Lys Asn
20 25 30

caa aac aag aca tta act gat caa tcg gag aaa gac aaa acc cta aag
144
Gln Asn Lys Thr Leu Thr Asp Gln Ser Glu Lys Asp Lys Thr Leu Lys
35 40 45

aaa cca acc aag att ctt cca tgt cca aga tgc aac agc atg gag act
192
Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Met Glu Thr
50 55 60

aag ttc tgt tac tac aac aac tac aac gta aac caa cct cgc cat ttt
240
Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg His Phe
65 70 75 80

tgt aaa gct tgt cag aga tat tgg acc tca ggt ggg acc atg aga agt
288
Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ser Gly Gly Thr Met Arg Ser
85 90 95

gtt cca atc gga gca gga cgg cgc aag aac aac aac tca cca act
336
Val Pro Ile Gly Ala Gly Arg Arg Lys Asn Lys Asn Asn Ser Pro Thr

100	105	110
tca cat tac cac cat gtg act atc tcc gaa aca aat ggt ccg gtc ctt		
384		
Ser His Tyr His His Val Thr Ile Ser Glu Thr Asn Gly Pro Val Leu		
115	120	125
agt ttc agc ctc gga gat gat caa aag gtc tcg agt aat agg ttt ggt		
432		
Ser Phe Ser Ser Leu Gly Asp Asp Gln Lys Val Ser Ser Asn Arg Phe Gly		
130	135	140
aat caa aag cta gtt gct agg ata gag aac aat gac gag cgc tct aat		
480		
Asn Gln Lys Leu Val Ala Arg Ile Glu Asn Asn Asp Glu Arg Ser Asn		
145	150	155
aac aac act tcg aac ggt ttg aat tgt ttt ccg gga gtt tcg tgg ccg		
528		
Asn Asn Thr Ser Asn Gly Leu Asn Cys Phe Pro Gly Val Ser Trp Pro		
165	170	175
tac acg tgg aat cct gcg ttt tac ccg gtt tac cct tat tgg agc atg		
576		
Tyr Thr Trp Asn Pro Ala Phe Tyr Pro Val Tyr Pro Tyr Trp Ser Met		
180	185	190
cca gtg ttg tct tct ccg gta agt tca agt cct act tct act ctt ggt		
624		
Pro Val Leu Ser Ser Pro Val Ser Ser Ser Pro Thr Ser Thr Leu Gly		
195	200	205
aag cat tcg aga gac gaa gac gag acg gtg aag caa aaa cag agg aat		
672		
Lys His Ser Arg Asp Glu Asp Glu Thr Val Lys Gln Lys Gln Arg Asn		
210	215	220
gga tct gta ttg gtt cca aag act ttg aga att gat gat cct aat gaa		
720		
Gly Ser Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu		
225	230	235
gct gca aag agt tcg ata tgg aca aca ctt ggg atc aag aac gaa gtt		
768		
Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Val		
245	250	255
atg ttc aat ggg ttt ggt tcg aag aaa gag gtt aag ctc agt aac aaa		
816		
Met Phe Asn Gly Phe Gly Ser Lys Lys Glu Val Lys Leu Ser Asn Lys		
260	265	270
gaa gaa aca gag acc tca ctt gtt ctt tgt gca aac cct gct gcg tta		
864		
Glu Glu Thr Glu Thr Ser Leu Val Leu Cys Ala Asn Pro Ala Ala Leu		
275	280	285
tca aga tca atc aat ttc cat gag cag atg tga		
897		
Ser Arg Ser Ile Asn Phe His Glu Gln Met		
290	295	

<210> 276 <211> 298 <212> PRT <213> Arabidopsis thaliana <400>
276

Met Leu Glu Thr Lys Asp Pro Ala Ile Lys Leu Phe Gly Met Lys Ile
1 5 10 15

Pro Phe Pro Thr Val Leu Glu Val Ala Asp Glu Glu Glu Glu Lys Asn
20 25 30

Gln Asn Lys Thr Leu Thr Asp Gln Ser Glu Lys Asp Lys Thr Leu Lys
35 40 45

Lys Pro Thr Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Met Glu Thr
50 55 60

Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg His Phe
65 70 75 80

Cys Lys Ala Cys Gln Arg Tyr Trp Thr Ser Gly Gly Thr Met Arg Ser
85 90 95

Val Pro Ile Gly Ala Gly Arg Arg Lys Asn Lys Asn Asn Ser Pro Thr
100 105 110

Ser His Tyr His His Val Thr Ile Ser Glu Thr Asn Gly Pro Val Leu
115 120 125

Ser Phe Ser Leu Gly Asp Asp Gln Lys Val Ser Ser Asn Arg Phe Gly
130 135 140

Asn Gln Lys Leu Val Ala Arg Ile Glu Asn Asn Asp Glu Arg Ser Asn
145 150 155 160

Asn Asn Thr Ser Asn Gly Leu Asn Cys Phe Pro Gly Val Ser Trp Pro
165 170 175

Tyr Thr Trp Asn Pro Ala Phe Tyr Pro Val Tyr Pro Tyr Trp Ser Met
180 185 190

Pro Val Leu Ser Ser Pro Val Ser Ser Ser Pro Thr Ser Thr Leu Gly
195 200 205

Lys His Ser Arg Asp Glu Asp Glu Thr Val Lys Gln Lys Gln Arg Asn
210 215 220

Gly Ser Val Leu Val Pro Lys Thr Leu Arg Ile Asp Asp Pro Asn Glu
225 230 235 240

Ala Ala Lys Ser Ser Ile Trp Thr Thr Leu Gly Ile Lys Asn Glu Val
245 250 255

Met Phe Asn Gly Phe Gly Ser Lys Lys Glu Val Lys Leu Ser Asn Lys
260 265 270

Glu Glu Thr Glu Thr Ser Leu Val Leu Cys Ala Asn Pro Ala Ala Leu
275 280 285

Ser Arg Ser Ile Asn Phe His Glu Gln Met
290 295

<210> 277 <211> 1200 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(1200) <223> G1903

<400> 277
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48
Met Ser Lys Ser Arg Asp Thr Glu Ile Lys Leu Phe Gly Arg Thr Ile
1 5 10 15

aca tct ctt tta gat gtg aat tgt tat gat ccg tcg tcg ttg tcc cct
96
Thr Ser Leu Leu Asp Val Asn Cys Tyr Asp Pro Ser Ser Leu Ser Pro
20 25 30

gtt cac gat gtt tct tct gat cca agc aag gag gat tcg tct tct tct
144
Val His Asp Val Ser Ser Asp Pro Ser Lys Glu Asp Ser Ser Ser Ser
35 40 45

tca tct tct tgt tct cca act att gga cca atc agg gtt ccg gtt aaa
192
Ser Ser Ser Cys Ser Pro Thr Ile Gly Pro Ile Arg Val Pro Val Lys
50 55 60

aaa agt gag caa gag agt aac aaa ttc aaa gat cca tat ata tta tcc
240
Lys Ser Glu Gln Glu Ser Asn Lys Phe Lys Asp Pro Tyr Ile Leu Ser
65 70 75 80

gat cta aac gaa cca cca aaa gca gta tct gag att tca tca cca aga
288
Asp Leu Asn Glu Pro Pro Lys Ala Val Ser Glu Ile Ser Ser Pro Arg
85 90 95

agt tcc aag aac aac tgt gat caa cag agc gag atc aca aca aca act
336
Ser Ser Lys Asn Asn Cys Asp Gln Gln Ser Glu Ile Thr Thr Thr Thr
100 105 110

acc aca agt act aca tca gga gag aaa tca acg gct ctc aag aaa ccg
384

Thr Thr Ser Thr Thr Ser Gly Glu Lys Ser Thr Ala Leu Lys Lys Pro
 115 120 125
 gac aag ctt att cca tgt cct aga tgt gaa agc gca aac acc aaa ttc
 432
 Asp Lys Leu Ile Pro Cys Pro Arg Cys Glu Ser Ala Asn Thr Lys Phe
 130 135 140
 tgt tat tac aac aac tac aac gtg aac cag cca cgt tac ttc tgc agg
 480
 Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg Tyr Phe Cys Arg
 145 150 155 160
 aac tgt cag agg tat tgg aca gct ggt gga tct atg agg aac gtt cct
 528
 Asn Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met Arg Asn Val Pro
 165 170 175
 gtt ggc tca ggt cgt cgc aag aac aaa gga tgg cct tct tca aac cat
 576
 Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Pro Ser Ser Asn His
 180 185 190
 tac ttg caa gtc act tct gag gat tgt gat aat aat aac tcg ggg acg
 624
 Tyr Leu Gln Val Thr Ser Glu Asp Cys Asp Asn Asn Asn Ser Gly Thr
 195 200 205
 atc ctt agt ttc ggt tct tcg gag tct tcg gtt aca gag act ggt aag
 672
 Ile Leu Ser Phe Gly Ser Ser Glu Ser Ser Val Thr Glu Thr Gly Lys
 210 215 220
 cat cag tca ggt gat aca gca aag ata agt gct gat tca gtt tct caa
 720
 His Gln Ser Gly Asp Thr Ala Lys Ile Ser Ala Asp Ser Val Ser Gln
 225 230 235 240
 gaa aat aaa agc tac caa ggg ttt ctt cct ccg caa gta atg tta cct
 768
 Glu Asn Lys Ser Tyr Gln Gly Phe Leu Pro Pro Gln Val Met Leu Pro
 245 250 255
 aat aat tct tct cct tgg cct tac caa tgg agt cca acg ggt cct aac
 816
 Asn Asn Ser Ser Pro Trp Pro Tyr Gln Trp Ser Pro Thr Gly Pro Asn
 260 265 270
 gct agt ttc tac cct gtc ccc ttc tac tgg gga tgc acg gtt ccg ata
 864
 Ala Ser Phe Tyr Pro Val Pro Phe Tyr Trp Gly Cys Thr Val Pro Ile
 275 280 285
 tac cct acc tca gag act tca tca tgt tta gga aaa cgg tca aga gat
 912
 Tyr Pro Thr Ser Glu Thr Ser Ser Cys Leu Gly Lys Arg Ser Arg Asp
 290 295 300
 caa act gaa gga aga atc aat gat act aat aca aca ata act act aca
 960
 Gln Thr Glu Gly Arg Ile Asn Asp Thr Asn Thr Thr Ile Thr Thr Thr

305 310 315 320
 aga gca aga ttg gtc tca gaa tct ctt aga atg aat atc gaa gct agt
 1008
 Arg Ala Arg Leu Val Ser Glu Ser Leu Arg Met Asn Ile Glu Ala Ser
 325 330 335

 aag agc gct gtg tgg tct aag tta ccg aca aaa ccc gag aaa aaa acg
 1056
 Lys Ser Ala Val Trp Ser Lys Leu Pro Thr Lys Pro Glu Lys Lys Thr
 340 345 350

 caa gga ttc agt ttg ttc aat gga ttt gac aca aag gga aac agc aac
 1104
 Gln Gly Phe Ser Leu Phe Asn Gly Phe Asp Thr Lys Gly Asn Ser Asn
 355 360 365

 aga agt agc ttg gtc tcc gaa act tct cac agt cta caa gca aac cct
 1152
 Arg Ser Ser Leu Val Ser Glu Thr Ser His Ser Leu Gln Ala Asn Pro
 370 375 380

 gca gcg atg tct aga gct atg aac ttc agg gag agc atg caa caa taa
 1200
 Ala Ala Met Ser Arg Ala Met Asn Phe Arg Glu Ser Met Gln Gln
 385 390 395

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 1 5 10 15

 Thr Ser Leu Leu Asp Val Asn Cys Tyr Asp Pro Ser Ser Leu Ser Pro
 20 25 30

 Val His Asp Val Ser Ser Asp Pro Ser Lys Glu Asp Ser Ser Ser Ser
 35 40 45

 Ser Ser Ser Cys Ser Pro Thr Ile Gly Pro Ile Arg Val Pro Val Lys
 50 55 60

 Lys Ser Glu Gln Glu Ser Asn Lys Phe Lys Asp Pro Tyr Ile Leu Ser
 65 70 75 80

 Asp Leu Asn Glu Pro Pro Lys Ala Val Ser Glu Ile Ser Ser Pro Arg
 85 90 95

 Ser Ser Lys Asn Asn Cys Asp Gln Gln Ser Glu Ile Thr Thr Thr Thr
 100 105 110

 Thr Thr Ser Thr Thr Ser Gly Glu Lys Ser Thr Ala Leu Lys Lys Pro
 115 120 125

Asp Lys Leu Ile Pro Cys Pro Arg Cys Glu Ser Ala Asn Thr Lys Phe
 130 135 140

Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg Tyr Phe Cys Arg
 145 150 155 160

Asn Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met Arg Asn Val Pro
 165 170 175

Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Pro Ser Ser Asn His
 180 185 190

Tyr Leu Gln Val Thr Ser Glu Asp Cys Asp Asn Asn Asn Ser Gly Thr
 195 200 205

Ile Leu Ser Phe Gly Ser Ser Glu Ser Ser Val Thr Glu Thr Gly Lys
 210 215 220

His Gln Ser Gly Asp Thr Ala Lys Ile Ser Ala Asp Ser Val Ser Gln
 225 230 235 240

Glu Asn Lys Ser Tyr Gln Gly Phe Leu Pro Pro Gln Val Met Leu Pro
 245 250 255

Asn Asn Ser Ser Pro Trp Pro Tyr Gln Trp Ser Pro Thr Gly Pro Asn
 260 265 270

Ala Ser Phe Tyr Pro Val Pro Phe Tyr Trp Gly Cys Thr Val Pro Ile
 275 280 285

Tyr Pro Thr Ser Glu Thr Ser Ser Cys Leu Gly Lys Arg Ser Arg Asp
 290 295 300

Gln Thr Glu Gly Arg Ile Asn Asp Thr Asn Thr Thr Ile Thr Thr Thr
 305 310 315 320

Arg Ala Arg Leu Val Ser Glu Ser Leu Arg Met Asn Ile Glu Ala Ser
 325 330 335

Lys Ser Ala Val Trp Ser Lys Leu Pro Thr Lys Pro Glu Lys Lys Thr
 340 345 350

Gln Gly Phe Ser Leu Phe Asn Gly Phe Asp Thr Lys Gly Asn Ser Asn
 355 360 365

Arg Ser Ser Leu Val Ser Glu Thr Ser His Ser Leu Gln Ala Asn Pro
 370 375 380

Ala Ala Met Ser Arg Ala Met Asn Phe Arg Glu Ser Met Gln Gln
 385 390 395

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Met Glu Ile Ala Thr
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gat aca gca aag cag atg aga gac gaa gag ttg ttc aaa gca gcg gaa
 104

Asp Thr Ala Lys Gln Met Arg Asp Glu Glu Leu Phe Lys Ala Ala Glu
 10 15 20

tgg gga gat tca tcg ttg ttc atg tca tta tct gaa gaa cag ctc tct
 152

Trp Gly Asp Ser Ser Leu Phe Met Ser Leu Ser Glu Glu Gln Leu Ser
 25 30 35

aaa tct ctc aat ttc aga aac gaa gat ggt cgc tct ctc ctc cat gtc
 200

Lys Ser Leu Asn Phe Arg Asn Glu Asp Gly Arg Ser Leu Leu His Val
 40 45 50

gct gct tcc ttc ggc cat tct caa ata gtg aag ttg tta tca agt tca
 248

Ala Ala Ser Phe Gly His Ser Gln Ile Val Lys Leu Leu Ser Ser Ser
 55 60 65

gat gaa gca aag act gta atc aat agc aag gat gat gaa gga tgg gct
 296

Asp Glu Ala Lys Thr Val Ile Asn Ser Lys Asp Asp Glu Gly Trp Ala
 70 75 80 85

cct ttg cat tcc gct gct agc atc ggt aat gct gag ctc gtt gag gtg
 344

Pro Leu His Ser Ala Ala Ser Ile Gly Asn Ala Glu Leu Val Glu Val
 90 95 100

ctt ttg acc aga ggt gct gat gtc aat gcc aaa aat aac ggt ggt cgc
 392

Leu Leu Thr Arg Gly Ala Asp Val Asn Ala Lys Asn Asn Gly Gly Arg
 105 110 115

act gct ctt cac tat gct gct agc aaa ggc cgg ttg gag att gct cag
 440

Thr Ala Leu His Tyr Ala Ala Ser Lys Gly Arg Leu Glu Ile Ala Gln
 120 125 130

ctt tta tta aca cac ggt gca aag att aac atc aca gac aag gtt ggt
 488

Leu Leu Leu Thr His Gly Ala Lys Ile Asn Ile Thr Asp Lys Val Gly

135 140 145
 tgc act ccg ctt cac agg gca gca agc gtg gga aag tta gaa gtt tgt
 536
 Cys Thr Pro Leu His Arg Ala Ala Ser Val Gly Lys Leu Glu Val Cys
 150 155 160 165
 gaa ttt ctt att gaa gaa gga gca gag atc gat gct acg gat aaa atg
 584
 Glu Phe Leu Ile Glu Glu Gly Ala Glu Ile Asp Ala Thr Asp Lys Met
 170 175 180
 ggt caa act gca ctc atg cat tca gtt atc tgc gat gac aaa cag gtt
 632
 Gly Gln Thr Ala Leu Met His Ser Val Ile Cys Asp Asp Lys Gln Val
 185 190 195
 gcg ttc ctg ctt ata aga cat ggt gca gat gtg gat gta gaa gac aag
 680
 Ala Phe Leu Leu Ile Arg His Gly Ala Asp Val Asp Val Glu Asp Lys
 200 205 210
 gaa ggc tac act gtt cta ggc cga gct acc aat gaa ttc cga cct gca
 728
 Glu Gly Tyr Thr Val Leu Gly Arg Ala Thr Asn Glu Phe Arg Pro Ala
 215 220 225
 ctt atc gat gct gct aag gcc atg ctt gaa gga taa aatgactctg
 774
 Leu Ile Asp Ala Ala Lys Ala Met Leu Glu Gly
 230 235 240
 gattacttta aaacttacta actctgagag ttgtttagtt acttaaaagg atttttcttt
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 actgtatcat gtttgcaaaa tggttctgcc ttatcaattc atgttctgt
 883

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 20 25 30
 Glu Glu Gln Leu Ser Lys Ser Leu Asn Phe Arg Asn Glu Asp Gly Arg
 35 40 45
 Ser Leu Leu His Val Ala Ala Ser Phe Gly His Ser Gln Ile Val Lys
 50 55 60
 Leu Leu Ser Ser Ser Asp Glu Ala Lys Thr Val Ile Asn Ser Lys Asp
 65 70 75 80

Asp Glu Gly Trp Ala Pro Leu His Ser Ala Ala Ser Ile Gly Asn Ala
85 90 95

Glu Leu Val Glu Val Leu Leu Thr Arg Gly Ala Asp Val Asn Ala Lys
100 105 110

Asn Asn Gly Gly Arg Thr Ala Leu His Tyr Ala Ala Ser Lys Gly Arg
115 120 125

Leu Glu Ile Ala Gln Leu Leu Thr His Gly Ala Lys Ile Asn Ile
130 135 140

Thr Asp Lys Val Gly Cys Thr Pro Leu His Arg Ala Ala Ser Val Gly
145 150 155 160

Lys Leu Glu Val Cys Glu Phe Leu Ile Glu Glu Gly Ala Glu Ile Asp
165 170 175

Ala Thr Asp Lys Met Gly Gln Thr Ala Leu Met His Ser Val Ile Cys
180 185 190

Asp Asp Lys Gln Val Ala Phe Leu Leu Ile Arg His Gly Ala Asp Val
195 200 205

Asp Val Glu Asp Lys Glu Gly Tyr Thr Val Leu Gly Arg Ala Thr Asn
210 215 220

Glu Phe Arg Pro Ala Leu Ile Asp Ala Ala Lys Ala Met Leu Glu Gly
225 230 235 240

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tcgtcttcct tggctcctgga ttgcttcacg aatttctagg acaaca atg gag gct
115

Met Glu Ala
1

cgt cca gtt cat aga tca ggt tcg aga gac ctc aca cgc act tct tca
163

Arg Pro Val His Arg Ser Gly Ser Arg Asp Leu Thr Arg Thr Ser Ser
5 10 15

atc cca tct aca caa aaa cct tca cca gta gaa gat agt ttc atg aga
211

Ile Pro Ser Thr Gln Lys Pro Ser Pro Val Glu Asp Ser Phe Met Arg

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20          25          30          35
tca gat aac aac agt cag tta atg tct aga cca tta gga caa acc tac
259
Ser Asp Asn Asn Ser Gln Leu Met Ser Arg Pro Leu Gly Gln Thr Tyr
          40          45          50
cat tta ctt tca tct agt aac ggt gga gct gtt gga cat ata tgt tct
307
His Leu Leu Ser Ser Ser Asn Gly Gly Ala Val Gly His Ile Cys Ser
          55          60          65
tct tca tca tct ggt ttt gca acc aat ctc cat tac tca act atg gta
355
Ser Ser Ser Ser Gly Phe Ala Thr Asn Leu His Tyr Ser Thr Met Val
          70          75          80
tct cat gag aaa caa caa cac tac aca gga agc agc agt aat aat gct
403
Ser His Glu Lys Gln Gln His Tyr Thr Gly Ser Ser Ser Asn Asn Ala
          85          90          95
gtg cag aca cca agc aac aac gat agt gct tgg tgt cat gat tca ttg
451
Val Gln Thr Pro Ser Asn Asn Asp Ser Ala Trp Cys His Asp Ser Leu
100          105          110          115
cca gga ggg ttt ctt gac ttc cat gaa acc aac ccg gcg att caa aac
499
Pro Gly Gly Phe Leu Asp Phe His Glu Thr Asn Pro Ala Ile Gln Asn
          120          125          130
aac tgt cag att gag gat ggt ggc att gcg gct gct ttt gat gac att
547
Asn Cys Gln Ile Glu Asp Gly Gly Ile Ala Ala Ala Phe Asp Asp Ile
          135          140          145
caa aaa cga agt gat tgg cat gaa tgg gct gac cat ttg atc act gat
595
Gln Lys Arg Ser Asp Trp His Glu Trp Ala Asp His Leu Ile Thr Asp
          150          155          160
gat gat cct ttg atg tct act aac tgg aat gat ctc ttg ctt gaa aca
643
Asp Asp Pro Leu Met Ser Thr Asn Trp Asn Asp Leu Leu Leu Glu Thr
          165          170          175
aat tcc aat tca gat tca aag gac cag aag aca ctg caa att ccg caa
691
Asn Ser Asn Ser Asp Ser Lys Asp Gln Lys Thr Leu Gln Ile Pro Gln
180          185          190          195
cct cag att gtt cag cag caa cct tct ccg tct gtg gaa ttg cga cct
739
Pro Gln Ile Val Gln Gln Gln Pro Ser Pro Ser Val Glu Leu Arg Pro
          200          205          210
gtt agc aca aca tct tca aac agc aat aac gga acg ggc aag gca cga
787
Val Ser Thr Thr Ser Ser Asn Ser Asn Asn Gly Thr Gly Lys Ala Arg
          215          220          225

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atg cgt tgg acg cca gag ctt cac gag gct ttt gtt gag gct gtc aac
 835
 Met Arg Trp Thr Pro Glu Leu His Glu Ala Phe Val Glu Ala Val Asn
 230 235 240

agt ctt ggc ggt agt gaa aga gct act cct aaa ggg gta ctg aag att
 883
 Ser Leu Gly Gly Ser Glu Arg Ala Thr Pro Lys Gly Val Leu Lys Ile
 245 250 255

atg aaa gtt gaa ggc ttg act ata tat cat gtt aaa agc cat tta cag
 931
 Met Lys Val Glu Gly Leu Thr Ile Tyr His Val Lys Ser His Leu Gln
 260 265 270 275

aaa tat agg aca gct aga tat cgg cca gaa cca tca gaa act ggt tcg
 979
 Lys Tyr Arg Thr Ala Arg Tyr Arg Pro Glu Pro Ser Glu Thr Gly Ser
 280 285 290

cca gaa agg aag ttg aca ccg ctt gaa cat ata aca tct ctt gat ttg
 1027
 Pro Glu Arg Lys Leu Thr Pro Leu Glu His Ile Thr Ser Leu Asp Leu
 295 300 305

aaa ggt ggg ata ggt att aca gag gct cta cga ctt cag atg gaa gta
 1075
 Lys Gly Gly Ile Gly Ile Thr Glu Ala Leu Arg Leu Gln Met Glu Val
 310 315 320

cag aag caa ctc cat gag cag ctc gag att caa aga aac ctg caa ctc
 1123
 Gln Lys Gln Leu His Glu Gln Leu Glu Ile Gln Arg Asn Leu Gln Leu
 325 330 335

cga ata gaa gaa caa ggc aag tac ctg caa atg atg ttc gag aag caa
 1171
 Arg Ile Glu Glu Gln Gly Lys Tyr Leu Gln Met Met Phe Glu Lys Gln
 340 345 350 355

aac tct ggt ctt acc aaa ggg aca gcc tca aca tca gat tcc gca gcc
 1219
 Asn Ser Gly Leu Thr Lys Gly Thr Ala Ser Thr Ser Asp Ser Ala Ala
 360 365 370

aaa tct gaa caa gaa gac aag aag act gct gat tcg aag gag gtt cca
 1267
 Lys Ser Glu Gln Glu Asp Lys Lys Thr Ala Asp Ser Lys Glu Val Pro
 375 380 385

gaa gaa gaa acc agg aaa tgt gag gaa cta gaa tct cca cag cca aag
 1315
 Glu Glu Glu Thr Arg Lys Cys Glu Glu Leu Glu Ser Pro Gln Pro Lys
 390 395 400

cgt ccc aaa atc gat aat tga aagtattggt cttttgctgg ataattctcg
 1366
 Arg Pro Lys Ile Asp Asn
 405

agtttcagag ttaacagtga tagagagaac gagctcttat cttgaggttc ttcaggactt
1426

ctctcgcggc cgctctag
1444

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20 25 30

Phe Met Arg Ser Asp Asn Asn Ser Gln Leu Met Ser Arg Pro Leu Gly
35 40 45

Gln Thr Tyr His Leu Leu Ser Ser Ser Asn Gly Gly Ala Val Gly His
50 55 60

Ile Cys Ser Ser Ser Ser Ser Gly Phe Ala Thr Asn Leu His Tyr Ser
65 70 75 80

Thr Met Val Ser His Glu Lys Gln Gln His Tyr Thr Gly Ser Ser Ser
85 90 95

Asn Asn Ala Val Gln Thr Pro Ser Asn Asn Asp Ser Ala Trp Cys His
100 105 110

Asp Ser Leu Pro Gly Gly Phe Leu Asp Phe His Glu Thr Asn Pro Ala
115 120 125

Ile Gln Asn Asn Cys Gln Ile Glu Asp Gly Gly Ile Ala Ala Ala Phe
130 135 140

Asp Asp Ile Gln Lys Arg Ser Asp Trp His Glu Trp Ala Asp His Leu
145 150 155 160

Ile Thr Asp Asp Asp Pro Leu Met Ser Thr Asn Trp Asn Asp Leu Leu
165 170 175

Leu Glu Thr Asn Ser Asn Ser Asp Ser Lys Asp Gln Lys Thr Leu Gln
180 185 190

Ile Pro Gln Pro Gln Ile Val Gln Gln Gln Pro Ser Pro Ser Val Glu
195 200 205

Leu Arg Pro Val Ser Thr Thr Ser Ser Asn Ser Asn Asn Gly Thr Gly
 210 215 220

Lys Ala Arg Met Arg Trp Thr Pro Glu Leu His Glu Ala Phe Val Glu
 225 230 235 240

Ala Val Asn Ser Leu Gly Gly Ser Glu Arg Ala Thr Pro Lys Gly Val
 245 250 255

Leu Lys Ile Met Lys Val Glu Gly Leu Thr Ile Tyr His Val Lys Ser
 260 265 270

His Leu Gln Lys Tyr Arg Thr Ala Arg Tyr Arg Pro Glu Pro Ser Glu
 275 280 285

Thr Gly Ser Pro Glu Arg Lys Leu Thr Pro Leu Glu His Ile Thr Ser
 290 295 300

Leu Asp Leu Lys Gly Gly Ile Gly Ile Thr Glu Ala Leu Arg Leu Gln
 305 310 315 320

Met Glu Val Gln Lys Gln Leu His Glu Gln Leu Glu Ile Gln Arg Asn
 325 330 335

Leu Gln Leu Arg Ile Glu Glu Gln Gly Lys Tyr Leu Gln Met Met Phe
 340 345 350

Glu Lys Gln Asn Ser Gly Leu Thr Lys Gly Thr Ala Ser Thr Ser Asp
 355 360 365

Ser Ala Ala Lys Ser Glu Gln Glu Asp Lys Lys Thr Ala Asp Ser Lys
 370 375 380

Glu Val Pro Glu Glu Glu Thr Arg Lys Cys Glu Glu Leu Glu Ser Pro
 385 390 395 400

Gln Pro Lys Arg Pro Lys Ile Asp Asn
 405

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113

Met Asn Ile Val Ser Trp Lys Asp Ala
1 5

aac gac gaa gtt gca ggc ggc gct acg aca aga cgt gaa aga gaa gta
161

Asn Asp Glu Val Ala Gly Gly Ala Thr Thr Arg Arg Glu Arg Glu Val
10 15 20 25

aaa gag gat caa gaa gaa acc gaa gtc aga gcc acc agt ggc aaa acc
209

Lys Glu Asp Gln Glu Glu Thr Glu Val Arg Ala Thr Ser Gly Lys Thr
30 35 40

gta att aaa aag cag cct aca tcg atc tct tct tct tct tct tct tgg
257

Val Ile Lys Lys Gln Pro Thr Ser Ile Ser Ser Ser Ser Ser Ser Trp
45 50 55

atg aaa tcc aag gat ccg agg att gtt agg gtt tca cgc gcc ttt gga
305

Met Lys Ser Lys Asp Pro Arg Ile Val Arg Val Ser Arg Ala Phe Gly
60 65 70

ggc aaa gac cgt cac agc aaa gtg tgt acg tta cgt gga cta cgt gac
353

Gly Lys Asp Arg His Ser Lys Val Cys Thr Leu Arg Gly Leu Arg Asp
75 80 85

aga cgc gtg aga tta tca gtc cca acg gct att cag ctc tac gat ctt
401

Arg Arg Val Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu
90 95 100 105

caa gaa cgg ctc ggt gtt gac cag cct agc aaa gcc gtt gac tgg ttg
449

Gln Glu Arg Leu Gly Val Asp Gln Pro Ser Lys Ala Val Asp Trp Leu
110 115 120

ctt gat gca gct aaa gag gag atc gac gag cta cct ccg tta cct atc
497

Leu Asp Ala Ala Lys Glu Glu Ile Asp Glu Leu Pro Pro Leu Pro Ile
125 130 135

tcg ccg gaa aat ttc agc atc ttc aac cat cat cag tcc ttc ttg aat
545

Ser Pro Glu Asn Phe Ser Ile Phe Asn His His Gln Ser Phe Leu Asn
140 145 150

ctt ggt caa cgg ccc ggt caa gat ccg acc caa ctc ggg ttt aaa atc
593

Leu Gly Gln Arg Pro Gly Gln Asp Pro Thr Gln Leu Gly Phe Lys Ile
155 160 165

aat gga tgt gta caa aag tct act act act agc cgc gaa gaa aac gat
641

Asn Gly Cys Val Gln Lys Ser Thr Thr Thr Ser Arg Glu Glu Asn Asp
170 175 180 185

aga gag aaa gga gaa aac gat gtc gtt tac aca aac aat cat cat gtt
689

Arg Glu Lys Gly Glu Asn Asp Val Val Tyr Thr Asn Asn His His Val
190 195 200

ggg tct tat gga act tat cac aac ctg gaa cat cat cat cat cat cac
737

Gly Ser Tyr Gly Thr Tyr His Asn Leu Glu His His His His His His
205 210 215

caa cat ttg agt tta cag gca gat tat cat agt cat caa cta cat agt
785

Gln His Leu Ser Leu Gln Ala Asp Tyr His Ser His Gln Leu His Ser
220 225 230

ctt gtc cca ttt cca tca caa att ttg gta tgt cca atg acg aca tca
833

Leu Val Pro Phe Pro Ser Gln Ile Leu Val Cys Pro Met Thr Thr Ser
235 240 245

cca aca act aca act ata caa tct ttg ttt cca tca tca tcg tca gct
881

Pro Thr Thr Thr Thr Ile Gln Ser Leu Phe Pro Ser Ser Ser Ser Ala
250 255 260 265

ggt tca ggg act atg gag aca tta gat ccg agg caa atg tag
923

Gly Ser Gly Thr Met Glu Thr Leu Asp Pro Arg Gln Met
270 275

caacaatggt ggtagagaca ttgataatcg gatgtcgtcg gtccaattca accgaactaa
983

tagcactaca acggctaaca tgtcgaggca tctaggctcg gagcgttgta caagtagagg
1043

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1103

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1120

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Glu Val Arg Ala Thr Ser Gly Lys Thr Val Ile Lys Lys Gln Pro Thr
35 40 45

Ser Ile Ser Ser Ser Ser Ser Ser Trp Met Lys Ser Lys Asp Pro Arg
50 55 60

Ile Val Arg Val Ser Arg Ala Phe Gly Gly Lys Asp Arg His Ser Lys
65 70 75 80

Val Cys Thr Leu Arg Gly Leu Arg Asp Arg Arg Val Arg Leu Ser Val
85 90 95

Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Glu Arg Leu Gly Val Asp
100 105 110

Gln Pro Ser Lys Ala Val Asp Trp Leu Leu Asp Ala Ala Lys Glu Glu
115 120 125

Ile Asp Glu Leu Pro Pro Leu Pro Ile Ser Pro Glu Asn Phe Ser Ile
130 135 140

Phe Asn His His Gln Ser Phe Leu Asn Leu Gly Gln Arg Pro Gly Gln
145 150 155 160

Asp Pro Thr Gln Leu Gly Phe Lys Ile Asn Gly Cys Val Gln Lys Ser
165 170 175

Thr Thr Thr Ser Arg Glu Glu Asn Asp Arg Glu Lys Gly Glu Asn Asp
180 185 190

Val Val Tyr Thr Asn Asn His His Val Gly Ser Tyr Gly Thr Tyr His
195 200 205

Asn Leu Glu His His His His His His Gln His Leu Ser Leu Gln Ala
210 215 220

Asp Tyr His Ser His Gln Leu His Ser Leu Val Pro Phe Pro Ser Gln
225 230 235 240

Ile Leu Val Cys Pro Met Thr Thr Ser Pro Thr Thr Thr Thr Ile Gln
245 250 255

Ser Leu Phe Pro Ser Ser Ser Ser Ala Gly Ser Gly Thr Met Glu Thr
260 265 270

Leu Asp Pro Arg Gln Met
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112

Met Asp Asn Ser Asp Ile Leu Met
1 5

aac atg atg atg cag cag atg gag aag ctt. cct gaa cac ttc tct aac
160

Asn Met Met Met Gln Gln Met Glu Lys Leu Pro Glu His Phe Ser Asn
10 15 20

tca aac cct aac cct aat ccc cat aac att atg atg ctt tct gaa tcc
208

Ser Asn Pro Asn Pro Asn Pro His Asn Ile Met Met Leu Ser Glu Ser
25 30 35 40

aac acc cac ccg ttc ttc ttc aac ccc act cat tct cat ctc cca ttt
256

Asn Thr His Pro Phe Phe Phe Asn Pro Thr His Ser His Leu Pro Phe
45 50 55

gac caa acc atg cct cac cac caa ccc ggt tta aat ttc cgg tac gcc
304

Asp Gln Thr Met Pro His His Gln Pro Gly Leu Asn Phe Arg Tyr Ala
60 65 70

ccc tcc ccg tca tca tct ctc ccg gag aag aga gga ggc tgc agc gac
352

Pro Ser Pro Ser Ser Ser Leu Pro Glu Lys Arg Gly Gly Cys Ser Asp
75 80 85

aac gcc aac atg gcg gcg atg aga gag atg atc ttt cga ata gcc gtg
400

Asn Ala Asn Met Ala Ala Met Arg Glu Met Ile Phe Arg Ile Ala Val
90 95 100

atg cag cct ata cat att gat ccg gaa tcc gta aag cca cca aag aga
448

Met Gln Pro Ile His Ile Asp Pro Glu Ser Val Lys Pro Pro Lys Arg
105 110 115 120

aag aac gtg agg atc tct aag gat cca cag agc gtg gca gct cgg cat
496

Lys Asn Val Arg Ile Ser Lys Asp Pro Gln Ser Val Ala Ala Arg His
125 130 135

cga agg gag agg ata agc gag ccg att ccg att ctt cag ccg ctt gtt
544

Arg Arg Glu Arg Ile Ser Glu Arg Ile Arg Ile Leu Gln Arg Leu Val
140 145 150

ccc ggt ggg act aag atg gat acg gcg tcg atg ctc gat gag gct atc
592

Pro Gly Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile
155 160 165

cat tac gtt aag ttt ctc aag aag caa gtg cag tcg ctg gag gaa cat
640

His Tyr Val Lys Phe Leu Lys Lys Gln Val Gln Ser Leu Glu Glu His

170 175 180
 gcg gtg gtt aac ggc gga gga atg acg gcg gtg gcc gga gga gca ctt
 688
 Ala Val Val Asn Gly Gly Gly Met Thr Ala Val Ala Gly Gly Ala Leu
 185 190 195 200
 gcg ggt act gtt ggt gga gga tat gga gga aaa ggg tgt ggc att atg
 736
 Ala Gly Thr Val Gly Gly Gly Tyr Gly Gly Lys Gly Cys Gly Ile Met
 205 210 215
 cgg tct gat cat cac cag atg ctt gga aat gca cag att ctt aga tga
 784
 Arg Ser Asp His His Gln Met Leu Gly Asn Ala Gln Ile Leu Arg
 220 225 230
 tgatgatgtt gattttttaa tatatatcat atgtttatta atatgacggg aaaaaatatt
 844
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 904
 tctttccggg ttctgataat gtttgggatg gttaattaac aattttaaag tcagacaact
 964
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 1024

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 Lys Leu Pro Glu His Phe Ser Asn Ser Asn Pro Asn Pro Asn Pro His
 20 25 30
 Asn Ile Met Met Leu Ser Glu Ser Asn Thr His Pro Phe Phe Phe Asn
 35 40 45
 Pro Thr His Ser His Leu Pro Phe Asp Gln Thr Met Pro His His Gln
 50 55 60
 Pro Gly Leu Asn Phe Arg Tyr Ala Pro Ser Pro Ser Ser Ser Leu Pro
 65 70 75 80
 Glu Lys Arg Gly Gly Cys Ser Asp Asn Ala Asn Met Ala Ala Met Arg
 85 90 95
 Glu Met Ile Phe Arg Ile Ala Val Met Gln Pro Ile His Ile Asp Pro
 100 105 110

Glu Ser Val Lys Pro Pro Lys Arg Lys Asn Val Arg Ile Ser Lys Asp
115 120 125

Pro Gln Ser Val Ala Ala Arg His Arg Arg Glu Arg Ile Ser Glu Arg
130 135 140

Ile Arg Ile Leu Gln Arg Leu Val Pro Gly Gly Thr Lys Met Asp Thr
145 150 155 160

Ala Ser Met Leu Asp Glu Ala Ile His Tyr Val Lys Phe Leu Lys Lys
165 170 175

Gln Val Gln Ser Leu Glu Glu His Ala Val Val Asn Gly Gly Gly Met
180 185 190

Thr Ala Val Ala Gly Gly Ala Leu Ala Gly Thr Val Gly Gly Gly Tyr
195 200 205

Gly Gly Lys Gly Cys Gly Ile Met Arg Ser Asp His His Gln Met Leu
210 215 220

Gly Asn Ala Gln Ile Leu Arg
225 230

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cctcaattcc aaatcttaaa ccctaaattt acagacacaa tcgagatcac ctgaaaaaag
120

agggtttaag attttagcaa ag atg gcg aat tca gga aat tat gga aag agg
172

Met Ala Asn Ser Gly Asn Tyr Gly Lys Arg
1 5 10

ccc ttt cga ggc gat gaa tcg gat gaa aag aaa gaa gcc gat gat gat
220

Pro Phe Arg Gly Asp Glu Ser Asp Glu Lys Lys Glu Ala Asp Asp Asp
15 20 25

gag aac ata ttc cct ttc ttc tct gcc cga tcc caa tat gac atg cgt
268

Glu Asn Ile Phe Pro Phe Phe Ser Ala Arg Ser Gln Tyr Asp Met Arg
30 35 40

gcc atg gtc tca gcc ttg act caa gtc att gga aac caa agc agc tct
316

Ala Met Val Ser Ala Leu Thr Gln Val Ile Gly Asn Gln Ser Ser Ser
45 50 55

cat gat aat aac caa cat caa cct gtt gtg tat aat caa caa gat cct
 364
 His Asp Asn Asn Gln His Gln Pro Val Val Tyr Asn Gln Gln Asp Pro
 60 65 70
 aac cca ccg gct cct cca act caa gat caa ggg cta ttg agg aag agg
 412
 Asn Pro Pro Ala Pro Pro Thr Gln Asp Gln Gly Leu Leu Arg Lys Arg
 75 80 85 90
 cac tat aga ggg gta aga caa cga cca tgg gga aag tgg gca gct gaa
 460
 His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
 95 100 105
 att cgg gat ccg caa aag gca gca cgg gtg tgg ctc ggg aca ttt gag
 508
 Ile Arg Asp Pro Gln Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu
 110 115 120
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 556
 Thr Ala Glu Ala Ala Ala Leu Ala Tyr Asp Asn Ala Ala Leu Lys Phe
 125 130 135
 aaa gga agc aaa gcc aaa ctc aat ttc cct gag aga gct caa cta gca
 604
 Lys Gly Ser Lys Ala Lys Leu Asn Phe Pro Glu Arg Ala Gln Leu Ala
 140 145 150
 agt aac act agt aca act acc ggt cca cca aac tat tat tct tct aat
 652
 Ser Asn Thr Ser Thr Thr Thr Gly Pro Pro Asn Tyr Tyr Ser Ser Asn
 155 160 165 170
 aat caa att tac tac tca aat ccg cag act aat ccg caa acc ata cct
 700
 Asn Gln Ile Tyr Tyr Ser Asn Pro Gln Thr Asn Pro Gln Thr Ile Pro
 175 180 185
 tat ttt aac caa tac tac tat aac caa tat ctt cat caa ggg ggg aat
 748
 Tyr Phe Asn Gln Tyr Tyr Tyr Asn Gln Tyr Leu His Gln Gly Gly Asn
 190 195 200
 agt aac gat gca tta agt tat agc ttg gcc ggt gga gaa acc gga ggc
 796
 Ser Asn Asp Ala Leu Ser Tyr Ser Leu Ala Gly Gly Glu Thr Gly Gly
 205 210 215
 tca atg tat aat cat cag acg tta tct act aca aat tct tca tct tct
 844
 Ser Met Tyr Asn His Gln Thr Leu Ser Thr Thr Asn Ser Ser Ser Ser
 220 225 230
 ggt gga tct tca agg caa caa gat gat gaa caa gat tac gcc aga tat
 892
 Gly Gly Ser Ser Arg Gln Gln Asp Asp Glu Gln Asp Tyr Ala Arg Tyr
 235 240 245 250

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934

Leu Arg Phe Gly Asp Ser Ser Pro Pro Asn Ser Gly Phe

255

260

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994

ttctaa

1000

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20 25 30

Phe Ser Ala Arg Ser Gln Tyr Asp Met Arg Ala Met Val Ser Ala Leu
35 40 45

Thr Gln Val Ile Gly Asn Gln Ser Ser Ser His Asp Asn Asn Gln His
50 55 60

Gln Pro Val Val Tyr Asn Gln Gln Asp Pro Asn Pro Pro Ala Pro Pro
65 70 75 80

Thr Gln Asp Gln Gly Leu Leu Arg Lys Arg His Tyr Arg Gly Val Arg
85 90 95

Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Gln Lys
100 105 110

Ala Ala Arg Val Trp Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala Ala
115 120 125

Leu Ala Tyr Asp Asn Ala Ala Leu Lys Phe Lys Gly Ser Lys Ala Lys
130 135 140

Leu Asn Phe Pro Glu Arg Ala Gln Leu Ala Ser Asn Thr Ser Thr Thr
145 150 155 160

Thr Gly Pro Pro Asn Tyr Tyr Ser Ser Asn Asn Gln Ile Tyr Tyr Ser
165 170 175

Asn Pro Gln Thr Asn Pro Gln Thr Ile Pro Tyr Phe Asn Gln Tyr Tyr
180 185 190

Tyr Asn Gln Tyr Leu His Gln Gly Gly Asn Ser Asn Asp Ala Leu Ser
 195 200 205

Tyr Ser Leu Ala Gly Gly Glu Thr Gly Gly Ser Met Tyr Asn His Gln
 210 215 220

Thr Leu Ser Thr Thr Asn Ser Ser Ser Ser Gly Gly Ser Ser Arg Gln
 225 230 235 240

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Ser Pro Pro Asn Ser Gly Phe
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gccgttatta caacgaggat tgtgtttgat ccg atg gaa gga ttg gaa tct gtg
 114

Met Glu Gly Leu Glu Ser Val
 1 5

tac gct caa gct atg tat gga atg aca cga gag agc aaa atc atg gag
 162

Tyr Ala Gln Ala Met Tyr Gly Met Thr Arg Glu Ser Lys Ile Met Glu
 10 15 20

cat caa gga tca gat ttg att tgg gga gga aat gag cta atg gct cga
 210

His Gln Gly Ser Asp Leu Ile Trp Gly Gly Asn Glu Leu Met Ala Arg
 25 30 35

gaa ctc tgt tct tct tct tct tat cac cac caa ctc att aat ccg aat
 258

Glu Leu Cys Ser Ser Ser Ser Tyr His His Gln Leu Ile Asn Pro Asn
 40 45 50 55

ctt agc agc tgt ttc atg tct gat ctt gga gtc tta ggt gag att caa
 306

Leu Ser Ser Cys Phe Met Ser Asp Leu Gly Val Leu Gly Glu Ile Gln
 60 65 70

cag cag caa cat gtt ggc aac aga gct agc tcg ata gat cca tca tca
 354

Gln Gln Gln His Val Gly Asn Arg Ala Ser Ser Ile Asp Pro Ser Ser
 75 80 85

ctc gat tgt ttg tta tct gcg acg tcg aat agc aac aac acc tcg acg
 402

Leu Asp Cys Leu Leu Ser Ala Thr Ser Asn Ser Asn Asn Thr Ser Thr
 90 95 100
 gag gac gat gaa gga ata tct gtg ctt ttc tca gat tgt cag act ctt
 450
 Glu Asp Asp Glu Gly Ile Ser Val Leu Phe Ser Asp Cys Gln Thr Leu
 105 110 115
 tgg agc ttt ggt gga gtc tca tct gca gag tct gag aac aga gag atc
 498
 Trp Ser Phe Gly Gly Val Ser Ser Ala Glu Ser Glu Asn Arg Glu Ile
 120 125 130 135
 act act gag acg aca aca acg ata aag cct aag cct ttg aag aga aac
 546
 Thr Thr Glu Thr Thr Thr Thr Ile Lys Pro Lys Pro Leu Lys Arg Asn
 140 145 150
 aga gga gga gat gga gga act act gag act aca aca aca aca aca aaa
 594
 Arg Gly Gly Asp Gly Gly Thr Thr Glu Thr Thr Thr Thr Thr Thr Lys
 155 160 165
 cct aag tct ttg aag aga aac aga gga gac gag aca gga agt cac ttt
 642
 Pro Lys Ser Leu Lys Arg Asn Arg Gly Asp Glu Thr Gly Ser His Phe
 170 175 180
 agt ctt gtt cat cct caa gat gat tcg gag aaa gga ggt ttc aag ctt
 690
 Ser Leu Val His Pro Gln Asp Asp Ser Glu Lys Gly Gly Phe Lys Leu
 185 190 195
 ata tac gat gag aat caa tcg aaa tca aag aaa cca aga aca gag aaa
 738
 Ile Tyr Asp Glu Asn Gln Ser Lys Ser Lys Lys Pro Arg Thr Glu Lys
 200 205 210 215
 gaa cga ggc ggt tct tcg aac att agt ttc caa cat tca act tgt ttg
 786
 Glu Arg Gly Gly Ser Ser Asn Ile Ser Phe Gln His Ser Thr Cys Leu
 220 225 230
 tct gac aat gtc gag ccc gat gct gag gcg att gca caa atg aag gag
 834
 Ser Asp Asn Val Glu Pro Asp Ala Glu Ala Ile Ala Gln Met Lys Glu
 235 240 245
 atg ata tac aga gcg gct gca ttt aga ccg gtg aat ttc ggg tta gag
 882
 Met Ile Tyr Arg Ala Ala Ala Phe Arg Pro Val Asn Phe Gly Leu Glu
 250 255 260
 att gtg gag aag cct aag agg aag aac gtc aag ata tcg acg gat cct
 930
 Ile Val Glu Lys Pro Lys Arg Lys Asn Val Lys Ile Ser Thr Asp Pro
 265 270 275
 caa acg gtt gca gcg aga cag aga agg gag agg ata agt gag aag att
 978
 Gln Thr Val Ala Ala Arg Gln Arg Arg Glu Arg Ile Ser Glu Lys Ile

280 285 290 295
 agg gtt tta caa aca ttg gtt cca ggt ggg acg aag atg gat act gca
 1026
 Arg Val Leu Gln Thr Leu Val Pro Gly Gly Thr Lys Met Asp Thr Ala
 300 305 310
 tca atg ctt gat gaa gct gct aat tat ctc aag ttc ctt aga gca caa
 1074
 Ser Met Leu Asp Glu Ala Ala Asn Tyr Leu Lys Phe Leu Arg Ala Gln
 315 320 325
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 1122
 Val Lys Ala Leu Glu Asn Leu Arg Pro Lys Leu Asp Gln Thr Asn Leu
 330 335 340
 tct ttc tct tct gct cct aca tcg ttt cca tta ttc cac cca tct ttt
 1170
 Ser Phe Ser Ser Ala Pro Thr Ser Phe Pro Leu Phe His Pro Ser Phe
 345 350 355
 ctt cca ttg caa aat cct aat caa atc cat cat cca gag tgt tga
 1215
 Leu Pro Leu Gln Asn Pro Asn Gln Ile His His Pro Glu Cys
 360 365 370
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 1275
 agcagttctc aagaaaggca acttctgtga caagggtggt gtcgggcagt gttgtttaca
 1335
 ctttccagtc tttgttttgc atttcttttt atataaagtt tgtattttat atagaatctg
 1395
 tggaattcga ggggtgaaat attgtgaaaa acagagccgc aagagggttaa ttacagtctc
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 20 25 30
 Gly Asn Glu Leu Met Ala Arg Glu Leu Cys Ser Ser Ser Ser Tyr His
 35 40 45
 His Gln Leu Ile Asn Pro Asn Leu Ser Ser Cys Phe Met Ser Asp Leu
 50 55 60

Gly Val Leu Gly Glu Ile Gln Gln Gln Gln His Val Gly Asn Arg Ala
 65 70 75 80
 Ser Ser Ile Asp Pro Ser Ser Leu Asp Cys Leu Leu Ser Ala Thr Ser
 85 90 95
 Asn Ser Asn Asn Thr Ser Thr Glu Asp Asp Glu Gly Ile Ser Val Leu
 100 105 110
 Phe Ser Asp Cys Gln Thr Leu Trp Ser Phe Gly Gly Val Ser Ser Ala
 115 120 125
 Glu Ser Glu Asn Arg Glu Ile Thr Thr Glu Thr Thr Thr Thr Ile Lys
 130 135 140
 Pro Lys Pro Leu Lys Arg Asn Arg Gly Gly Asp Gly Gly Thr Thr Glu
 145 150 155 160
 Thr Thr Thr Thr Thr Thr Lys Pro Lys Ser Leu Lys Arg Asn Arg Gly
 165 170 175
 Asp Glu Thr Gly Ser His Phe Ser Leu Val His Pro Gln Asp Asp Ser
 180 185 190
 Glu Lys Gly Gly Phe Lys Leu Ile Tyr Asp Glu Asn Gln Ser Lys Ser
 195 200 205
 Lys Lys Pro Arg Thr Glu Lys Glu Arg Gly Gly Ser Ser Asn Ile Ser
 210 215 220
 Phe Gln His Ser Thr Cys Leu Ser Asp Asn Val Glu Pro Asp Ala Glu
 225 230 235 240
 Ala Ile Ala Gln Met Lys Glu Met Ile Tyr Arg Ala Ala Ala Phe Arg
 245 250 255
 Pro Val Asn Phe Gly Leu Glu Ile Val Glu Lys Pro Lys Arg Lys Asn
 260 265 270
 Val Lys Ile Ser Thr Asp Pro Gln Thr Val Ala Ala Arg Gln Arg Arg
 275 280 285
 Glu Arg Ile Ser Glu Lys Ile Arg Val Leu Gln Thr Leu Val Pro Gly
 290 295 300

Gly Thr Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ala Asn Tyr
 305 310 315 320

Leu Lys Phe Leu Arg Ala Gln Val Lys Ala Leu Glu Asn Leu Arg Pro
 325 330 335

Lys Leu Asp Gln Thr Asn Leu Ser Phe Ser Ser Ala Pro Thr Ser Phe
 340 345 350

Pro Leu Phe His Pro Ser Phe Leu Pro Leu Gln Asn Pro Asn Gln Ile
 355 360 365

His His Pro Glu Cys
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 97

Thr Asn Gln Thr His Asn Asn Ala Lys Glu Ile Arg Tyr Arg Gly Val
 15 20 25

agg aag cgt cct tgg ggc cgt tat gcc gcc gag atc cga gat ccg ggc
 145

Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp Pro Gly
 30 35 40

aag aaa acc cgc gtc tgg ctt ggc act ttc gat acg gct gaa gag gcg
 193

Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala
 45 50 55 60

gcg cgt gct tac gat acg gcg gcg cgt gat ttt cgt ggt gct aag gct
 241

Ala Arg Ala Tyr Asp Thr Ala Ala Arg Asp Phe Arg Gly Ala Lys Ala
 65 70 75

aag acc aat ttc cca act ttt ctc gag ctg agt gac cag aag gtc cct
 289

Lys Thr Asn Phe Pro Thr Phe Leu Glu Leu Ser Asp Gln Lys Val Pro
 80 85 90

acc ggt ttc gcg cgt agc cct agc cag agc agc acg ctc gac tgt gct
 337

Thr Gly Phe Ala Arg Ser Pro Ser Gln Ser Ser Thr Leu Asp Cys Ala
 95 100 105

tct cct ccg acg tta gtt gtg cct tca gcg acg gct ggg aat gtt ccc
 385

Ser Pro Pro Thr Leu Val Val Pro Ser Ala Thr Ala Gly Asn Val Pro
 110 115 120

ccg cag ctc gag ctt agt ctc ggc gga gga ggc ggc ggc tcg tgt tat
 433

Pro Gln Leu Glu Leu Ser Leu Gly Gly Gly Gly Gly Gly Ser Cys Tyr
 125 130 135 140

cag atc ccg atg tcg cgt cct gtc tac ttt ttg gac ctg atg ggg atc
 481

Gln Ile Pro Met Ser Arg Pro Val Tyr Phe Leu Asp Leu Met Gly Ile
 145 150 155

ggc aac gta ggt cgt ggt cag cct cct cct gtg aca tcg gcg ttt aga
 529

Gly Asn Val Gly Arg Gly Gln Pro Pro Pro Val Thr Ser Ala Phe Arg
 160 165 170

tcg ccg gtg gtg cat gtt gcg acg aag atg gct tgt ggt gcc caa agc
 577

Ser Pro Val Val His Val Ala Thr Lys Met Ala Cys Gly Ala Gln Ser
 175 180 185

gac tct gat tcg tca tcg gtc gtt gat ttc gaa ggt ggc atg gag aag
 625

Asp Ser Asp Ser Ser Ser Val Val Asp Phe Glu Gly Gly Met Glu Lys
 190 195 200

aga tct cag ctg tta gat cta gat ctt aat ttg cct cct cca tcg gaa
 673

Arg Ser Gln Leu Leu Asp Leu Asp Leu Asn Leu Pro Pro Pro Ser Glu
 205 210 215 220

cag gcc tga gcttttaacg gtgtcgtttc aattcgaagc gcatgcgttt
 722

Gln Ala

cttcttcttt ttgagctgtg aaaattcggt ttctcatagt tttcctctc tctctctctc
 782

agtctaaatt tattaccagt ttttagaaag aaaaaacaga ttaaatctga gagagaaaaa
 842

tataatttta gctgacatgg atcggtatgt acatattatt acataaccgg agatctgaac
 902

ttttgttgtg tgcttttaaat tttttgcgac ttggtttcac cccatgttgt ttctctattt
 962

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 1022

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 1023

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516

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113
Met Asp Ser Ser Cys Ile Asp Glu Ile Ser Ser
1 5 10
tcc act tca gaa tct ttc tcc gcc acc acc gcc aag aag ctc tct cct
161
Ser Thr Ser Glu Ser Phe Ser Ala Thr Thr Ala Lys Lys Leu Ser Pro
15 20 25
cct ccc gcg gcg gcg tta cgc ctc tac cgg atg gga agc ggc ggg agc
209
Pro Pro Ala Ala Ala Leu Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser
30 35 40
agc gtc gtg ttg gat ccc gag aac ggc cta gag acg gag tca cga aag
257
Ser Val Val Leu Asp Pro Glu Asn Gly Leu Glu Thr Glu Ser Arg Lys
45 50 55
cta cca tct tca aaa tac aaa ggt gtt gtt cct cag cct aac gga aga
305
Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg
60 65 70 75
tgg gga gct cag atc tac gag aag cac caa cga gta tgg ctc ggg act
353
Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr
80 85 90
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401
Phe Asn Glu Gln Glu Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys
95 100 105
aga ttc cgt ggc cgc gac gcc gtc gtc aac ttc aag aac gtt ctg gaa
449
Arg Phe Arg Gly Arg Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu
110 115 120
gac ggc gat tta gct ttt ctt gaa gct cac tca aag gcc gag atc gtc
497
Asp Gly Asp Leu Ala Phe Leu Glu Ala His Ser Lys Ala Glu Ile Val
125 130 135
gac atg ttg aga aaa cac act tac gcc gac gag ctt gaa cag aac aat
545
Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Leu Glu Gln Asn Asn
140 145 150 155
aaa cgg cag ttg ttt ctc tcc gtc gac gct aac gga aaa cgt aac gga
593
Lys Arg Gln Leu Phe Leu Ser Val Asp Ala Asn Gly Lys Arg Asn Gly
160 165 170
tcg agt act act caa aac gac aaa gtt tta aag acg tgt gaa gtt ctt
641
Ser Ser Thr Thr Gln Asn Asp Lys Val Leu Lys Thr Cys Glu Val Leu
175 180 185

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689
Phe Glu Lys Ala Val Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu
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gtg ata cct aaa caa cac gcc gag aaa cac ttt ccg tta ccg tca ccg
737
Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro Ser Pro
      205      210      215

tca ccg gca gtg act aaa gga gtt ttg atc aac ttc gaa gac gtt aac
785
Ser Pro Ala Val Thr Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn
220      225      230      235

ggt aaa gtg tgg agg ttc cgt tac tca tac tgg aac agt agt caa agt
833
Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser
      240      245      250

tac gtg ttg acc aag gga tgg agt cga ttc gtc aag gag aag aat ctt
881
Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu
      255      260      265

cga gcc ggt gat gtt gtt act ttc gag aga tcg acc gga cta gag cgg
929
Arg Ala Gly Asp Val Val Thr Phe Glu Arg Ser Thr Gly Leu Glu Arg
      270      275      280

cag tta tat att gat tgg aaa gtt cgg tct ggt ccg aga gaa aac ccg
977
Gln Leu Tyr Ile Asp Trp Lys Val Arg Ser Gly Pro Arg Glu Asn Pro
      285      290      295

gtt cag gtg gtg gtt cgg ctt ttc gga gtt gat atc ttt aat gtg acc
1025
Val Gln Val Val Val Arg Leu Phe Gly Val Asp Ile Phe Asn Val Thr
300      305      310      315

acc gtg aag cca aac gac gtc gtg gcc gtt tgc ggt gga aag aga tct
1073
Thr Val Lys Pro Asn Asp Val Val Ala Val Cys Gly Gly Lys Arg Ser
      320      325      330

cga gat gtt gat gat atg ttt gcg tta cgg tgt tcc aag aag cag gcg
1121
Arg Asp Val Asp Asp Met Phe Ala Leu Arg Cys Ser Lys Lys Gln Ala
      335      340      345

ata atc aat gct ttg tga catatttcct tttccgattt tatgctttcg
1169
Ile Ile Asn Ala Leu
      350

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1229

ggaaaagaga taagacc
1246

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Leu Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser Ser Val Val Leu Asp
35 40 45

Pro Glu Asn Gly Leu Glu Thr Glu Ser Arg Lys Leu Pro Ser Ser Lys
50 55 60

Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
65 70 75 80

Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Gln Glu
85 90 95

Glu Ala Ala Arg Ser Tyr Asp Ile Ala Ala Cys Arg Phe Arg Gly Arg
100 105 110

Asp Ala Val Val Asn Phe Lys Asn Val Leu Glu Asp Gly Asp Leu Ala
115 120 125

Phe Leu Glu Ala His Ser Lys Ala Glu Ile Val Asp Met Leu Arg Lys
130 135 140

His Thr Tyr Ala Asp Glu Leu Glu Gln Asn Asn Lys Arg Gln Leu Phe
145 150 155 160

Leu Ser Val Asp Ala Asn Gly Lys Arg Asn Gly Ser Ser Thr Thr Gln
165 170 175

Asn Asp Lys Val Leu Lys Thr Cys Glu Val Leu Phe Glu Lys Ala Val
180 185 190

Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
195 200 205

His Ala Glu Lys His Phe Pro Leu Pro Ser Pro Ser Pro Ala Val Thr
210 215 220

Lys Gly Val Leu Ile Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg

225 230 235 240
 Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys
 245 250 255
 Gly Trp Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val
 260 265 270
 Val Thr Phe Glu Arg Ser Thr Gly Leu Glu Arg Gln Leu Tyr Ile Asp
 275 280 285
 Trp Lys Val Arg Ser Gly Pro Arg Glu Asn Pro Val Gln Val Val Val
 290 295 300
 Arg Leu Phe Gly Val Asp Ile Phe Asn Val Thr Thr Val Lys Pro Asn
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 325 330 335
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Met Asp Gln Gly Gly
 1 5

cgt agc agt ggt agt gga gga gga gga gcc gag caa ggg aag tac cgt
 103

Arg Ser Ser Gly Ser Gly Gly Gly Gly Ala Glu Gln Gly Lys Tyr Arg
 10 15 20

gga gta agg aga cga cct tgg ggt aaa tac gcc gcg gaa ata aga gat
 151

Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp
 25 30 35

tcg agg aag cac gga gag cgt gtg tgg cta ggg aca ttc gac act gcg
 199

Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
 40 45 50

gaa gac gcg gct cga gcc tat gac cga gcc gcc tat tca atg aga ggc
 247

Glu Asp Ala Ala Arg Ala Tyr Asp Arg Ala Ala Tyr Ser Met Arg Gly
 55 60 65

aaa gct gcc att ctc aac ttc cct cac gag tat aac atg gga acc gga

295

Lys Ala Ala Ile Leu Asn Phe Pro His Glu Tyr Asn Met Gly Thr Gly
70 75 80 85

tcc tca tcc act gcg gct aat tct tct tcc tcg tcg cag caa gtt ttt

343

Ser Ser Ser Thr Ala Ala Asn Ser Ser Ser Ser Ser Gln Gln Val Phe
90 95 100

gag ttt gag tac ttg gac gat agc gtt ttg gat gaa ctt ctt gaa tat

391

Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Asp Glu Leu Leu Glu Tyr
105 110 115

gga gag aac tat aac aag act cat aat atc aac atg ggc aag agg caa

439

Gly Glu Asn Tyr Asn Lys Thr His Asn Ile Asn Met Gly Lys Arg Gln
120 125 130

taa agggaatata atcggtatta actgaaagtt atgtgaaaga ccattttcag

492

ttataacaaa taaaataaaa tcccaagcgt acaaagctgt ttctaaaaaa aaaaaaaaaa

552

a

553

<210> 296 <211> 133 <212> PRT <213> Arabidopsis thaliana <400>

296

Met Asp Gln Gly Gly Arg Ser Ser Gly Ser Gly Gly Gly Gly Ala Glu

1 5 10 15

Gln Gly Lys Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala

20

25

30

Ala Glu Ile Arg Asp Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly

35

40

45

Thr Phe Asp Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Arg Ala Ala

50

55

60

Tyr Ser Met Arg Gly Lys Ala Ala Ile Leu Asn Phe Pro His Glu Tyr

65

70

75

80

Asn Met Gly Thr Gly Ser Ser Ser Thr Ala Ala Asn Ser Ser Ser Ser

85

90

95

Ser Gln Gln Val Phe Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Asp

100

105

110

Glu Leu Leu Glu Tyr Gly Glu Asn Tyr Asn Lys Thr His Asn Ile Asn
 115 120 125

Met Gly Lys Arg Gln
 130

<210> 297 <211> 929 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (164)..(805) <223> G40

<400> 297
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 60

agacagatat actatctttt attaatccaa aaagactgag aactctagta actacgtact
 120

acttaaacct tatccagttt cttgaaacag agtactctga tca atg aac tca ttt
 175

Met Asn Ser Phe
 1

tca gct ttt tct gaa atg ttt ggc tcc gat tac gag cct caa ggc gga
 223
 Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu Pro Gln Gly Gly
 5 10 15 20

gat tat tgt ccg acg ttg gcc acg agt tgt ccg aag aaa ccg gcg ggc
 271
 Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly
 25 30 35

cgt aag aag ttt cgt gag act cgt cac cca att tac aga gga gtt cgt
 319
 Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg
 40 45 50

caa aga aac tcc ggt aag tgg gtt tct gaa gtg aga gag cca aac aag
 367
 Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg Glu Pro Asn Lys
 55 60 65

aaa acc agg att tgg ctc ggg act ttc caa acc gct gag atg gca gct
 415
 Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala
 70 75 80

cgt gct cac gac gtc gct gca tta gcc ctc cgt ggc cga tca gca tgt
 463
 Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys
 85 90 95 100

ctc aac ttc gct gac tcg gct tgg cgg cta cga atc ccg gag tca aca
 511
 Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr
 105 110 115

tgc gcc aag gat atc caa aaa gcg gct gct gaa gcg gcg ttg gct ttt
 559
 Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Ala Phe

120 125 130
 caa gat gag acg tgt gat acg acg acc acg aat cat ggc ctg gac atg
 607
 Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His Gly Leu Asp Met
 135 140 145
 gag gag acg atg gtg gaa gct att tat acä ccg gaa cag agc gaa ggt
 655
 Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Glu Gly
 150 155 160
 gcg ttt tat atg gat gag gag aca atg ttt ggg atg ccg act ttg ttg
 703
 Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met Pro Thr Leu Leu
 165 170 175 180
 gat aat atg gct gaa ggc atg ctt tta ccg ccg cct gtt caa tgg
 751
 Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro Ser Val Gln Trp
 185 190 195
 aat cat aat tat gac ggc gaa gga gat ggt gac gtg tcg ctt tgg agt
 799
 Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val Ser Leu Trp Ser
 200 205 210
 tac taa tattcgatag tcgtttccat tttgtacta tagtttgaaa atattctagt
 855
 Tyr
 tccttttttt agaatgggtc cttcatttta ttttatttta ttgttgtaga aacgagtgga
 915
 aaataattca atac
 929
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 298
 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
 1 5 -10 15
 Pro Gln Gly Gly Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys
 20 25 30
 Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr
 35 40 45
 Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg
 50 55 60
 Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala
 65 70 75 80

Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly
 85 90 95
 Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile
 100 105 110
 Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala
 115 120 125
 Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His
 130 135 140
 Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu
 145 150 155 160
 Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met
 165 170 175
 Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro
 180 185 190
 Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val
 195 200 205
 Ser Leu Trp Ser Tyr
 210

<210> 299 <211> 803 <212> DNA <213> Arabidopsis thaliana <220>
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 55

 Met Phe Gly Ser Asp Tyr Glu
 1 5

tct ccg gtt tcc tca ggc ggt gat tac agt ccg aag ctt gcc acg agc
 103
 Ser Pro Val Ser Ser Gly Gly Asp Tyr Ser Pro Lys Leu Ala Thr Ser
 10 15 20

tgc ccc aag aaa cca gcg gga agg aag aag ttt cgt gag act cgt cac
 151
 Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
 25 30 35

cca att tac aga gga gtt cgt caa aga aac tcc ggt aag tgg gtg tgt
 199
 Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Cys
 40 45 50 55

gag ttg aga gag cca aac aag aaa acg agg att tgg ctc ggg act ttc
 247
 Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
 60 65 70
 caa acc gct gag atg gca gct cgt gct cac gac gtc gcc gcc ata gct
 295
 Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Ile Ala
 75 80 85
 ctc cgt ggc aga tct gcc tgt ctc aat ttc gct gac tcg gct tgg cgg
 343
 Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
 90 95 100
 cta cga atc ccg gaa tca acc tgt gcc aag gaa atc caa aag gcg gcg
 391
 Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala
 105 110 115
 gct gaa gcc gcg ttg aat ttt caa gat gag atg tgt cat atg acg acg
 439
 Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys His Met Thr Thr
 120 125 130 135
 gat gct cat ggt ctt gac atg gag gag acc ttg gtg gag gct att tat
 487
 Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr
 140 145 150
 acg ccg gaa cag agc caa gat gcg ttt tat atg gat gaa gag gcg atg
 535
 Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp Glu Glu Ala Met
 155 160 165
 ttg ggg atg tct agt ttg ttg gat aac atg gcc gaa ggg atg ctt tta
 583
 Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu
 170 175 180
 ccg tcg ccg tcg gtt caa tgg aac tat aat ttt gat gtc gag gga gat
 631
 Pro Ser Pro Ser Val Gln Trp Asn Tyr Asn Phe Asp Val Glu Gly Asp
 185 190 195
 gat gac gtg tcc tta tgg agc tat taa aattcgattt ttatttccat
 678
 Asp Asp Val Ser Leu Trp Ser Tyr
 200 205
 ttttggtatt atagcttttt atacatttga tcctttttta gaatggatct tcttcttttt
 738
 ttggttga gaaacgaatg taaatggtaa aagttgtgt. caaatgcaaa tgtttttgag
 798
 tgcag
 803

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Met Phe Gly Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr
1 5 10 15

Ser Pro Lys Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly Arg Lys
20 25 30

Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg
35 40 45

Asn Ser Gly Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr
50 55 60

Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala
65 70 75 80

His Asp Val Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn
85 90 95

Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala
100 105 110

Lys Glu Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp
115 120 125

Glu Met Cys His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu
130 135 140

Thr Leu Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe
145 150 155 160

Tyr Met Asp Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn
165 170 175

Met Ala Glu Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr
180 185 190

Asn Phe Asp Val Glu Gly Asp Asp Asp Val Ser Leu Trp Ser Tyr
195 200 205

<210> 301 <211> 908 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (119)..(769) <223> G42

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gacagagatc ttttagttac cttatccagt ttcttgaaac agagtactct tctgatca
 118
 atg aac tca ttt tct gct ttt tct gaa atg ttt ggc tcc gat tac gag
 166
 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
 1 5 10 15
 tct tcg gtt tcc tca ggc ggt gat tat att ccg acg ctt gcg agc agc
 214
 Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
 20 25 30
 tgc ccc aag aaa ccg gcg ggt cgt aag aag ttt cgt gag act cgt cac
 262
 Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
 35 40 45
 cca ata tac aga gga gtt cgt cgg aga aac tcc ggt aag tgg gtt tgt
 310
 Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
 50 55 60
 gag gtt aga gaa cca aac aag aaa aca agg att tgg ctc gga aca ttt
 358
 Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
 65 70 75 80
 caa acc gct gag atg gca gct cga gct cac gac gtt gcc gct tta gcc
 406
 Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
 85 90 95
 ctt cgt ggc cga tca gcc tgt ctc aat ttc gct gac tcg gct tgg aga
 454
 Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
 100 105 110
 ctc cga atc ccg gaa tca act tgc gct aag gac atc caa aag gcg gcg
 502
 Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
 115 120 125
 gct gaa gct gcg ttg gcg ttt cag gat gag atg tgt gat gcg acg acg
 550
 Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
 130 135 140
 gat cat ggc ttc gac atg gag gag acg ttg gtg gag gct att tac acg
 598
 Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
 145 150 155 160
 gcg gaa cag agc gaa aat gcg ttt tat atg cac gat gag gcg atg ttt
 646
 Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
 165 170 175
 gag atg ccg agt ttg ttg gct aat atg gca gaa ggg atg ctt ttg ccg
 694

Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
 180 185 190

ctt ccg tcc gta cag tgg aat cat aat cat gaa gtc gac ggc gat gat
 742

Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp
 195 200 205

gac gac gta tcg tta tgg agt tat taa aactcagatt attatttcca
 789

Asp Asp Val Ser Leu Trp Ser Tyr
 210 215

tttttagtac gatacttttt attttattat tattttttaga tcctttttta gaatggaatc
 849

tacattatgt ttgtaaaact gagaaacgag tgtaaattaa attgattcag tttcagtat
 908

<210> 302 <211> 216 <212> PRT <213> Arabidopsis thaliana <400>
 302

Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
 1 5 10 15

Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
 20 25 30

Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
 35 40 45

Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
 50 55 60

Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
 65 70 75 80

Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
 85 90 95

Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
 100 105 110

Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
 115 120 125

Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
 130 135 140

Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
 145 150 155 160

Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
165 170 175

Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
180 185 190

Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp
195 200 205

Asp Asp Val Ser Leu Trp Ser Tyr
210 215

<210> 303 <211> 959 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (50)..(733) <223> G152

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58

Met Gly Arg
1

ggg aag att gtg atc cag aag atc gat gat.tcc acg agt aga caa gtc
106

Gly Lys Ile Val Ile Gln Lys Ile Asp Asp Ser Thr Ser Arg Gln Val
5 10 15

act ttc tcc aaa aga aga aag ggt ctc atc aag aaa gct aaa gaa ctt
154

Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala Lys Glu Leu
20 25 30 35

gct att ctc tgc gac gcc gag gtc tgt ctc atc att ttc tcc aac act
202

Ala Ile Leu Cys Asp Ala Glu Val Cys Leu Ile Ile Phe Ser Asn Thr
40 45 50

gac aag ctc tat gac ttt gcc agc tcc agt gtg aaa tct act att gaa
250

Asp Lys Leu Tyr Asp Phe Ala Ser Ser Ser Val Lys Ser Thr Ile Glu
55 60 65

cga ttc aat acg gct aag atg gag gag caa gaa cta atg aac cct gca
298

Arg Phe Asn Thr Ala Lys Met Glu Glu Gln Glu Leu Met Asn Pro Ala
70 75 80

tca gaa gtt aag ttt tgg cag aga gag gct gaa act cta agg caa gaa
346

Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Glu Thr Leu Arg Gln Glu
85 90 95

ttg cac tca ttg caa gaa aat tat cgg caa cta acg gga gtg gaa tta
394

Leu His Ser Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly Val Glu Leu
100 105 110 115

aat ggt ttg agc gtt aag gag tta caa aac ata gag agt caa ctt gaa
 442
 Asn Gly Leu Ser Val Lys Glu Leu Gln Asn Ile Glu Ser Gln Leu Glu
 120 125 130

atg agt tta cgt gga att cgt atg aaa agg gaa caa att ttg acc aat
 490
 Met Ser Leu Arg Gly Ile Arg Met Lys Arg Glu Gln Ile Leu Thr Asn
 135 140 145

gaa att aaa gag cta acc aga aag agg aat ctt gtt cat cat gaa aac
 538
 Glu Ile Lys Glu Leu Thr Arg Lys Arg Asn Leu Val His His Glu Asn
 150 155 160

ctc gaa ttg tcg aga aaa gta caa agg att cat caa gaa aat gtc gaa
 586
 Leu Glu Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu Asn Val Glu
 165 170 175

cta tac aag aag gct tat gga acg tcg aac aca aat gga ttg gga cat
 634
 Leu Tyr Lys Lys Ala Tyr Gly Thr Ser Asn Thr Asn Gly Leu Gly His
 180 185 190 195

cat gag cta gta gat gca gtt tat gaa tcc cat gaa cag gtt agg ctg
 682
 His Glu Leu Val Asp Ala Val Tyr Glu Ser His Ala Gln Val Arg Leu
 200 205 210

cag cta agc cag cct gag cag tcc cat tat aag aca tct tca aac agc
 730
 Gln Leu Ser Gln Pro Glu Gln Ser His Tyr Lys Thr Ser Ser Asn Ser
 215 220 225

taa gatcatataa gagatatata acaaattggt cgttcttgat tatctcaaaa
 783

ccctttcaaa tatatatatcgc tgcatattat atatgaagac tcgtttgact atgtcaatat
 843

atatgttttc atgcaggagt aagtgtgagt gtaatcatgt cggagagcaa accaaagggt
 903

tgatttgtag gatatatatc tatatatggt ctcaagtgaag agcaatggaa cagctt
 959

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 304

Met Gly Arg Gly Lys Ile Val Ile Gln Lys Ile Asp Asp Ser Thr Ser
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Lys Gly Leu Ile Lys Lys Ala
 20 25 30

Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Cys Leu Ile Ile Phe

35 40 45
 Ser Asn Thr Asp Lys Leu Tyr Asp Phe Ala Ser Ser Ser Val Lys Ser
 50 55 60
 Thr Ile Glu Arg Phe Asn Thr Ala Lys Met Glu Glu Gln Glu Leu Met
 65 70 75 80
 Asn Pro Ala Ser Glu Val Lys Phe Trp Gln Arg Glu Ala Glu Thr Leu
 85 90 95
 Arg Gln Glu Leu His Ser Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
 100 105 110
 Val Glu Leu Asn Gly Leu Ser Val Lys Glu Leu Gln Asn Ile Glu Ser
 115 120 125
 Gln Leu Glu Met Ser Leu Arg Gly Ile Arg Met Lys Arg Glu Gln Ile
 130 135 140
 Leu Thr Asn Glu Ile Lys Glu Leu Thr Arg Lys Arg Asn Leu Val His
 145 150 155 160
 His Glu Asn Leu Glu Leu Ser Arg Lys Val Gln Arg Ile His Gln Glu
 165 170 175
 Asn Val Glu Leu Tyr Lys Lys Ala Tyr Gly Thr Ser Asn Thr Asn Gly
 180 185 190
 Leu Gly His His Glu Leu Val Asp Ala Val Tyr Glu Ser His Ala Gln
 195 200 205
 Val Arg Leu Gln Leu Ser Gln Pro Glu Gln Ser His Tyr Lys Thr Ser
 210 215 220
 Ser Asn Ser
 225

<210> 305 <211> 1098 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (97)..(801) <223> G153

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tcaattggtt ttggtgtag tcttttggg agagag atg ggg aga ggg aag ata
 114

Met Gly Arg Gly Lys Ile

1

5

gtt ata cga agg atc gat aac tct aca agt aga caa gtg act ttc tcc
 162
 Val Ile Arg Arg Ile Asp Asn Ser Thr Ser Arg Gln Val Thr Phe Ser
 10 15 20

aag aga agg agt ggt ttg ctt aag aag gct aaa gag tta tcg atc ctt
 210
 Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala Lys Glu Leu Ser Ile Leu
 25 30 35

tgt gat gca gaa gtt ggt gtt atc ata ttc tct agc acc gga aag ctc
 258
 Cys Asp Ala Glu Val Gly Val Ile Ile Phe Ser Ser Thr Gly Lys Leu
 40 45 50

tac gac tac gca agc aat tca agt atg aaa aca atc att gag cgg tac
 306
 Tyr Asp Tyr Ala Ser Asn Ser Ser Met Lys Thr Ile Ile Glu Arg Tyr
 55 60 65 70

aac aga gta aaa gag gag cag cat caa ctt ctg aat cat gcc tca gag
 354
 Asn Arg Val Lys Glu Glu Gln His Gln Leu Leu Asn His Ala Ser Glu
 75 80 85

ata aag ttt tgg caa aga gag gtt gca agt ttg cag cag cag ctc caa
 402
 Ile Lys Phe Trp Gln Arg Glu Val Ala Ser Leu Gln Gln Gln Leu Gln
 90 95 100

cat cta caa gaa tgc cac agg aaa cta gtg gga gag gaa ctt tct gga
 450
 His Leu Gln Glu Cys His Arg Lys Leu Val Gly Glu Glu Leu Ser Gly
 105 110 115

atg aat gct aac gac cta caa aat ctt gaa gac cag cta gta aca agt
 498
 Met Asn Ala Asn Asp Leu Gln Asn Leu Glu Asp Gln Leu Val Thr Ser
 120 125 130

cta aaa ggt gtt cgt ctc aaa aag gat caa ctt atg aca aat gaa atc
 546
 Leu Lys Gly Val Arg Leu Lys Lys Asp Gln Leu Met Thr Asn Glu Ile
 135 140 145 150

aga gaa ctt aat cgt aag gga caa atc atc caa aaa gag aat cac gag
 594
 Arg Glu Leu Asn Arg Lys Gly Gln Ile Ile Gln Lys Glu Asn His Glu
 155 160 165

cta caa aat att gta gat ata atg cgt aag gaa aat att aaa ttg caa
 642
 Leu Gln Asn Ile Val Asp Ile Met Arg Lys Glu Asn Ile Lys Leu Gln
 170 175 180

aag aag gtt cat gga aga aca aat gtg att gaa ggc aat tca agt gta
 690
 Lys Lys Val His Gly Arg Thr Asn Val Ile Glu Gly Asn Ser Ser Val
 185 190 195

gat cca ata agc aat gga acc aca aca tat gca cca ccg caa ctt caa
738

Asp Pro Ile Ser Asn Gly Thr Thr Thr Tyr Ala Pro Pro Gln Leu Gln
200 205 210

ctc ata caa cta caa cca gct cct aga gaa aaa tca atc aga cta ggg
786

Leu Ile Gln Leu Gln Pro Ala Pro Arg Glu Lys Ser Ile Arg Leu Gly
215 220 225 230

cta caa ctt tcc tag caaaacatgt gggacatcga acaatatacg aaaagagttt
841

Leu Gln Leu Ser

gtatgtcatc ttcagtaaca accaagctgg atcatttcat tcttggttat gtaattctgt
901

ttactacttt ggagtttaat atgttatatg acaagtttct ctttgtcaag ttacttgtgt
961

atgtacatca taaaataatg atgtgatgtg agtgccgaac atactagaca tcattttacc
1021

gtgtgttttt ttcgggtaca ttaaattgtac aaaatccagt ctaattggca tttttataca
1081

aaaaaaaaa aaaaaaa
1098

<210> 306 <211> 234 <212> PRT <213> Arabidopsis thaliana <400>
306

Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser
1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Ser Gly Leu Leu Lys Lys Ala
20 25 30

Lys Glu Leu Ser Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe
35 40 45

Ser Ser Thr Gly Lys Leu Tyr Asp Tyr Ala Ser Asn Ser Ser Met Lys
50 55 60

Thr Ile Ile Glu Arg Tyr Asn Arg Val Lys Glu Glu Gln His Gln Leu
65 70 75 80

Leu Asn His Ala Ser Glu Ile Lys Phe Trp Gln Arg Glu Val Ala Ser
85 90 95

Leu Gln Gln Gln Leu Gln His Leu Gln Glu Cys His Arg Lys Leu Val
100 105 110

Gly Glu Glu Leu Ser Gly Met Asn Ala Asn Asp Leu Gln Asn Leu Glu
 115 120 125

Asp Gln Leu Val Thr Ser Leu Lys Gly Val Arg Leu Lys Lys Asp Gln
 130 135 140

Leu Met Thr Asn Glu Ile Arg Glu Leu Asn Arg Lys Gly Gln Ile Ile
 145 150 155 160

Gln Lys Glu Asn His Glu Leu Gln Asn Ile Val Asp Ile Met Arg Lys
 165 170 175

Glu Asn Ile Lys Leu Gln Lys Lys Val His Gly Arg Thr Asn Val Ile
 180 185 190

Glu Gly Asn Ser Ser Val Asp Pro Ile Ser Asn Gly Thr Thr Thr Tyr
 195 200 205

Ala Pro Pro Gln Leu Gln Leu Ile Gln Leu Gln Pro Ala Pro Arg Glu
 210 215 220

Lys Ser Ile Arg Leu Gly Leu Gln Leu Ser
 225 230

<210> 307 <211> 1952 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (100)..(1761) <223> G186

<400> 307
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 60

ctccttcgtt aatctcgtga tctctttctt tttctatat atg gac aga gga tgg
 114

Met Asp Arg Gly Trp
 1 5

tct ggt ctc act ctt gat tca tct tct ctt gat ctt tta aac cct aat
 162

Ser Gly Leu Thr Leu Asp Ser Ser Ser Leu Asp Leu Leu Asn Pro Asn
 10 15 20

cgt att tct cat aag aat cac cga cgt ttc tca aat cct ttg gcg atg
 210

Arg Ile Ser His Lys Asn His Arg Arg Phe Ser Asn Pro Leu Ala Met
 25 30 35

tct aga att gac gaa gaa gat gat cag aag acg aga ata tca acc aac
 258

Ser Arg Ile Asp Glu Glu Asp Asp Gln Lys Thr Arg Ile Ser Thr Asn
 40 45 50

ggt agt gaa ttt agg ttt ccg gtg agt ctc tca ggt att cgt gat cgt
 306
 Gly Ser Glu Phe Arg Phe Pro Val Ser Leu Ser Gly Ile Arg Asp Arg
 55 60 65

gaa gat gaa gat ttt tca tct ggc gtt gct gga gat aat gac cgt gaa
 354
 Glu Asp Glu Asp Phe Ser Ser Gly Val Ala Gly Asp Asn Asp Arg Glu
 70 75 80 85

gtt ccc ggc gaa gtg gat ttc ttc tcc gac aag aaa tct agg gtt tgt
 402
 Val Pro Gly Glu Val Asp Phe Phe Ser Asp Lys Lys Ser Arg Val Cys
 90 95 100

cgt gaa gac gac gaa gga ttt cgt gtg aag aag gaa gaa caa gat gat
 450
 Arg Glu Asp Asp Glu Gly Phe Arg Val Lys Lys Glu Glu Gln Asp Asp
 105 110 115

cga acg gac gta aat acc ggt ttg aat ctt cga aca act ggt aat aca
 498
 Arg Thr Asp Val Asn Thr Gly Leu Asn Leu Arg Thr Thr Gly Asn Thr
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aag agt gat gag tca atg atc gat gat gga gaa tct tcc gaa atg gaa
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 Lys Ser Asp Glu Ser Met Ile Asp Asp Gly Glu Ser Ser Glu Met Glu
 135 140 145

gat aag cgt gcg aaa aat gag ttg gtg aaa tta caa gat gag ttg aag
 594
 Asp Lys Arg Ala Lys Asn Glu Leu Val Lys Leu Gln Asp Glu Leu Lys
 150 155 160 165

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 642
 Lys Met Thr Met Asp Asn Gln Lys Leu Arg Glu Leu Leu Thr Gln Val
 170 175 180

agc aac agt tac act tca ctt cag atg cat ctt gtt tca cta atg cag
 690
 Ser Asn Ser Tyr Thr Ser Leu Gln Met His Leu Val Ser Leu Met Gln
 185 190 195

caa cag caa caa cag aac aat aag gta ata gaa gct gct gag aag cct
 738
 Gln Gln Gln Gln Asn Asn Lys Val Ile Glu Ala Ala Glu Lys Pro
 200 205 210

gag gag acg ata gta cca agg caa ttt att gat tta ggc cct acg aga
 786
 Glu Glu Thr Ile Val Pro Arg Gln Phe Ile Asp Leu Gly Pro Thr Arg
 215 220 225

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 834
 Ala Val Gly Glu Ala Glu Asp Val Ser Asn Ser Ser Ser Glu Asp Arg
 230 235 240 245

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 882
 Thr Arg Ser Gly Gly Ser Ser Ala Ala Glu Arg Arg Ser Asn Gly Lys
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 930
 Arg Leu Gly Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Lys Ile Gln
 265 270 275
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 978
 Lys Val Asn Ser Thr Thr Pro Thr Thr Phe Asp Gln Thr Ala Glu Ala
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 1026
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 330 335 340
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 Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro Pro
 360 365 370
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 1266
 Ala Ala Val Ala Met Ala Ser Thr Thr Thr Ala Ala Ala Asn Met Leu
 375 380 385
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 1314
 Leu Ser Gly Ser Met Ser Ser His Asp Gly Met Met Asn Pro Thr Asn
 390 395 400 405
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 1362
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 410 415 420
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 1410
 Ser Ala Ser Ala Pro Phe Pro Thr Val Thr Leu Asp Leu Thr His Ser
 425 430 435

cct ccg cct cct aat ggt tcc aat cct tcc tct tcc gcg gct acc aac
1458

Pro Pro Pro Pro Asn Gly Ser Asn Pro Ser Ser Ser Ala Ala Thr Asn
440 445 450

aac aac cac aac tca ctg atg cag cgg ccg caa caa caa caa cag caa
1506

Asn Asn His Asn Ser Leu Met Gln Arg Pro Gln Gln Gln Gln Gln Gln
455 460 465

atg acg aac tta cct ccg gga atg cta cct cat gta ata ggc cag gca
1554

Met Thr Asn Leu Pro Pro Gly Met Leu Pro His Val Ile Gly Gln Ala
470 475 480 485

ttg tat aac caa tcc aag ttc tcg ggg ctg cag ttc tct ggt ggc tct
1602

Leu Tyr Asn Gln Ser Lys Phe Ser Gly Leu Gln Phe Ser Gly Gly Ser
490 495 500

ccc tcg acg gca gcg ttt tct cag tca cac gcg gtg gct gat aca ata
1650

Pro Ser Thr Ala Ala Phe Ser Gln Ser His Ala Val Ala Asp Thr Ile
505 510 515

acg gca ctc aca gct gac ccg aat ttc acg gcg gct ctt gca gcc gtt
1698

Thr Ala Leu Thr Ala Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Val
520 525 530

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1746

Ile Ser Ser Met Ile Asn Gly Thr Asn His His Asp Gly Glu Gly Asn
535 540 545

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1801

Asn Lys Asn Gln
550

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1861

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1921

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1952

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Asn Pro Leu Ala Met Ser Arg Ile Asp Glu Glu Asp Asp Gln Lys Thr
 35 40 45
 Arg Ile Ser Thr Asn Gly Ser Glu Phe Arg Phe Pro Val Ser Leu Ser
 50 55 60
 Gly Ile Arg Asp Arg Glu Asp Glu Asp Phe Ser Ser Gly Val Ala Gly
 65 70 75 80
 Asp Asn Asp Arg Glu Val Pro Gly Glu Val Asp Phe Phe Ser Asp Lys
 85 90 95
 Lys Ser Arg Val Cys Arg Glu Asp Asp Glu Gly Phe Arg Val Lys Lys
 100 105 110
 Glu Glu Gln Asp Asp Arg Thr Asp Val Asn Thr Gly Leu Asn Leu Arg
 115 120 125
 Thr Thr Gly Asn Thr Lys Ser Asp Glu Ser Met Ile Asp Asp Gly Glu
 130 135 140
 Ser Ser Glu Met Glu Asp Lys Arg Ala Lys Asn Glu Leu Val Lys Leu
 145 150 155 160
 Gln Asp Glu Leu Lys Lys Met Thr Met Asp Asn Gln Lys Leu Arg Glu
 165 170 175
 Leu Leu Thr Gln Val Ser Asn Ser Tyr Thr Ser Leu Gln Met His Leu
 180 185 190
 Val Ser Leu Met Gln Gln Gln Gln Gln Gln Asn Asn Lys Val Ile Glu
 195 200 205
 Ala Ala Glu Lys Pro Glu Glu Thr Ile Val Pro Arg Gln Phe Ile Asp
 210 215 220
 Leu Gly Pro Thr Arg Ala Val Gly Glu Ala Glu Asp Val Ser Asn Ser
 225 230 235 240
 Ser Ser Glu Asp Arg Thr Arg Ser Gly Gly Ser Ser Ala Ala Glu Arg
 245 250 255
 Arg Ser Asn Gly Lys Arg Leu Gly Arg Glu Glu Ser Pro Glu Thr Glu
 260 265 270
 Ser Asn Lys Ile Gln Lys Val Asn Ser Thr Thr Pro Thr Thr Phe Asp

275 280 285
 Gln Thr Ala Glu Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala
 290 295 300
 Arg Ser Glu Ala Pro Met Ile Ser Asp Gly Cys Gln Trp Arg Lys Tyr
 305 310 315 320
 Gly Gln Lys Met Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg
 325 330 335
 Cys Thr Met Ala Thr Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys
 340 345 350
 Ala Glu Asp Arg Ser Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn
 355 360 365
 His Pro Leu Pro Pro Ala Ala Val Ala Met Ala Ser Thr Thr Thr Ala
 370 375 380
 Ala Ala Asn Met Leu Leu Ser Gly Ser Met Ser Ser His Asp Gly Met
 385 390 395 400
 Met Asn Pro Thr Asn Leu Leu Ala Arg Ala Val Leu Pro Cys Ser Thr
 405 410 415
 Ser Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Val Thr Leu
 420 425 430
 Asp Leu Thr His Ser Pro Pro Pro Pro Asn Gly Ser Asn Pro Ser Ser
 435 440 445
 Ser Ala Ala Thr Asn Asn Asn His Asn Ser Leu Met Gln Arg Pro Gln
 450 455 460
 Gln Gln Gln Gln Gln Met Thr Asn Leu Pro Pro Gly Met Leu Pro His
 465 470 475 480
 Val Ile Gly Gln Ala Leu Tyr Asn Gln Ser Lys Phe Ser Gly Leu Gln
 485 490 495
 Phe Ser Gly Gly Ser Pro Ser Thr Ala Ala Phe Ser Gln Ser His Ala
 500 505 510
 Val Ala Asp Thr Ile Thr Ala Leu Thr Ala Asp Pro Asn Phe Thr Ala
 515 520 525

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ctctctctct ttgtctctct tactctcttt ttacctctct cttcattggt cttcacc
 117

atg tct aat gaa acc aga gat ctc tac aac tac caa tac cct tca tcg
 165
 Met Ser Asn Glu Thr Arg Asp Leu Tyr Asn Tyr Gln Tyr Pro Ser Ser
 1 5 10 15

ttt tcg ttg cac gaa atg atg aat ctg cct act tca aat cca tct tct
 213
 Phe Ser Leu His Glu Met Met Asn Leu Pro Thr Ser Asn Pro Ser Ser
 20 25 30

tat gga aac ctc cca tca caa aac ggt ttt aat cca tct act tat tcc
 261
 Tyr Gly Asn Leu Pro Ser Gln Asn Gly Phe Asn Pro Ser Thr Tyr Ser
 35 40 45

ttc acc gat tgt ctc caa agt tct cca gca gcg tat gaa tct cta ctt
 309
 Phe Thr Asp Cys Leu Gln Ser Ser Pro Ala Ala Tyr Glu Ser Leu Leu
 50 55 60

cag aaa act ttt ggt ctt tct ccc tct tcc tca gag gtt ttc aat tct
 357
 Gln Lys Thr Phe Gly Leu Ser Pro Ser Ser Ser Glu Val Phe Asn Ser
 65 70 75 80

tcg atc gat caa gaa ccg aac cgt gat gtt act aat gac gta atc aat
 405
 Ser Ile Asp Gln Glu Pro Asn Arg Asp Val Thr Asn Asp Val Ile Asn
 85 90 95

ggt ggt gca tgc aac gag act gaa act agg gtt tct cct tct aat tct
 453
 Gly Gly Ala Cys Asn Glu Thr Glu Thr Arg Val Ser Pro Ser Asn Ser
 100 105 110

tcc tct agt gag gct gat cac ccc ggt gaa gat tcc ggt aag agc cgg
 501
 Ser Ser Ser Glu Ala Asp His Pro Gly Glu Asp Ser Gly Lys Ser Arg
 115 120 125

agg aaa cga gag tta gtc ggt gaa gaa gat caa att tcc aaa aaa gtt
 549
 Arg Lys Arg Glu Leu Val Gly Glu Glu Asp Gln Ile Ser Lys Lys Val
 130 135 140

ggg aaa acg aaa aag act gag gtg aag aaa caa aga gag cca cga gtc
 597
 Gly Lys Thr Lys Lys Thr Glu Val Lys Lys Gln Arg Glu Pro Arg Val
 145 150 155 160

tcg ttt atg act aaa agt gaa gtt gat cat ctt gaa gat ggt tat aga
 645
 Ser Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg
 165 170 175

tgg aga aaa tac ggc caa aag gct gta aaa aat agc cct tat cca agg
 693
 Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg
 180 185 190

agt tac tat aga tgt aca aca caa aag tgc aac gtg aag aaa cga gtg
 741
 Ser Tyr Tyr Arg Cys Thr Thr Gln Lys Cys Asn Val Lys Lys Arg Val
 195 200 205

gag aga tcg ttc caa gat cca acg gtt gtg att aca act tac gag ggt
 789
 Glu Arg Ser Phe Gln Asp Pro Thr Val Val Ile Thr Thr Tyr Glu Gly
 210 215 220

caa cac aac cac ccg att ccg act aat ctt cga gga agt tct gcc gcg
 837
 Gln His Asn His Pro Ile Pro Thr Asn Leu Arg Gly Ser Ser Ala Ala
 225 230 235 240

gct gct atg ttc tcc gca gac ctc atg act cca aga agc ttt gca cat
 885
 Ala Ala Met Phe Ser Ala Asp Leu Met Thr Pro Arg Ser Phe Ala His
 245 250 255

gat atg ttt agg acg gca gct tat act aac ggc ggt tct gtg gcg gcg
 933
 Asp Met Phe Arg Thr Ala Ala Tyr Thr Asn Gly Gly Ser Val Ala Ala
 260 265 270

gct ttg gat tat gga tat gga caa agt ggt tat ggt agt gtg aat tca
 981
 Ala Leu Asp Tyr Gly Tyr Gly Gln Ser Gly Tyr Gly Ser Val Asn Ser
 275 280 285

aac cct agt tct cac caa gtg tat cat caa ggg ggt gag tat gag ctc
 1029
 Asn Pro Ser Ser His Gln Val Tyr His Gln Gly Gly Glu Tyr Glu Leu
 290 295 300

ttg agg gag att ttt cct bca att ttc ttt aag caa gag cct tga
 1074
 Leu Arg Glu Ile Phe Pro Ser Ile Phe Phe Lys Gln Glu Pro
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1136

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20 25 30

Tyr Gly Asn Leu Pro Ser Gln Asn Gly Phe Asn Pro Ser Thr Tyr Ser
35 40 45

Phe Thr Asp Cys Leu Gln Ser Ser Pro Ala Ala Tyr Glu Ser Leu Leu
50 55 60

Gln Lys Thr Phe Gly Leu Ser Pro Ser Ser Ser Glu Val Phe Asn Ser
65 70 75 80

Ser Ile Asp Gln Glu Pro Asn Arg Asp Val Thr Asn Asp Val Ile Asn
85 90 95

Gly Gly Ala Cys Asn Glu Thr Glu Thr Arg Val Ser Pro Ser Asn Ser
100 105 110

Ser Ser Ser Glu Ala Asp His Pro Gly Glu Asp Ser Gly Lys Ser Arg
115 120 125

Arg Lys Arg Glu Leu Val Gly Glu Glu Asp Gln Ile Ser Lys Lys Val
130 135 140

Gly Lys Thr Lys Lys Thr Glu Val Lys Lys Gln Arg Glu Pro Arg Val
145 150 155 160

Ser Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg
165 170 175

Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Tyr Pro Arg
180 185 190

Ser Tyr Tyr Arg Cys Thr Thr Gln Lys Cys Asn Val Lys Lys Arg Val
195 200 205

Glu Arg Ser Phe Gln Asp Pro Thr Val Val Ile Thr Thr Tyr Glu Gly
 210 215 220

Gln His Asn His Pro Ile Pro Thr Asn Leu Arg Gly Ser Ser Ala Ala
 225 230 235 240

Ala Ala Met Phe Ser Ala Asp Leu Met Thr Pro Arg Ser Phe Ala His
 245 250 255

Asp Met Phe Arg Thr Ala Ala Tyr Thr Asn Gly Gly Ser Val Ala Ala
 260 265 270

Ala Leu Asp Tyr Gly Tyr Gly Gln Ser Gly Tyr Gly Ser Val Asn Ser
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Asn Pro Ser Ser His Gln Val Tyr His Gln Gly Gly Glu Tyr Glu Leu
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 120

ttatttcttt gacctctcaa aaca atg ggt aga tca ccg tgt tgt gac aaa
 171

Met Gly Arg Ser Pro Cys Cys Asp Lys
 1 5

ttg ggt ttg aag aaa gga cct tgg aca cca gag gag gat cag aaa ctt
 219

Leu Gly Leu Lys Lys Gly Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu
 10 15 20 25

tta gct tat att gaa gaa cat ggt cat gga agt tgg cgt tca ttg cct
 267

Leu Ala Tyr Ile Glu Glu His Gly His Gly Ser Trp Arg Ser Leu Pro
 30 35 40

gag aaa gct ggt ctc cat cga tgc gga aag agt tgt aga cta aga tgg
 315

Glu Lys Ala Gly Leu His Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp
 45 50 55

act aac tac cta aga cct gac atc aaa aga ggc aaa ttc aac tta caa
 363

Thr Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Lys Phe Asn Leu Gln
 60 65 70
 gaa gaa caa acc att atc caa ctc cat gct ctg tta gga aac aga tgg
 411
 Glu Glu Gln Thr Ile Ile Gln Leu His Ala Leu Leu Gly Asn Arg Trp
 75 80 85
 tca gcg att gct act cat ttg cca aag aga aca gac aac gag atc aag
 459
 Ser Ala Ile Ala Thr His Leu Pro Lys Arg Thr Asp Asn Glu Ile Lys
 90 95 100 105
 aac tat tgg aac act cat ttg aag aaa cgg tta gtg aaa atg ggg att
 507
 Asn Tyr Trp Asn Thr His Leu Lys Lys Arg Leu Val Lys Met Gly Ile
 110 115 120
 gat cca gtg act cat aaa ccc aaa aac gag act cct tta tct tct ctt
 555
 Asp Pro Val Thr His Lys Pro Lys Asn Glu Thr Pro Leu Ser Ser Leu
 125 130 135
 ggt cta tcc aag aac gca gct ata ctt agc cac act gct caa tgg gaa
 603
 Gly Leu Ser Lys Asn Ala Ala Ile Leu Ser His Thr Ala Gln Trp Glu
 140 145 150
 agt gca agg ctt gaa gct gaa gca aga cta gct aga gaa tca aag ctt
 651
 Ser Ala Arg Leu Glu Ala Glu Ala Arg Leu Ala Arg Glu Ser Lys Leu
 155 160 165
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 699
 Leu His Leu Gln His Tyr Gln Thr Lys Thr Ser Ser Gln Pro His His
 170 175 180 185
 cat cat gga ttc act cac aag tca ttg tta cct aat tgg aca aca aaa
 747
 His His Gly Phe Thr His Lys Ser Leu Leu Pro Asn Trp Thr Thr Lys
 190 195 200
 cca cac gaa gat caa caa cag ctt gaa tct ccg aca tct aca gtg tca
 795
 Pro His Glu Asp Gln Gln Gln Leu Glu Ser Pro Thr Ser Thr Val Ser
 205 210 215
 ttc tct gag atg aag gaa tca atc ccg gcg aag ata gag ttt gtc gga
 843
 Phe Ser Glu Met Lys Glu Ser Ile Pro Ala Lys Ile Glu Phe Val Gly
 220 225 230
 tca tca act ggt gtg act ctg atg aaa gaa cct gaa cac gat tgg atc
 891
 Ser Ser Thr Gly Val Thr Leu Met Lys Glu Pro Glu His Asp Trp Ile
 235 240 245
 aat tca acg atg cac gag ttt gaa act acg cag atg gga gaa gga atc
 939
 Asn Ser Thr Met His Glu Phe Glu Thr Thr Gln Met Gly Glu Gly Ile

250 255 260 265
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 987
 Glu Glu Gly Phe Thr Gly Leu Leu Leu Gly Gly Asp Ser Ile Asp Arg
 270 275 280
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 1035
 Ser Phe Ser Gly Asp Lys Asn Glu Thr Ala Gly Glu Ser Ser Gly Gly
 285 290 295
 gac tgc aac tac tat gag gac aac aag aac tac ttg gac agc att ttc
 1083
 Asp Cys Asn Tyr Tyr Glu Asp Asn Lys Asn Tyr Leu Asp Ser Ile Phe
 300 305 310
 aac ttt gta gat cct tca ccg tcg gat tca ccg atg ttc tga
 1125
 Asn Phe Val Asp Pro Ser Pro Ser Asp Ser Pro Met Phe
 315 320 325
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 1245
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 1252

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 35 40 45
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60
 Ile Lys Arg Gly Lys Phe Asn Leu Gln Glu Glu Gln Thr Ile Ile Gln
 65 70 75 80
 Leu His Ala Leu Leu Gly Asn Arg Trp Ser Ala Ile Ala Thr His Leu
 85 90 95
 Pro Lys Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Leu
 100 105 110

Lys Lys Arg Leu Val Lys Met Gly Ile Asp Pro Val Thr His Lys Pro
 115 120 125

Lys Asn Glu Thr Pro Leu Ser Ser Leu Gly Leu Ser Lys Asn Ala Ala
 130 135 140

Ile Leu Ser His Thr Ala Gln Trp Glu Ser Ala Arg Leu Glu Ala Glu
 145 150 155 160

Ala Arg Leu Ala Arg Glu Ser Lys Leu Leu His Leu Gln His Tyr Gln
 165 170 175

Thr Lys Thr Ser Ser Gln Pro His His His His Gly Phe Thr His Lys
 180 185 190

Ser Leu Leu Pro Asn Trp Thr Thr Lys Pro His Glu Asp Gln Gln Gln
 195 200 205

Leu Glu Ser Pro Thr Ser Thr Val Ser Phe Ser Glu Met Lys Glu Ser
 210 215 220

Ile Pro Ala Lys Ile Glu Phe Val Gly Ser Ser Thr Gly Val Thr Leu
 225 230 235 240

Met Lys Glu Pro Glu His Asp Trp Ile Asn Ser Thr Met His Glu Phe
 245 250 255

Glu Thr Thr Gln Met Gly Glu Gly Ile Glu Glu Gly Phe Thr Gly Leu
 260 265 270

Leu Leu Gly Gly Asp Ser Ile Asp Arg Ser Phe Ser Gly Asp Lys Asn
 275 280 285

Glu Thr Ala Gly Glu Ser Ser Gly Gly Asp Cys Asn Tyr Tyr Glu Asp
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 305 310 315 320

Ser Asp Ser Pro Met Phe
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101
Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Asp Leu Leu Gln Arg Leu
15 20 25

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149
Val Gln Lys His Gly Pro Arg Asn Trp Ser Leu Ile Ser Lys Ser Ile
30 35 40

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197
Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Cys Asn Gln Leu
45 50 55

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245
Ser Pro Glu Val Glu His Arg Ala Phe Ser Gln Glu Glu Asp Glu Thr
60 65 70 75

att att cga gct cac gct cgg ttt ggt aac aag tgg gct acg atc tct
293
Ile Ile Arg Ala His Ala Arg Phe Gly Asn Lys Trp Ala Thr Ile Ser
80 85 90

cgt ctt ctc aat gga cga acc gat aac gct atc aag aat cat tgg aac
341
Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn
95 100 105

tcg acg ctg aag cga aaa tgc agc gtc gaa ggg caa agt tgt gat ttt
389
Ser Thr Leu Lys Arg Lys Cys Ser Val Glu Gly Gln Ser Cys Asp Phe
110 115 120

ggt ggt aat gga ggg tat gat ggt aat tta gga gaa gag caa ccg ttg
437
Gly Gly Asn Gly Gly Tyr Asp Gly Asn Leu Gly Glu Glu Gln Pro Leu
125 130 135

aaa cgt acg gcg agt ggt ggt ggt gtc tcg act ggc ttg tat atg
485
Lys Arg Thr Ala Ser Gly Gly Gly Gly Val Ser Thr Gly Leu Tyr Met
140 145 150 155

agt ccc gga agt cca tcg gga tct gac gtc agc gag caa tct agt ggt
533
Ser Pro Gly Ser Pro Ser Gly Ser Asp Val Ser Glu Gln Ser Ser Gly
160 165 170

ggt gca cac gtg ttt aaa cca acg gtt aga tct gag gtt aca gcg tca
581
Gly Ala His Val Phe Lys Pro Thr Val Arg Ser Glu Val Thr Ala Ser
175 180 185

tcg tct ggt gaa gat cct cca act tat ctt agt ttg tct ctt cct tgg
629

Ser Ser Gly Glu Asp Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro Trp
190 195 200

act gac gag acg gtt cga gtc aac gag ccg gtt caa ctt aac cag aat
677

Thr Asp Glu Thr Val Arg Val Asn Glu Pro Val Gln Leu Asn Gln Asn
205 210 215

acg gtt atg gac ggt ggt tat acg gcg gag ctg ttt ccg gtt aga aag
725

Thr Val Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys
220 225 230 235

gaa gag caa gtg gaa gta gaa gaa gaa gaa gcg aag ggg ata tct ggt
773

Glu Glu Gln Val Glu Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly
240 245 250

gga ttc ggt ggt gag ttc atg acg gtg gtt cag gag atg ata agg acg
821

Gly Phe Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg Thr
255 260 265

gag gtg agg agt tac atg gcg gat tta cag cga gga aac gtc ggt ggt
869

Glu Val Arg Ser Tyr Met Ala Asp Leu Gln Arg Gly Asn Val Gly Gly
270 275 280

agt agt tct ggc ggc gga ggt ggc ggt tcg tgt atg cca caa agt gta
917

Ser Ser Ser Gly Gly Gly Gly Gly Gly Ser Cys Met Pro Gln Ser Val
285 290 295

aac agc cgt cgt gtt ggg ttt aga gag ttt ata gtg aac caa atc gga
965

Asn Ser Arg Arg Val Gly Phe Arg Glu Phe Ile Val Asn Gln Ile Gly
300 305 310 315

att ggg aag atg gag tag gcggcc
989

Ile Gly Lys Met Glu
320

<210> 314 <211> 320 <212> PRT <213> Arabidopsis thaliana <400>
314

Met Ser Asn Pro Thr Arg Lys Asn Met Glu Arg Ile Lys Gly Pro Trp
1 5 10 15

Ser Pro Glu Glu Asp Asp Leu Leu Gln Arg Leu Val Gln Lys His Gly
20 25 30

Pro Arg Asn Trp Ser Leu Ile Ser Lys Ser Ile Pro Gly Arg Ser Gly
35 40 45

Lys Ser Cys Arg Leu Arg Trp Cys Asn Gln Leu Ser Pro Glu Val Glu
 50 55 60
 His Arg Ala Phe Ser Gln Glu Glu Asp Glu Thr Ile Ile Arg Ala His
 65 70 75 80
 Ala Arg Phe Gly Asn Lys Trp Ala Thr Ile Ser Arg Leu Leu Asn Gly
 85 90 95
 Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn Ser Thr Leu Lys Arg
 100 105 110
 Lys Cys Ser Val Glu Gly Gln Ser Cys Asp Phe Gly Gly Asn Gly Gly
 115 120 125
 Tyr Asp Gly Asn Leu Gly Glu Glu Gln Pro Leu Lys Arg Thr Ala Ser
 130 135 140
 Gly Gly Gly Gly Val Ser Thr Gly Leu Tyr Met Ser Pro Gly Ser Pro
 145 150 155 160
 Ser Gly Ser Asp Val Ser Glu Gln Ser Ser Gly Gly Ala His Val Phe
 165 170 175
 Lys Pro Thr Val Arg Ser Glu Val Thr Ala Ser Ser Ser Gly Glu Asp
 180 185 190
 Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro Trp Thr Asp Glu Thr Val
 195 200 205
 Arg Val Asn Glu Pro Val Gln Leu Asn Gln Asn Thr Val Met Asp Gly
 210 215 220
 Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys Glu Glu Gln Val Glu
 225 230 235 240
 Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe Gly Gly Glu
 245 250 255
 Phe Met Thr Val Val Gln Glu Met Ile Arg Thr Glu Val Arg Ser Tyr
 260 265 270
 Met Ala Asp Leu Gln Arg Gly Asn Val Gly Gly Ser Ser Ser Gly Gly
 275 280 285
 Gly Gly Gly Gly Ser Cys Met Pro Gln Ser Val Asn Ser Arg Arg Val

290 295 300

Gly Phe Arg Glu Phe Ile Val Asn Gln Ile Gly Ile Gly Lys Met Glu
 305 310 315 320

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 48
 Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser
 1 5 10 15
 cct gaa gaa gac gag aag cta agg agc ttc atc ctc tct tat ggc cat
 96
 Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His
 20 25 30
 tct tgc tgg acc act gtt ccc atc aaa gct ggg tta caa agg aat ggg
 144
 Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly
 35 40 45
 aag agc tgc aga tta aga tgg att aat tac cta aga cca ggg tta aag
 192
 Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys
 50 55 60
 agg gat atg att agt gca gaa gaa gag act atc ttg acg ttt cat
 240
 Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His
 65 70 75 80
 tct ccc ttg ggt aac aag tgg tcg caa ata gct aaa ttc tta ccg gga
 288
 Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly
 85 90 95
 aga aca gac aat gag ata aag aac tat tgg cac tct cat ttg aaa aag
 336
 Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys
 100 105 110
 aaa tgg ctc aag tct cag agc tta caa gat gca aaa tot att tcc cct
 384
 Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro
 115 120 125
 cct tcg tct tca tca tca tca ctt gtt gct tgt gga gaa aga aat ccg
 432
 Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro
 130 135 140
 gaa acc ttg atc tcg aat cac gtg ttc tcc ctc cag aga ctt cta gag
 480
 Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu
 145 150 155 160

aac aaa tct tca tct ccc tca caa gaa agc aac gga aat aac agc cat
 528
 Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His
 165 170 175

caa tgt tct tct gct cct gag att cca agg ctt ttc ttc tct gaa tgg
 576
 Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp
 180 185 190

ctt tct tct tca tat ccc cac acc gat tat tcc tct gag ttt acc gac
 624
 Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp
 195 200 205

tct aag cac agt caa gct cca aat gtc gaa gag act ctc tca gct tat
 672
 Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr
 210 215 220

gaa gaa atg ggt gat gtt gat cag ttc cat tac aac gaa atg atg atc
 720
 Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile
 225 230 235 240

aac aac agc aac tgg act ctt aac gac att gtg ttt ggt tcc aaa tgt
 768
 Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys
 245 250 255

aag aag cag gag cat cat att tat aga gag gct tca gat tgt aat tct
 816
 Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser
 260 265 270

tct gct gaa ttc ttt tct cca cca aca acg acg taa attgcgttta
 862
 Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr
 275 280

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 920

<210> 316 <211> 283 <212> PRT <213> Arabidopsis thaliana <400>
 316

Met Ala Lys Thr Lys Tyr Gly Glu Arg His Arg Lys Gly Leu Trp Ser
 1 5 10 15

Pro Glu Glu Asp Glu Lys Leu Arg Ser Phe Ile Leu Ser Tyr Gly His
 20 25 30

Ser Cys Trp Thr Thr Val Pro Ile Lys Ala Gly Leu Gln Arg Asn Gly
 35 40 45

Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Gly Leu Lys
 50 55 60

Arg Asp Met Ile Ser Ala Glu Glu Glu Glu Thr Ile Leu Thr Phe His
65 70 75 80

Ser Pro Leu Gly Asn Lys Trp Ser Gln Ile Ala Lys Phe Leu Pro Gly
85 90 95

Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp His Ser His Leu Lys Lys
100 105 110

Lys Trp Leu Lys Ser Gln Ser Leu Gln Asp Ala Lys Ser Ile Ser Pro
115 120 125

Pro Ser Ser Ser Ser Ser Ser Leu Val Ala Cys Gly Glu Arg Asn Pro
130 135 140

Glu Thr Leu Ile Ser Asn His Val Phe Ser Leu Gln Arg Leu Leu Glu
145 150 155 160

Asn Lys Ser Ser Ser Pro Ser Gln Glu Ser Asn Gly Asn Asn Ser His
165 170 175

Gln Cys Ser Ser Ala Pro Glu Ile Pro Arg Leu Phe Phe Ser Glu Trp
180 185 190

Leu Ser Ser Ser Tyr Pro His Thr Asp Tyr Ser Ser Glu Phe Thr Asp
195 200 205

Ser Lys His Ser Gln Ala Pro Asn Val Glu Glu Thr Leu Ser Ala Tyr
210 215 220

Glu Glu Met Gly Asp Val Asp Gln Phe His Tyr Asn Glu Met Met Ile
225 230 235 240

Asn Asn Ser Asn Trp Thr Leu Asn Asp Ile Val Phe Gly Ser Lys Cys
245 250 255

Lys Lys Gln Glu His His Ile Tyr Arg Glu Ala Ser Asp Cys Asn Ser
260 265 270

Ser Ala Glu Phe Phe Ser Pro Pro Thr Thr Thr
275 280

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 Met Asp Val Tyr Gly Met Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
 1 5 10 15
 ctt ctc gat ttc tcc aac gac gaa atc ttc tct tcc tct tcc acc gtc
 96
 Leu Leu Asp Phe Ser Asn Asp Glu Ile Phe Ser Ser Ser Ser Thr Val
 20 25 30
 act tcc tcc gcc gct tcc tcc gcc gct tct tcc gaa aac cct ttc agc
 144
 Thr Ser Ser Ala Ala Ser Ser Ala Ala Ser Ser Glu Asn Pro Phe Ser
 35 40 45
 ttt cct tct tcc acc tac act tct cct act ctc ctc acc gac ttc act
 192
 Phe Pro Ser Ser Thr Tyr Thr Ser Pro Thr Leu Leu Thr Asp Phe Thr
 50 55 60
 cac gat ctc tgc gtt ccc agt gac gac gca gct cat ctc gaa tgg tta
 240
 His Asp Leu Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu Trp Leu
 65 70 75 80
 tcg cga ttc gtt gac gat tca ttc tcc gat ttc cca gca aat cct tta
 288
 Ser Arg Phe Val Asp Asp Ser Phe Ser Asp Phe Pro Ala Asn Pro Leu
 85 90 95
 acc atg acc gtt aga ccc gag att tca ttc acc gga aaa cct aga agt
 336
 Thr Met Thr Val Arg Pro Glu Ile Ser Phe Thr Gly Lys Pro Arg Ser
 100 105 110
 cgc cga tca aga gca cca gca cct tcc gta gct gga act tgg gct ccg
 384
 Arg Arg Ser Arg Ala Pro Ala Pro Ser Val Ala Gly Thr Trp Ala Pro
 115 120 125
 atg tct gaa tca gag ctt tgt cac tcc gtc gct aaa cct .aaa ccg aag
 432
 Met Ser Glu Ser Glu Leu Cys His Ser Val Ala Lys Pro Lys Pro Lys
 130 135 140
 aaa gtc tac aac gct gaa tcg gtt acg gcg gat gga gcg agg cgg tgc
 480
 Lys Val Tyr Asn Ala Glu Ser Val Thr Ala Asp Gly Ala Arg Arg Cys
 145 150 155 160
 acg cac tgt gcc tcg gag aaa acg cca cag tgg aga act gga ccg ctt
 528
 Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp Arg Thr Gly Pro Leu
 165 170 175
 gga cct aaa aca ctt tgt aac gct tgt gga gtt cgt tac aaa tca ggg
 576
 Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val Arg Tyr Lys Ser Gly
 180 185 190

agg ctt gta ccg gaa tac aga ccg gcg tcg agt ccg acg ttt gta ttg
624

Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser Pro Thr Phe Val Leu
195 200 205

act cag cat tcg aac tct cat cgg aaa gtt atg gag ctg cgg cga cag
672

Thr Gln His Ser Asn Ser His Arg Lys Val Met Glu Leu Arg Arg Gln
210 215 220

aag gaa caa caa gaa tct tgc gtt cga att ccg ccg ttt cag ccg cag
720

Lys Glu Gln Gln Glu Ser Cys Val Arg Ile Pro Pro Phe Gln Pro Gln
225 230 235 240

taa
723

<210> 318 <211> 240 <212> PRT <213> Arabidopsis thaliana <400>
318

Met Asp Val Tyr Gly Met Ser Ser Pro Asp Leu Leu Arg Ile Asp Asp
1 5 10 15

Leu Leu Asp Phe Ser Asn Asp Glu Ile Phe Ser Ser Ser Ser Thr Val
20 25 30

Thr Ser Ser Ala Ala Ser Ser Ala Ala Ser Ser Glu Asn Pro Phe Ser
35 40 45

Phe Pro Ser Ser Thr Tyr Thr Ser Pro Thr Leu Leu Thr Asp Phe Thr
50 55 60

His Asp Leu Cys Val Pro Ser Asp Asp Ala Ala His Leu Glu Trp Leu
65 70 75 80

Ser Arg Phe Val Asp Asp Ser Phe Ser Asp Phe Pro Ala Asn Pro Leu
85 90 95

Thr Met Thr Val Arg Pro Glu Ile Ser Phe Thr Gly Lys Pro Arg Ser
100 105 110

Arg Arg Ser Arg Ala Pro Ala Pro Ser Val Ala Gly Thr Trp Ala Pro
115 120 125

Met Ser Glu Ser Glu Leu Cys His Ser Val Ala Lys Pro Lys Pro Lys
130 135 140

Lys Val Tyr Asn Ala Glu Ser Val Thr Ala Asp Gly Ala Arg Arg Cys
145 150 155 160

Thr His Cys Ala Ser Glu Lys Thr Pro Gln Trp Arg Thr Gly Pro Leu
165 170 175

Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val Arg Tyr Lys Ser Gly
180 185 190

Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser Pro Thr Phe Val Leu
195 200 205

Thr Gln His Ser Asn Ser His Arg Lys Val Met Glu Leu Arg Arg Gln
210 215 220

Lys Glu Gln Gln Glu Ser Cys Val Arg Ile Pro Pro Phe Gln Pro Gln
225 230 235 240

<210> 319 <211> 932 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (43)..(759) <223> G350

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54

Met Ala Leu Glu
1

act ctt act tct cca aga tta tct tct ccg atg ccg act ctg ttt caa
102

Thr Leu Thr Ser Pro Arg Leu Ser Ser Pro Met Pro Thr Leu Phe Gln
5 10 15 20

gat tca gca cta ggg ttt cat gga agc aaa ggc aaa cga tct aag cga
150

Asp Ser Ala Leu Gly Phe His Gly Ser Lys Gly Lys Arg Ser Lys Arg
25 30 35

tca aga tct gaa ttc gac cgt cag agt ctc acg gag gat gaa tat atc
198

Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu Asp Glu Tyr Ile
40 45 50

gct tta tgt ctc atg ctt ctt gct cgc gac gga gat aga aac cgt gac
246

Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp Arg Asn Arg Asp
55 60 65

ctt gac ctg cct tct tct tcg tct tca cct cct ctg ctt cct cct ctt
294

Leu Asp Leu Pro Ser Ser Ser Ser Pro Pro Leu Leu Pro Pro Leu
70 75 80

cct act ccg atc tac aag tgt agc gtc tgt gac aag gcg ttt tcg tct
342

Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys Ala Phe Ser Ser
85 90 95 100

tac cag gct ctt ggt gga cac aag gca agt cac cgg aaa agc ttt tcg
 390
 Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Ser Phe Ser
 105 110 115
 ctt act caa tct gcc gga gga gat gag ctg tcg aca tcg tcg gcg ata
 438
 Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr Ser Ser Ala Ile
 120 125 130
 acc acg tct ggt ata tcc ggt ggc ggg gga gga agt gtg aag tcg cac
 486
 Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Gly Ser Val Lys Ser His
 135 140 145
 gtt tgc tct atc tgt cat aaa tcg ttc gcc acc ggt caa gct ctc ggc
 534
 Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly Gln Ala Leu Gly
 150 155 160
 ggc cac aaa cgg tgc cac tac gaa gga aag aac gga ggc ggt gtg agt
 582
 Gly His Lys Arg Cys His Tyr Glu Gly Lys Asn Gly Gly Gly Val Ser
 165 170 175 180
 agt agc gtg tcg aat tct gaa gat gtg ggg tct aca agc cac gtc agc
 630
 Ser Ser Val Ser Asn Ser Glu Asp Val Gly Ser Thr Ser His Val Ser
 185 190 195
 agt ggc cac cgt ggg ttt gac ctc aac ata ccg ccg ata ccg gaa ttc
 678
 Ser Gly His Arg Gly Phe Asp Leu Asn Ile Pro Pro Ile Pro Glu Phe
 200 205 210
 tcg atg gtc aac gga gac gaa gag gtg atg agt cct atg ccg gcg aag
 726
 Ser Met Val Asn Gly Asp Glu Glu Val Met Ser Pro Met Pro Ala Lys
 215 220 225
 aaa ctc cgg ttt gac ttc ccg gag aaa ccc taa acataaacct aggaaaaact
 779
 Lys Leu Arg Phe Asp Phe Pro Glu Lys Pro
 230 235
 ttacagaatt cattttatag gaaattgttt tactgtatat acaaatatcg attttgattg
 839
 atgttcttct tcactgaaaa attatgattc tttgttgtat aattgatgtt tctgaaaaag
 899
 atataacttt ttattaaaaa aaaaaaaaaa aaa
 932
 <210> 320 <211> 238 <212> PRT <213> Arabidopsis thaliana <400>
 320
 Met Ala Leu Glu Thr Leu Thr Ser Pro Arg Leu Ser Ser Pro Met Pro
 1 5 10 15

Thr Leu Phe Gln Asp Ser Ala Leu Gly Phe His Gly Ser Lys Gly Lys
20 25 30

Arg Ser Lys Arg Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu
35 40 45

Asp Glu Tyr Ile Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp
50 55 60

Arg Asn Arg Asp Leu Asp Leu Pro Ser Ser Ser Ser Ser Pro Pro Leu
65 70 75 80

Leu Pro Pro Leu Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys
85 90 95

Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
100 105 110

Lys Ser Phe Ser Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr
115 120 125

Ser Ser Ala Ile Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Ser
130 135 140

Val Lys Ser His Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly
145 150 155 160

Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly Lys Asn Gly
165 170 175

Gly Gly Val Ser Ser Ser Val Ser Asn Ser Glu Asp Val Gly Ser Thr
180 185 190

Ser His Val Ser Ser Gly His Arg Gly Phe Asp Leu Asn Ile Pro Pro
195 200 205

Ile Pro Glu Phe Ser Met Val Asn Gly Asp Glu Glu Val Met Ser Pro
210 215 220

Met Pro Ala Lys Lys Leu Arg Phe Asp Phe Pro Glu Lys Pro
225 230 235

<210> 321 <211> 2940 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (336)..(2492) <223> G384

<400> 321

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atccaccggt tatgtcttga cgggctttaa gcctataaac tgatgcccta agacaccttt
120

ttaggtttct caataattct ccgcatctat cttttcttct ccacaagtaa' gggaaccaga
180

aaaccaggga agaatccgag caagctaggg ttctattgtg tgcacaaaat gggatataca
240

ggcagaagaa aatcgagata aatcaactaa atgatttgga taatcatctt gaagatttga
300

aggatttcga gactaagtcc ggcgagaag tcacc atg gag aat cct tta gaa
353

Met Glu Asn Pro Leu Glu
1 5

gaa gag ctt caa gat cct aat cag cgt ccc aac aaa aag aag cgt tac
401

Glu Glu Leu Gln Asp Pro Asn Gln Arg Pro Asn Lys Lys Lys Arg Tyr
10 15 20

cac cgt cac aca caa cgc cag att caa gag cta gag tcg ttc ttc aag
449

His Arg His Thr Gln Arg Gln Ile Gln Glu Leu Glu Ser Phe Phe Lys
25 30 35

gaa tgt cct cat cca gac gat aag caa aga aag gag ctg agt cgc gag
497

Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Glu Leu Ser Arg Glu
40 45 50

cta agc tta gaa cct ctt caa gtc aag ttc tgg ttc caa aac aaa cgc
545

Leu Ser Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn Lys Arg
55 60 65 70

act caa atg aag gca caa cat gag agg cac gag aac cag ata ctg aag
593

Thr Gln Met Lys Ala Gln His Glu Arg His Glu Asn Gln Ile Leu Lys
75 80 85

tca gaa aat gac aag ctc cga gca gag aac aat agg tac aag gat gct
641

Ser Glu Asn Asp Lys Leu Arg Ala Glu Asn Asn Arg Tyr Lys Asp Ala
90 95 100

cta agc aac gca aca tgc cca aac tgt ggt ggt ccg gca gct ata gga
689

Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly Gly Pro Ala Ala Ile Gly
105 110 115

gaa atg tcc ttc gac gaa cag cat tta agg atc gaa aat gct cgt tta
737

Glu Met Ser Phe Asp Glu Gln His Leu Arg Ile Glu Asn Ala Arg Leu
120 125 130

cgc gaa gag att gac aga atc tct gcc ata gct gct aaa tac gta ggg
 785
 Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr Val Gly
 135 140 145 150
 aag cct tta atg gct aat tcc tct tct ttc cct cag ctc tct tct tca
 833
 Lys Pro Leu Met Ala Asn Ser Ser Ser Phe Pro Gln Leu Ser Ser Ser
 155 160 165
 cac cac att ccc tcg cgc tcg ctt gat ctt gaa gtt ggg aac ttt ggg
 881
 His His Ile Pro Ser Arg Ser Leu Asp Leu Glu Val Gly Asn Phe Gly
 170 175 180
 aac aat aac aat agc cac act ggt ttc gtt ggg gaa atg ttt gga agc
 929
 Asn Asn Asn Asn Ser His Thr Gly Phe Val Gly Glu Met Phe Gly Ser
 185 190 195
 agc gac att ttg agg tcg gtt tcg ata cct tct gag gct gat aag cct
 977
 Ser Asp Ile Leu Arg Ser Val Ser Ile Pro Ser Glu Ala Asp Lys Pro
 200 205 210
 atg att gtt gag tta gct gtt gca gca atg gaa gag ctt gtg aga atg
 1025
 Met Ile Val Glu Leu Ala Val Ala Ala Met Glu Glu Leu Val Arg Met
 215 220 225 230
 gct caa act ggt gat ccc tta tgg gtt tca agc gat aat tct gtt gag
 1073
 Ala Gln Thr Gly Asp Pro Leu Trp Val Ser Ser Asp Asn Ser Val Glu
 235 240 245
 att ctc aat gaa gaa gag tat ttt agg acg ttt cct aga gga att gga
 1121
 Ile Leu Asn Glu Glu Glu Tyr Phe Arg Thr Phe Pro Arg Gly Ile Gly
 250 255 260
 ccg aaa cct atc ggt ttg aga tca gaa gct tca aga gag tct act gtt
 1169
 Pro Lys Pro Ile Gly Leu Arg Ser Glu Ala Ser Arg Glu Ser Thr Val
 265 270 275
 gtt atc atg aat cat atc aat ctc att gag att cta atg gat gtg aat
 1217
 Val Ile Met Asn His Ile Asn Leu Ile Glu Ile Leu Met Asp Val Asn
 280 285 290
 caa tgg tct agt gtg ttc tgc ggg att gta tca aga gca ttg act cta
 1265
 Gln Trp Ser Ser Val Phe Cys Gly Ile Val Ser Arg Ala Leu Thr Leu
 295 300 305 310
 gaa gtt ctc tca act ggc gta cga ggg aac tac aat ggg gca ttg caa
 1313
 Glu Val Leu Ser Thr Gly Val Arg Gly Asn Tyr Asn Gly Ala Leu Gln
 315 320 325

gtg atg aca gca gag ttc caa gtc cca tcg ccg ctt gtc cct act cgt
 1361
 Val Met Thr Ala Glu Phe Gln Val Pro Ser Pro Leu Val Pro Thr Arg
 330 335 340

gag aac tac ttt gta agg tac tgt aaa cag cac agt gac ggt att tgg
 1409
 Glu Asn Tyr Phe Val Arg Tyr Cys Lys Gln His Ser Asp Gly Ile Trp
 345 350 355

gcg gtt gtg gat gtc tct ttg gac agc cta aga cca agt ccg atc act
 1457
 Ala Val Val Asp Val Ser Leu Asp Ser Leu Arg Pro Ser Pro Ile Thr
 360 365 370

aga agc aga aga aga ccc tct ggt tgt ctg att caa gaa ttg cag aat
 1505
 Arg Ser Arg Arg Arg Pro Ser Gly Cys Leu Ile Gln Glu Leu Gln Asn
 375 380 385 390

ggt tac tcc aag gtg aca tgg gta gag cat att gag gtg gat gat aga
 1553
 Gly Tyr Ser Lys Val Thr Trp Val Glu His Ile Glu Val Asp Asp Arg
 395 400 405

tcg gtt cac aac atg tat aaa ccg ttg gtt aat acc ggt tta gct ttc
 1601
 Ser Val His Asn Met Tyr Lys Pro Leu Val Asn Thr Gly Leu Ala Phe
 410 415 420

ggt gca aaa cgt tgg gtg gct aca ctt gac cgc caa tgt gag cgg ctc
 1649
 Gly Ala Lys Arg Trp Val Ala Thr Leu Asp Arg Gln Cys Glu Arg Leu
 425 430 435

gcc agt tcc atg gcc agc aac att ccg gct tgt gat ctt tcc gtg ata
 1697
 Ala Ser Ser Met Ala Ser Asn Ile Pro Ala Cys Asp Leu Ser Val Ile
 440 445 450

acg agt cct gag ggg aga aag agc atg ctg aaa cta gcg gag aga atg
 1745
 Thr Ser Pro Glu Gly Arg Lys Ser Met Leu Lys Leu Ala Glu Arg Met
 455 460 465 470

gtg atg agc ttc tgt acc gga gtc ggc gcg tca acc gcc gat gcc tgg
 1793
 Val Met Ser Phe Cys Thr Gly Val Gly Ala Ser Thr Ala Asp Ala Trp
 475 480 485

act aca ttg tcg acc aca gga tcc gac gac gtt cgg gtc atg acc cga
 1841
 Thr Thr Leu Ser Thr Thr Gly Ser Asp Asp Val Arg Val Met Thr Arg
 490 495 500

aag agc atg gat gat ccg gga aga cct cca ggc atc gtt ctc agc gcc
 1889
 Lys Ser Met Asp Asp Pro Gly Arg Pro Pro Gly Ile Val Leu Ser Ala
 505 510 515

gct act tct ttc tgg atc cct gta gct cca aaa cga gtg ttc gat ttt
 1937
 Ala Thr Ser Phe Trp Ile Pro Val Ala Pro Lys Arg Val Phe Asp Phe
 520 525 530

ctc aga gat gaa aac tca aga agc gag tgg gat ata ctt tcc aat gga
 1985
 Leu Arg Asp Glu Asn Ser Arg Ser Glu Trp Asp Ile Leu Ser Asn Gly
 535 540 545 550

ggc ttg gtt caa gaa atg gct cat atc gca aat ggt cgt gat cct ggg
 2033
 Gly Leu Val Gln Glu Met Ala His Ile Ala Asn Gly Arg Asp Pro Gly
 555 560 565

aat agt gtc tcc ttg ctt cga gtc aat agt ggg aac tca ggg cag agc
 2081
 Asn Ser Val Ser Leu Leu Arg Val Asn Ser Gly Asn Ser Gly Gln Ser
 570 575 580

aac atg ttg atc tta caa gaa agt tgt acg gac gca tca ggg tcc tat
 2129
 Asn Met Leu Ile Leu Gln Glu Ser Cys Thr Asp Ala Ser Gly Ser Tyr
 585 590 595

gtg ata tac gca cca gtt gat ata ata gct atg aac gtt gtc ctg agt
 2177
 Val Ile Tyr Ala Pro Val Asp Ile Ile Ala Met Asn Val Val Leu Ser
 600 605 610

ggt ggt gat ccg gat tat gtc gct ttg tta cca tcc gga ttc gct att
 2225
 Gly Gly Asp Pro Asp Tyr Val Ala Leu Leu Pro Ser Gly Phe Ala Ile
 615 620 625 630

ttg ccg gat ggc tct gct aga gga gga gga ggt agt gct aat gcc agt
 2273
 Leu Pro Asp Gly Ser Ala Arg Gly Gly Gly Gly Ser Ala Asn Ala Ser
 635 640 645

gct gga gcc gga gtt gaa gga gga gga gag ggg aat aat ctt gaa gtg
 2321
 Ala Gly Ala Gly Val Glu Gly Gly Gly Glu Gly Asn Asn Leu Glu Val
 650 655 660

gtt act act act ggg agt tgt ggc ggt tca cta ctc aca gtt gcg ttt
 2369
 Val Thr Thr Thr Gly Ser Cys Gly Gly Ser Leu Leu Thr Val Ala Phe
 665 670 675

cag ata ctt gtt gac tct gtt cct acc gct aaa ctc tct ctc ggt tca
 2417
 Gln Ile Leu Val Asp Ser Val Pro Thr Ala Lys Leu Ser Leu Gly Ser
 680 685 690

gtt gct aca gtc aat agt ctg atc aaa tgc act gtc gag cgg att aaa
 2465
 Val Ala Thr Val Asn Ser Leu Ile Lys Cys Thr Val Glu Arg Ile Lys
 695 700 705 710

gcc gct ctg gcc tgc gac gga gcc taa tcgatgtttt cggaaggtaa
2512

Ala Ala Leu Ala Cys Asp Gly Ala
715

gagtgaagg ggaggttttag ggagtttatg ataatgtttg tgttcttttg gtttttaaag
2572

tcttttgaga ttctccaaag gaagtcaaga acgctccttt ttgcgtttta tctcatttcc
2632

gcgtttgtta gcggacgggc caaagaaaga ggcttgagaa agaaaaggta aagaggttcg
2692

ggtattgact tctgctggaa ccaaaaaaaaa aggaatcggg tttgttgtgt ttcggcgggt
2752

tagcattttg cgttttcttt gttattattt atcattgact agtgaacagt ttagcgttct
2812

gcttttcgcg tctactgtga aactccttgt tattaagcca ctctagtggg actgtcatta
2872

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2932

tctcttct
2940

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20 25 30

Leu Glu Ser Phe Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg
35 40 45

Lys Glu Leu Ser Arg Glu Leu Ser Leu Glu Pro Leu Gln Val Lys Phe
50 55 60

Trp Phe Gln Asn Lys Arg Thr Gln Met Lys Ala Gln His Glu Arg His
65 70 75 80

Glu Asn Gln Ile Leu Lys Ser Glu Asn Asp Lys Leu Arg Ala Glu Asn
85 90 95

Asn Arg Tyr Lys Asp Ala Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly
100 105 110

Gly Pro Ala Ala Ile Gly Glu Met Ser Phe Asp Glu Gln His Leu Arg
 115 120 125

Ile Glu Asn Ala Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile
 130 135 140

Ala Ala Lys Tyr Val Gly Lys Pro Leu Met Ala Asn Ser Ser Ser Phe
 145 150 155 160

Pro Gln Leu Ser Ser Ser His His Ile Pro Ser Arg Ser Leu Asp Leu
 165 170 175

Glu Val Gly Asn Phe Gly Asn Asn Asn Asn Ser His Thr Gly Phe Val
 180 185 190

Gly Glu Met Phe Gly Ser Ser Asp Ile Leu Arg Ser Val Ser Ile Pro
 195 200 205

Ser Glu Ala Asp Lys Pro Met Ile Val Glu Leu Ala Val Ala Ala Met
 210 215 220

Glu Glu Leu Val Arg Met Ala Gln Thr Gly Asp Pro Leu Trp Val Ser
 225 230 235 240

Ser Asp Asn Ser Val Glu Ile Leu Asn Glu Glu Glu Tyr Phe Arg Thr
 245 250 255

Phe Pro Arg Gly Ile Gly Pro Lys Pro Ile Gly Leu Arg Ser Glu Ala
 260 265 270

Ser Arg Glu Ser Thr Val Val Ile Met Asn His Ile Asn Leu Ile Glu
 275 280 285

Ile Leu Met Asp Val Asn Gln Trp Ser Ser Val Phe Cys Gly Ile Val
 290 295 300

Ser Arg Ala Leu Thr Leu Glu Val Leu Ser Thr Gly Val Arg Gly Asn
 305 310 315 320

Tyr Asn Gly Ala Leu Gln Val Met Thr Ala Glu Phe Gln Val Pro Ser
 325 330 335

Pro Leu Val Pro Thr Arg Glu Asn Tyr Phe Val Arg Tyr Cys Lys Gln
 340 345 350

His Ser Asp Gly Ile Trp Ala Val Val Asp Val Ser Leu Asp Ser Leu

355 360 365
 Arg Pro Ser Pro Ile Thr Arg Ser Arg Arg Arg Pro Ser Gly Cys Leu
 370 375 380
 Ile Gln Glu Leu Gln Asn Gly Tyr Ser Lys Val Thr Trp Val Glu His
 385 390 395 400
 Ile Glu Val Asp Asp Arg Ser Val His Asn Met Tyr Lys Pro Leu Val
 405 410 415
 Asn Thr Gly Leu Ala Phe Gly Ala Lys Arg Trp Val Ala Thr Leu Asp
 420 425 430
 Arg Gln Cys Glu Arg Leu Ala Ser Ser Met Ala Ser Asn Ile Pro Ala
 435 440 445
 Cys Asp Leu Ser Val Ile Thr Ser Pro Glu Gly Arg Lys Ser Met Leu
 450 455 460
 Lys Leu Ala Glu Arg Met Val Met Ser Phe Cys Thr Gly Val Gly Ala
 465 470 475 480
 Ser Thr Ala Asp Ala Trp Thr Thr Leu Ser Thr Thr Gly Ser Asp Asp
 485 490 495
 Val Arg Val Met Thr Arg Lys Ser Met Asp Asp Pro Gly Arg Pro Pro
 500 505 510
 Gly Ile Val Leu Ser Ala Ala Thr Ser Phe Trp Ile Pro Val Ala Pro
 515 520 525
 Lys Arg Val Phe Asp Phe Leu Arg Asp Glu Asn Ser Arg Ser Glu Trp
 530 535 540
 Asp Ile Leu Ser Asn Gly Gly Leu Val Gln Glu Met Ala His Ile Ala
 545 550 555 560
 Asn Gly Arg Asp Pro Gly Asn Ser Val Ser Leu Leu Arg Val Asn Ser
 565 570 575
 Gly Asn Ser Gly Gln Ser Asn Met Leu Ile Leu Gln Glu Ser Cys Thr
 580 585 590
 Asp Ala Ser Gly Ser Tyr Val Ile Tyr Ala Pro Val Asp Ile Ile Ala
 595 600 605

Met Asn Val Val Leu Ser Gly Gly Asp Pro Asp Tyr Val Ala Leu Leu
610 615 620

Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly Ser Ala Arg Gly Gly Gly
625 630 635 640

Gly Ser Ala Asn Ala Ser Ala Gly Ala Gly Val Glu Gly Gly Gly Glu
645 650 655

Gly Asn Asn Leu Glu Val Val Thr Thr Thr Gly Ser Cys Gly Gly Ser
660 665 670

Leu Leu Thr Val Ala Phe Gln Ile Leu Val Asp Ser Val Pro Thr Ala
675 680 685

Lys Leu Ser Leu Gly Ser Val Ala Thr Val Asn Ser Leu Ile Lys Cys
690 695 700

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120

ctttcaaaag actctttctt tcttttggat tgattttgga ttctagggct ctctttcttt
180

tagtggtttt ttgttgttgt tgttgtgggc tctctg atg att act gaa ctt gag
234

Met Ile Thr Glu Leu Glu
1 5

atg ggg aaa ggt gag agt gag ctt gag ctt ggt cta ggg ctg agt ctt
282

Met Gly Lys Gly Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu
10 15 20

ggc ggt gga acg gcg gcc aag att ggt aaa tca ggt ggt ggt ggc gcg
330

Gly Gly Gly Thr Ala Ala Lys Ile Gly Lys Ser Gly Gly Gly Gly Ala
25 30 35

tgg gga gag cgt gga agg ctt ttg acg gct aag gat ttt cct tct gtt
378

Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala Lys Asp Phe Pro Ser Val

40 45 50
 ggt tct aaa cgt gct gct gat tct gct tct cat gct ggt tca tct cct
 426
 Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser His Ala Gly Ser Ser Pro
 55 60 65 70
 cct cgt tca agt caa gtt gtt gga tgg cct cct ata ggg tca cac agg
 474
 Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Ser His Arg
 75 80 85
 atg aac agt ttg gtt aat aac caa gct aca aag tca gca aga gaa gaa
 522
 Met Asn Ser Leu Val Asn Asn Gln Ala Thr Lys Ser Ala Arg Glu Glu
 90 95 100
 gaa gaa gct ggt aag aag aaa gtg aaa gat gat gaa cct aaa gat gtg
 570
 Glu Glu Ala Gly Lys Lys Lys Val Lys Asp Asp Glu Pro Lys Asp Val
 105 110 115
 aca aag aaa gtg aat ggg aaa gta caa gtt gga ttt att aag gtg aac
 618
 Thr Lys Lys Val Asn Gly Lys Val Gln Val Gly Phe Ile Lys Val Asn
 120 125 130
 atg gat gga gtt gct ata gga aga aaa gtg gat ttg aat gct cat tct
 666
 Met Asp Gly Val Ala Ile Gly Arg Lys Val Asp Leu Asn Ala His Ser
 135 140 145 150
 tct tac gag aat ttg gcg caa aca ttg gaa gat atg ttc ttt cgc act
 714
 Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Asp Met Phe Phe Arg Thr
 155 160 165
 aat ccg ggt act gtc ggg tta acc agt cag ttc act aaa ccg ttg agg
 762
 Asn Pro Gly Thr Val Gly Leu Thr Ser Gln Phe Thr Lys Pro Leu Arg
 170 175 180
 ctt tta gat gga tcg tct gag ttt gta ctt act tat gaa gat aag gaa
 810
 Leu Leu Asp Gly Ser Ser Glu Phe Val Leu Thr Tyr Glu Asp Lys Glu
 185 190 195
 gga gat tgg atg ctt gtt ggt gat gtt cca tgg aga atg ttc atc aac
 858
 Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn
 200 205 210
 tcg gtg aaa agg cta cgt gtg atg aaa acc tct gaa gct aat gga ctc
 906
 Ser Val Lys Arg Leu Arg Val Met Lys Thr Ser Glu Ala Asn Gly Leu
 215 220 225 230
 gct gca cga aat caa gaa cca aac gag aga cag cga aag cag ccg gtt
 954
 Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg Gln Arg Lys Gln Pro Val
 235 240 245

tag atctcttttc gacgttacgg tgttacaggt tttatatttt ggggttttgc
1007

aagtctgaga tacttctgaa gcaagcataa gctagattga tcttatatcc agtttgtgta
1067

ttttcttggt tcttataatg gtttttactg gttttcttta gttttttttt ttgctgtctt
1127

ttaattttcg gttgcgattt cactatatac tatggatgga agagaatgct ctttatactt
1187

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1247

tgacgtagcc tcgag
1262

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20 25 30

Ser Gly Gly Gly Gly Ala Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala
35 40 45

Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser
50 55 60

His Ala Gly Ser Ser Pro Pro Arg Ser Ser Gln Val Val Gly Trp Pro
65 70 75 80

Pro Ile Gly Ser His Arg Met Asn Ser Leu Val Asn Asn Gln Ala Thr
85 90 95

Lys Ser Ala Arg Glu Glu Glu Glu Ala Gly Lys Lys Lys Val Lys Asp
100 105 110

Asp Glu Pro Lys Asp Val Thr Lys Lys Val Asn Gly Lys Val Gln Val
115 120 125

Gly Phe Ile Lys Val Asn Met Asp Gly Val Ala Ile Gly Arg Lys Val
130 135 140

Asp Leu Asn Ala His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu
145 150 155 160

Asp Met Phe Phe Arg Thr Asn Pro Gly Thr Val Gly Leu Thr Ser Gln
 165 170 175

Phe Thr Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser Glu Phe Val Leu
 180 185 190

Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val Gly Asp Val Pro
 195 200 205

Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg Val Met Lys Thr
 210 215 220

Ser Glu Ala Asn Gly Leu Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg
 225 230 235 240

Gln Arg Lys Gln Pro Val
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 ttc tcc tcc tct ggt ttt agt gac cct aag gag act aga aat gtc tcc
 96
 Phe Ser Ser Ser Gly Phe Ser Asp Pro Lys Glu Thr Arg Asn Val Ser
 20 25 30
 gtc gcc ggc gag ggg caa aaa agt aat tct acc cga tcc gct gcg gct
 144
 Val Ala Gly Glu Gly Gln Lys Ser Asn Ser Thr Arg Ser Ala Ala Ala
 35 40 45
 gag cgt gct ttg gac cct gag gct gct ctt tac aga gag cta tgg cac
 192
 Glu Arg Ala Leu Asp Pro Glu Ala Ala Leu Tyr Arg Glu Leu Trp His
 50 55 60
 gct tgt gct ggt ccg ctt gtg acg gtt cct aga caa gac gac cga gtc
 240
 Ala Cys Ala Gly Pro Leu Val Thr Val Pro Arg Gln Asp Asp Arg Val
 65 70 75 80
 ttc tat ttt cct caa gga cac atc gag cag gtg gag gct tcg acg aac
 288
 Phe Tyr Phe Pro Gln Gly His Ile Glu Gln Val Glu Ala Ser Thr Asn
 85 90 95

cag gcg gca gaa caa cag atg cct ctc tat gat ctt ccg tca aag ctt
 336
 Gln Ala Ala Glu Gln Gln Met Pro Leu Tyr Asp Leu Pro Ser Lys Leu
 100 105 110

ctc tgt cga gtt att aat gta gat tta aag gca gag gca gat aca gat
 384
 Leu Cys Arg Val Ile Asn Val Asp Leu Lys Ala Glu Ala Asp Thr Asp
 115 120 125

gaa gtt tat gcg cag att act ctt ctt cct gag gct aat caa gac gag
 432
 Glu Val Tyr Ala Gln Ile Thr Leu Leu Pro Glu Ala Asn Gln Asp Glu
 130 135 140

aat gca att gag aaa gaa gcg cct ctt cct cca cct ccg agg ttc cag
 480
 Asn Ala Ile Glu Lys Glu Ala Pro Leu Pro Pro Pro Pro Arg Phe Gln
 145 150 155 160

gtg cat tcg ttc tgc aaa acc ttg act gca tcc gac aca agt aca cat
 528
 Val His Ser Phe Cys Lys Thr Leu Thr Ala Ser Asp Thr Ser Thr His
 165 170 175

ggt gga ttt tct gtt ctt agg cga cat gcg gat gaa tgt ctc cca cct
 576
 Gly Gly Phe Ser Val Leu Arg Arg His Ala Asp Glu Cys Leu Pro Pro
 180 185 190

ctg gat atg tct cga cag cct ccc act caa gag tta gtt gca aag gat
 624
 Leu Asp Met Ser Arg Gln Pro Pro Thr Gln Glu Leu Val Ala Lys Asp
 195 200 205

ttg cat gca aat gag tgg cga ttc aga cat ata ttc cgg ggt caa cca
 672
 Leu His Ala Asn Glu Trp Arg Phe Arg His Ile Phe Arg Gly Gln Pro
 210 215 220

cgg agg cat ttg cta cag agt ggg tgg agt gtg ttt gtt agc tcc aaa
 720
 Arg Arg His Leu Leu Gln Ser Gly Trp Ser Val Phe Val Ser Ser Lys
 225 230 235 240

agg cta gtt gca ggc gat gcg ttt ata ttt cta agg ggc gag aat gga
 768
 Arg Leu Val Ala Gly Asp Ala Phe Ile Phe Leu Arg Gly Glu Asn Gly
 245 250 255

gaa tta aga gtt ggt gta agg cgt gcg atg cga caa caa gga aac gtg
 816
 Glu Leu Arg Val Gly Val Arg Arg Ala Met Arg Gln Gln Gly Asn Val
 260 265 270

ccg tct tct gtt ata tct agc cat agc atg cat ctt gga gta ctg gcc
 864
 Pro Ser Ser Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala
 275 280 285

acc gca tgg cat gcc att tca aca ggg act atg ttt aca gtc tac tac
 912
 Thr Ala Trp His Ala Ile Ser Thr Gly Thr Met Phe Thr Val Tyr Tyr
 290 295 300
 aaa ccc agg acg agc cca tct gag ttt att gtt ccg ttc gat cag tat
 960
 Lys Pro Arg Thr Ser Pro Ser Glu Phe Ile Val Pro Phe Asp Gln Tyr
 305 310 315 320
 atg gag tct gtt aag aat aac tac tct att ggc atg aga ttc aaa atg
 1008
 Met Glu Ser Val Lys Asn Asn Tyr Ser Ile Gly Met Arg Phe Lys Met
 325 330 335
 aga ttt gaa ggc gaa gag gct cct gag cag agg ttt act ggc aca atc
 1056
 Arg Phe Glu Gly Glu Glu Ala Pro Glu Gln Arg Phe Thr Gly Thr Ile
 340 345 350
 gtt ggg att gaa gag tct gat cct act agg tgg cca aaa tca aag tgg
 1104
 Val Gly Ile Glu Glu Ser Asp Pro Thr Arg Trp Pro Lys Ser Lys Trp
 355 360 365
 aga tcc ctc aag gtg aga tgg gat gag act tct agt att cct cga cct
 1152
 Arg Ser Leu Lys Val Arg Trp Asp Glu Thr Ser Ser Ile Pro Arg Pro
 370 375 380
 gat aga gta tct ccg tgg aaa gta gag cca gct ctt gct cct cct gct
 1200
 Asp Arg Val Ser Pro Trp Lys Val Glu Pro Ala Leu Ala Pro Pro Ala
 385 390 395 400
 ttg agt cct gtt cca atg cct agg cct aag agg ccc aga tca aat ata
 1248
 Leu Ser Pro Val Pro Met Pro Arg Pro Lys Arg Pro Arg Ser Asn Ile
 405 410 415
 gca cct tca tct cct gac tct tcg atg ctt acc aga gaa ggt aca act
 1296
 Ala Pro Ser Ser Pro Asp Ser Ser Met Leu Thr Arg Glu Gly Thr Thr
 420 425 430
 aag gca aac atg gac cct tta cca gca agc gga ctt tca agg gtc ttg
 1344
 Lys Ala Asn Met Asp Pro Leu Pro Ala Ser Gly Leu Ser Arg Val Leu
 435 440 445
 caa ggt caa gaa tac tcg acc ttg agg acg aaa cat act gag agt gta
 1392
 Gln Gly Gln Glu Tyr Ser Thr Leu Arg Thr Lys His Thr Glu Ser Val
 450 455 460
 gag tgt gat gct cct gag aat tct gtt gtc tgg caa tct tca gcg gat
 1440
 Glu Cys Asp Ala Pro Glu Asn Ser Val Val Trp Gln Ser Ser Ala Asp
 465 470 475 480

gat gat aag gtt gac gtg gtt tcg ggt tct aga aga tat gga tct gag
 1488
 Asp Asp Lys Val Asp Val Val Ser Gly Ser Arg Arg Tyr Gly Ser Glu
 485 490 495

aac tgg atg tcc tca gcc agg cat gaa cct act tac aca gat ttg ctc
 1536
 Asn Trp Met Ser Ser Ala Arg His Glu Pro Thr Tyr Thr Asp Leu Leu
 500 505 510

tcc ggc ttt ggg act aac ata gat cca tcc cat ggt cag cgg ata cct
 1584
 Ser Gly Phe Gly Thr Asn Ile Asp Pro Ser His Gly Gln Arg Ile Pro
 515 520 525

ttt tat gac cat tca tca tca cct tct atg cct gca aag aga atc ttg
 1632
 Phe Tyr Asp His Ser Ser Ser Pro Ser Met Pro Ala Lys Arg Ile Leu
 530 535 540

agt gat tca gaa ggc aag ttc gat tat ctt gct aac cag tgg cag atg
 1680
 Ser Asp Ser Glu Gly Lys Phe Asp Tyr Leu Ala Asn Gln Trp Gln Met
 545 550 555 560

ata cac tct ggt ctc tcc ctg aag tta cat gaa tct cct aag gta cct
 1728
 Ile His Ser Gly Leu Ser Leu Lys Leu His Glu Ser Pro Lys Val Pro
 565 570 575

gca gca act gat gcg tct ctc caa ggg cga tgc aat gtt aaa tac agc
 1776
 Ala Ala Thr Asp Ala Ser Leu Gln Gly Arg Cys Asn Val Lys Tyr Ser
 580 585 590

gaa tat cct gtt ctt aat ggt cta tcg act gag aat gct ggt ggt aac
 1824
 Glu Tyr Pro Val Leu Asn Gly Leu Ser Thr Glu Asn Ala Gly Gly Asn
 595 600 605

tgg cca ata cgt cca cgt gct ttg aat tat tat gag gaa gtg gtc aat
 1872
 Trp Pro Ile Arg Pro Arg Ala Leu Asn Tyr Tyr Glu Glu Val Val Asn
 610 615 620

gct caa gcg caa gct cag gct agg gag caa gta aca aaa caa ccc ttc
 1920
 Ala Gln Ala Gln Ala Gln Ala Arg Glu Gln Val Thr Lys Gln Pro Phe
 625 630 635 640

acg ata caa gag gag aca gca aag tca aga gaa ggg aac tgc agg ctc
 1968
 Thr Ile Gln Glu Glu Thr Ala Lys Ser Arg Glu Gly Asn Cys Arg Leu
 645 650 655

ttt ggc att cct ctg acc aac aac atg aat ggg aca gac tca acc atg
 2016
 Phe Gly Ile Pro Leu Thr Asn Asn Met Asn Gly Thr Asp Ser Thr Met
 660 665 670

tct cag aga aac aac ttg aat gat gct gcg ggg ctt aca cag ata gca
 2064
 Ser Gln Arg Asn Asn Leu Asn Asp Ala Ala Gly Leu Thr Gln Ile Ala
 675 680 685
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 2112
 Ser Pro Lys Val Gln Asp Leu Ser Asp Gln Ser Lys Gly Ser Lys Ser
 690 695 700
 aca aac gat cat cgt gaa cag gga aga cca ttc cag act aat aat cct
 2160
 Thr Asn Asp His Arg Glu Gln Gly Arg Pro Phe Gln Thr Asn Asn Pro
 705 710 715 720
 cat ccg aag gat gct caa acg aaa acc aac tca agt agg agt tgc aca
 2208
 His Pro Lys Asp Ala Gln Thr Lys Thr Asn Ser Ser Arg Ser Cys Thr
 725 730 735
 aag gtt cac aag cag gga att gca ctt ggc cgt tca gtg gat ctt tca
 2256
 Lys Val His Lys Gln Gly Ile Ala Leu Gly Arg Ser Val Asp Leu Ser
 740 745 750
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 2304
 Lys Phe Gln Asn Tyr Glu Glu Leu Val Ala Glu Leu Asp Arg Leu Phe
 755 760 765
 gag ttc aat gga gag ttg atg gct cct aag aaa gat tgg ttg ata gtt
 2352
 Glu Phe Asn Gly Glu Leu Met Ala Pro Lys Lys Asp Trp Leu Ile Val
 770 775 780
 tac aca gat gaa gag aat gat atg atg ctt gtt ggt gac gat cct tgg
 2400
 Tyr Thr Asp Glu Glu Asn Asp Met Met Leu Val Gly Asp Asp Pro Trp
 785 790 795 800
 cag gag ttt tgt tgc atg gtt cgc aaa atc ttc ata tac acg aaa gag
 2448
 Gln Glu Phe Cys Cys Met Val Arg Lys Ile Phe Ile Tyr Thr Lys Glu
 805 810 815
 gaa gtg agg aag atg aac ccg ggg act tta agc tgt agg agc gag gaa
 2496
 Glu Val Arg Lys Met Asn Pro Gly Thr Leu Ser Cys Arg Ser Glu Glu
 820 825 830
 gaa gca gtt gtt ggg gaa gga tca gat gca aag gac gcc aag tct gca
 2544
 Glu Ala Val Val Gly Glu Gly Ser Asp Ala Lys Asp Ala Lys Ser Ala
 835 840 845
 tca aat cct tca ttg tcc agc gct ggg aac tct taa
 2580
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 850 855

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326

Met Ala Ser Ser Glu Val Ser Met Lys Gly Asn Arg Gly Gly Asp Asn
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20 25 30

Val Ala Gly Glu Gly Gln Lys Ser Asn Ser Thr Arg Ser Ala Ala Ala
35 40 45

Glu Arg Ala Leu Asp Pro Glu Ala Ala Leu Tyr Arg Glu Leu Trp His
50 55 60

Ala Cys Ala Gly Pro Leu Val Thr Val Pro Arg Gln Asp Asp Arg Val
65 70 75 80

Phe Tyr Phe Pro Gln Gly His Ile Glu Gln Val Glu Ala Ser Thr Asn
85 90 95

Gln Ala Ala Glu Gln Gln Met Pro Leu Tyr Asp Leu Pro Ser Lys Leu
100 105 110

Leu Cys Arg Val Ile Asn Val Asp Leu Lys Ala Glu Ala Asp Thr Asp
115 120 125

Glu Val Tyr Ala Gln Ile Thr Leu Leu Pro Glu Ala Asn Gln Asp Glu
130 135 140

Asn Ala Ile Glu Lys Glu Ala Pro Leu Pro Pro Pro Pro Arg Phe Gln
145 150 155 160

Val His Ser Phe Cys Lys Thr Leu Thr Ala Ser Asp Thr Ser Thr His
165 170 175

Gly Gly Phe Ser Val Leu Arg Arg His Ala Asp Glu Cys Leu Pro Pro
180 185 190

Leu Asp Met Ser Arg Gln Pro Pro Thr Gln Glu Leu Val Ala Lys Asp
195 200 205

Leu His Ala Asn Glu Trp Arg Phe Arg His Ile Phe Arg Gly Gln Pro
210 215 220

Arg Arg His Leu Leu Gln Ser Gly Trp Ser Val Phe Val Ser Ser Lys
225 230 235 240

Arg Leu Val Ala Gly Asp Ala Phe Ile Phe Leu Arg Gly Glu Asn Gly
 245 250 255

Glu Leu Arg Val Gly Val Arg Arg Ala Met Arg Gln Gln Gly Asn Val
 260 265 270

Pro Ser Ser Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala
 275 280 285

Thr Ala Trp His Ala Ile Ser Thr Gly Thr Met Phe Thr Val Tyr Tyr
 290 295 300

Lys Pro Arg Thr Ser Pro Ser Glu Phe Ile Val Pro Phe Asp Gln Tyr
 305 310 315 320

Met Glu Ser Val Lys Asn Asn Tyr Ser Ile Gly Met Arg Phe Lys Met
 325 330 335

Arg Phe Glu Gly Glu Glu Ala Pro Glu Gln Arg Phe Thr Gly Thr Ile
 340 345 350

Val Gly Ile Glu Glu Ser Asp Pro Thr Arg Trp Pro Lys Ser Lys Trp
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Arg Ser Leu Lys Val Arg Trp Asp Glu Thr Ser Ser Ile Pro Arg Pro
 370 375 380

Asp Arg Val Ser Pro Trp Lys Val Glu Pro Ala Leu Ala Pro Pro Ala
 385 390 395 400

Leu Ser Pro Val Pro Met Pro Arg Pro Lys Arg Pro Arg Ser Asn Ile
 405 410 415

Ala Pro Ser Ser Pro Asp Ser Ser Met Leu Thr Arg Glu Gly Thr Thr
 420 425 430

Lys Ala Asn Met Asp Pro Leu Pro Ala Ser Gly Leu Ser Arg Val Leu
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Gln Gly Gln Glu Tyr Ser Thr Leu Arg Thr Lys His Thr Glu Ser Val
 450 455 460

Glu Cys Asp Ala Pro Glu Asn Ser Val Val Trp Gln Ser Ser Ala Asp
 465 470 475 480

Asp Asp Lys Val Asp Val Val Ser Gly Ser Arg Arg Tyr Gly Ser Glu
485 490 495

Asn Trp Met Ser Ser Ala Arg His Glu Pro Thr Tyr Thr Asp Leu Leu
500 505 510

Ser Gly Phe Gly Thr Asn Ile Asp Pro Ser His Gly Gln Arg Ile Pro
515 520 525

Phe Tyr Asp His Ser Ser Ser Pro Ser Met Pro Ala Lys Arg Ile Leu
530 535 540

Ser Asp Ser Glu Gly Lys Phe Asp Tyr Leu Ala Asn Gln Trp Gln Met
545 550 555 560

Ile His Ser Gly Leu Ser Leu Lys Leu His Glu Ser Pro Lys Val Pro
565 570 575

Ala Ala Thr Asp Ala Ser Leu Gln Gly Arg Cys Asn Val Lys Tyr Ser
580 585 590

Glu Tyr Pro Val Leu Asn Gly Leu Ser Thr Glu Asn Ala Gly Gly Asn
595 600 605

Trp Pro Ile Arg Pro Arg Ala Leu Asn Tyr Tyr Glu Glu Val Val Asn
610 615 620

Ala Gln Ala Gln Ala Gln Ala Arg Glu Gln Val Thr Lys Gln Pro Phe
625 630 635 640

Thr Ile Gln Glu Glu Thr Ala Lys Ser Arg Glu Gly Asn Cys Arg Leu
645 650 655

Phe Gly Ile Pro Leu Thr Asn Asn Met Asn Gly Thr Asp Ser Thr Met
660 665 670

Ser Gln Arg Asn Asn Leu Asn Asp Ala Ala Gly Leu Thr Gln Ile Ala
675 680 685

Ser Pro Lys Val Gln Asp Leu Ser Asp Gln Ser Lys Gly Ser Lys Ser
690 695 700

Thr Asn Asp His Arg Glu Gln Gly Arg Pro Phe Gln Thr Asn Asn Pro
705 710 715 720

His Pro Lys Asp Ala Gln Thr Lys Thr Asn Ser Ser Arg Ser Cys Thr
725 730 735

Lys Val His Lys Gln Gly Ile Ala Leu Gly Arg Ser Val Asp Leu Ser
740 745 750

Lys Phe Gln Asn Tyr Glu Glu Leu Val Ala Glu Leu Asp Arg Leu Phe
755 760 765

Glu Phe Asn Gly Glu Leu Met Ala Pro Lys Lys Asp Trp Leu Ile Val
770 775 780

Tyr Thr Asp Glu Glu Asn Asp Met Met Leu Val Gly Asp Asp Pro Trp
785 790 795 800

Gln Glu Phe Cys Cys Met Val Arg Lys Ile Phe Ile Tyr Thr Lys Glu
805 810 815

Glu Val Arg Lys Met Asn Pro Gly Thr Leu Ser Cys Arg Ser Glu Glu
820 825 830

Glu Ala Val Val Gly Glu Gly Ser Asp Ala Lys Asp Ala Lys Ser Ala
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120

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180

tacgcaccct tcttttatct tcgactgttt cagcttcggt ttcttcacgc gagagagata
240

gagagactgt gtgttttggt gtgactgata gaagatttaa tcagctg atg gca aat
296

Met Ala Asn
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cgc gga ggt gaa tat ctg tac gat gag tta tgg aaa tta tgc gcg gga
344

Arg Gly Gly Glu Tyr Leu Tyr Asp Glu Leu Trp Lys Leu Cys Ala Gly
5 10 15

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392
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Gln Gly His Met Glu Gln Leu Glu Ala Ser Thr Gln Gln Val Asp Leu
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aat acg atg aag cct ctt ttt gtt ctt cct cct aag att ctc tgc aat
488
Asn Thr Met Lys Pro Leu Phe Val Leu Pro Pro Lys Ile Leu Cys Asn
      55      60      65

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536
Val Met Asn Val Ser Leu Gln Ala Glu Lys Asp Thr Asp Glu Val Tyr
      70      75      80

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584
Ala Gln Ile Thr Leu Ile Pro Val Gly Thr Glu Val Asp Glu Pro Met
      85      90      95

agt cct gat ccc tct cct cct gag ttg caa agg ccg aaa gtt cac tct
632
Ser Pro Asp Pro Ser Pro Pro Glu Leu Gln Arg Pro Lys Val His Ser
100      105      110      115

ttc agc aag gtt ttg aca gcg tct gat aca agc acc cat ggt ggc ttt
680
Phe Ser Lys Val Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe
      120      125      130

tct gtt cta agg aaa cat gcc acg gaa tgt ctt cct ccg ctg gat atg
728
Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Pro Leu Asp Met
      135      140      145

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776
Thr Gln Gln Thr Pro Thr Gln Glu Leu Val Ala Glu Asp Val His Gly
      150      155      160

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824
Tyr Gln Trp Lys Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His
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Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Thr Ser Lys Arg Leu Val
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920
Ala Gly Asp Thr Phe Val Phe Leu Arg Gly Glu Asn Gly Glu Leu Arg
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 Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala Thr Ala Arg
 230 235 240

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 1064
 His Ala Thr Gln Thr Lys Thr Met Phe Ile Val Tyr Tyr Lys Pro Arg
 245 250 255

aca agc caa ttc atc att agc ttg aac aaa tat cta gaa gcc atg agc
 1112
 Thr Ser Gln Phe Ile Ile Ser Leu Asn Lys Tyr Leu Glu Ala Met Ser
 260 265 270 275

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 Asn Lys Phe Ser Val Gly Met Arg Phe Lys Met Arg Phe Glu Gly Glu
 280 285 290

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 Asp Ser Pro Glu Arg Arg Tyr Ser Gly Thr Val Ile Gly Val Lys Asp
 295 300 305

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 1256
 Cys Ser Pro His Trp Lys Asp Ser Lys Trp Arg Cys Leu Glu Val His
 310 315 320

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 Trp Asp Glu Pro Ala Ser Ile Ser Arg Pro Asn Lys Val Ser Pro Trp
 325 330 335

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 1352
 Glu Ile Glu Pro Phe Val Asn Ser Glu Asn Val Pro Lys Ser Val Met
 340 345 350 355

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 360 365 370

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 Val Gly Ile Thr Ala Ser Asn Leu Trp Ser Ser Val Leu Thr Gln Pro
 375 380 385

cat gag ttt gca caa tcg tgc atc acc tca cag tgg agt tct cct cag
 1496
 His Glu Phe Ala Gln Ser Cys Ile Thr Ser Gln Trp Ser Ser Pro Gln
 390 395 400

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 Gln Cys His Arg Asp Ala Asn Glu Asp Ala Lys Lys Ser Asp Trp Leu
 405 410 415
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 1592
 Asn Asn Ser Tyr Ser Val Ser Asn Val Ala Lys Asp Ser Thr Leu Asn
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 1688
 Asn Tyr Arg Leu Phe Gly Ile Asp Leu Met Ser Ser Ser Leu Ala Val
 455 460 465
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 1736
 Pro Glu Glu Lys Thr Ala Pro Met Arg Pro Ile Asn Ile Ser Lys Pro
 470 475 480
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 1784
 Thr Met Asp Ser His Ser Asp Pro Lys Ser Glu Ile Ser Lys Val Ser
 485 490 495
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 1832
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 1880
 Ser Lys Gln Ser Ser Ser Thr Arg Ser Arg Thr Lys Val Gln Met Gln
 520 525 530
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 1928
 Gly Val Pro Val Gly Arg Ala Val Asp Leu Asn Ala Leu Lys Gly Tyr
 535 540 545
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 1976
 Asn Glu Leu Ile Asp Asp Ile Glu Lys Leu Phe Asp Ile Lys Gly Glu
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 565 570 575
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 2072
 Asp Met Met Leu Val Gly Asp Asp Pro Trp Pro Glu Phe Cys Asn Met
 580 585 590 595

gtg aag aga ata ttc ata tgg tcg aaa gag gaa gtg aag aaa atg acg
2120

Val Lys Arg Ile Phe Ile Trp Ser Lys Glu Glu Val Lys Lys Met Thr
600 605 610

cct ggg aac caa ctc cgg atg ctg tta agg gaa gtt gaa aca aca cta
2168

Pro Gly Asn Gln Leu Arg Met Leu Leu Arg Glu Val Glu Thr Thr Leu
615 620 625

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2214

Thr Thr Thr Ser Lys Thr Asp Asn His Ser Asn
630 635

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35 40 45

Val Asp Leu Asn Thr Met Lys Pro Leu Phe Val Leu Pro Pro Lys Ile
50 55 60

Leu Cys Asn Val Met Asn Val Ser Leu Gln Ala Glu Lys Asp Thr Asp
65 70 75 80

Glu Val Tyr Ala Gln Ile Thr Leu Ile Pro Val Gly Thr Glu Val Asp
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Glu Pro Met Ser Pro Asp Pro Ser Pro Pro Glu Leu Gln Arg Pro Lys
100 105 110

Val His Ser Phe Ser Lys Val Leu Thr Ala Ser Asp Thr Ser Thr His
115 120 125

Gly Gly Phe Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Pro
130 135 140

Leu Asp Met Thr Gln Gln Thr Pro Thr Gln Glu Leu Val Ala Glu Asp
145 150 155 160

Val His Gly Tyr Gln Trp Lys Phe Lys His Ile Phe Arg Gly Gln Pro
165 170 175

Arg Arg His Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Thr Ser Lys
180 185 190

Arg Leu Val Ala Gly Asp Thr Phe Val Phe Leu Arg Gly Glu Asn Gly
195 200 205

Glu Leu Arg Val Gly Val Arg Arg Ala Asn Leu Gln Gln Ser Ser Met
210 215 220

Pro Ser Ser Val Ile Ser Ser His Ser Met His Leu Gly Val Leu Ala
225 230 235 240

Thr Ala Arg His Ala Thr Gln Thr Lys Thr Met Phe Ile Val Tyr Tyr
245 250 255

Lys Pro Arg Thr Ser Gln Phe Ile Ile Ser Leu Asn Lys Tyr Leu Glu
260 265 270

Ala Met Ser Asn Lys Phe Ser Val Gly Met Arg Phe Lys Met Arg Phe
275 280 285

Glu Gly Glu Asp Ser Pro Glu Arg Arg Tyr Ser Gly Thr Val Ile Gly
290 295 300

Val Lys Asp Cys Ser Pro His Trp Lys Asp Ser Lys Trp Arg Cys Leu
305 310 315 320

Glu Val His Trp Asp Glu Pro Ala Ser Ile Ser Arg Pro Asn Lys Val
325 330 335

Ser Pro Trp Glu Ile Glu Pro Phe Val Asn Ser Glu Asn Val Pro Lys
340 345 350

Ser Val Met Leu Lys Asn Lys Arg Pro Arg Gln Val Ser Glu Val Ser
355 360 365

Ala Leu Asp Val Gly Ile Thr Ala Ser Asn Leu Trp Ser Ser Val Leu
370 375 380

Thr Gln Pro His Glu Phe Ala Gln Ser Cys Ile Thr Ser Gln Trp Ser

385 390 395 400
 Ser Pro Gln Gln Cys His Arg Asp Ala Asn Glu Asp Ala Lys Lys Ser
 405 410 415
 Asp Trp Leu Asn Asn Ser Tyr Ser Val Ser Asn Val Ala Lys Asp Ser
 420 425 430
 Thr Leu Asn Asp Gln Met Val Ser Pro Val Glu Gln Lys Lys Pro Glu
 435 440 445
 Thr Thr Ala Asn Tyr Arg Leu Phe Gly Ile Asp Leu Met Ser Ser Ser
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 465 470 475 480
 Ser Lys Pro Thr Met Asp Ser His Ser Asp Pro Lys Ser Glu Ile Ser
 485 490 495
 Lys Val Ser Glu Glu Lys Lys Gln Glu Pro Ala Glu Gly Ser Pro Lys
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 Glu Val Gln Ser Lys Gln Ser Ser Ser Thr Arg Ser Arg Thr Lys Val
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 Gln Met Gln Gly Val Pro Val Gly Arg Ala Val Asp Leu Asn Ala Leu
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 Lys Gly Tyr Asn Glu Leu Ile Asp Asp Ile Glu Lys Leu Phe Asp Ile
 545 550 555 560
 Lys Gly Glu Leu Arg Ser Arg Asn Gln Trp Glu Ile Val Phe Thr Asp
 565 570 575
 Asp Glu Gly Asp Met Met Leu Val Gly Asp Asp Pro Trp Pro Glu Phe
 580 585 590
 Cys Asn Met Val Lys Arg Ile Phe Ile Trp Ser Lys Glu Glu Val Lys
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attagggttt caattgttta cttttgttt gctttttata tcaagta atg gat cag
 176

Met Asp Gln
 1

gtc tct cgc tct ctt cct cca cct ttt ctc tca aga gat ctc cat ctt
 224

Val Ser Arg Ser Leu Pro Pro Phe Leu Ser Arg Asp Leu His Leu
 5 10 15

cac cca cac cat caa ttc cag cat cag cag cag cag cag caa cag aat
 272

His Pro His His Gln Phe Gln His Gln Gln Gln Gln Gln Gln Asn
 20 25 30 35

cac ggc cac gat ata gac cag cac cga atc ggt ggg cta aaa cgt gac
 320

His Gly His Asp Ile Asp Gln His Arg Ile Gly Gly Leu Lys Arg Asp
 40 45 50

cga gat gct gat atc gat ccc aac gag cac tct tca gcc gga aaa gat
 368

Arg Asp Ala Asp Ile Asp Pro Asn Glu His Ser Ser Ala Gly Lys Asp
 55 60 65

caa agt act cct ggc tcc ggt gga gaa agc ggc ggc gga gga gga gga
 416

Gln Ser Thr Pro Gly Ser Gly Gly Glu Ser Gly Gly Gly Gly Gly Gly
 70 75 80

gat aat cac atc acg aga agg cca cgt ggc aga cca gcg gga tct aag
 464

Asp Asn His Ile Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
 85 90 95

aac aaa cca aaa ccg cca atc atc atc act cga gac agc gca aac gct
 512

Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala
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ctc aaa tct cat gtc atg gaa gta gca aac gga tgt gac gtc atg gaa
 560

Leu Lys Ser His Val Met Glu Val Ala Asn Gly Cys Asp Val Met Glu
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 608

Ser Val Thr Val Phe Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu
 135 140 145

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 Ser Gly Asn Gly Ala Val Thr Asn Val Thr Ile Arg Gln Pro Ala Ser
 150 155 160

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 Val Pro Gly Gly Gly Ser Ser Val Val Asn Leu His Gly Arg Phe Glu
 165 170 175

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 Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala
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 Ala Ser Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val
 200 205 210

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 848
 Gly Gly Ser Val Val Gly Pro Leu Met Ala Ser Gly Pro Val Val Ile
 215 220 225

atg gca gct tcg ttt gga aac gct gcg tat gag aga ctg ccg ttg gag
 896
 Met Ala Ala Ser Phe Gly Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu
 230 235 240

gaa gac gat caa gaa gag caa aca gct gga gcg gtt gct aat aat atc
 944
 Glu Asp Asp Gln Glu Glu Gln Thr Ala Gly Ala Val Ala Asn Asn Ile
 245 250 255

gat gga aac gca aca atg ggt ggt gga acg caa acg caa act cag acg
 992
 Asp Gly Asn Ala Thr Met Gly Gly Gly Thr Gln Thr Gln Thr Gln Thr
 260 265 270 275

cag cag caa cag caa caa cag ttg atg caa gat ccg acg tcg ttt ata
 1040
 Gln Gln Gln Gln Gln Gln Gln Leu Met Gln Asp Pro Thr Ser Phe Ile
 280 285 290

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 1088
 Gln Gly Leu Pro Pro Asn Leu Met Asn Ser Val Gln Leu Pro Ala Glu
 295 300 305

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 1141
 Ala Tyr Trp Gly Thr Pro Arg Pro Ser Phe
 310 315

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 1201

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 1261

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1394

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Gln Gln Asn His Gly His Asp Ile Asp Gln His Arg Ile Gly Gly Leu
35 40 45

Lys Arg Asp Arg Asp Ala Asp Ile Asp Pro Asn Glu His Ser Ser Ala
50 55 60

Gly Lys Asp Gln Ser Thr Pro Gly Ser Gly Gly Glu Ser Gly Gly Gly
65 70 75 80

Gly Gly Gly Asp Asn His Ile Thr Arg Arg Pro Arg Gly Arg Pro Ala
85 90 95

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser
100 105 110

Ala Asn Ala Leu Lys Ser His Val Met Glu Val Ala Asn Gly Cys Asp
115 120 125

Val Met Glu Ser Val Thr Val Phe Ala Arg Arg Arg Gln Arg Gly Ile
130 135 140

Cys Val Leu Ser Gly Asn Gly Ala Val Thr Asn Val Thr Ile Arg Gln
145 150 155 160

Pro Ala Ser Val Pro Gly Gly Gly Ser Ser Val Val Asn Leu His Gly
165 170 175

Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala
180 185 190

Pro Pro Ala Ala Ser Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly
195 200 205

Gln Val Val Gly Gly Ser Val Val Gly Pro Leu Met Ala Ser Gly Pro
210 215 220

Val Val Ile Met Ala Ala Ser Phe Gly Asn Ala Ala Tyr Glu Arg Leu
225 230 235 240

Pro Leu Glu Glu Asp Asp Gln Glu Glu Gln Thr Ala Gly Ala Val Ala
245 250 255

Asn Asn Ile Asp Gly Asn Ala Thr Met Gly Gly Gly Thr Gln Thr Gln
260 265 270

Thr Gln Thr Gln Gln Gln Gln Gln Gln Leu Met Gln Asp Pro Thr
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Ser Phe Ile Gln Gly Leu Pro Pro Asn Leu Met Asn Ser Val Gln Leu
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120

tatgcataat tgagag atg gtg gtc aaa agg aag tta aat tgt ggt ggc tct
172

Met Val Val Lys Arg Lys Leu Asn Cys Gly Gly Ser
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220

Asp Gly Phe Asp Phe Pro Asn Ile Pro Lys Ala Pro Arg Ser Ser Arg
15 20 25

agg aag gtc tca ggt aag aga tct gat gat gaa agt gag atc tgt gca
268

Arg Lys Val Ser Gly Lys Arg Ser Asp Asp Glu Ser Glu Ile Cys Ala
30 35 40

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316

Ile Asp Leu Leu Ala Ser Leu Ala Gly Lys Leu Leu Glu Glu Ser Glu

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412			
Leu Gly Gly Leu Ile Lys Gln Glu Leu Glu Asp Gly Tyr Thr Thr Lys			
	80	85	90
cct tgt aaa tcc gag ttt ttc gat cca gga aac cct gct tca aag tcc			
460			
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	95	100	105
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508			
Thr Ser Glu Asn Thr Ser Val Thr Cys Leu Pro Phe Ser Ser Phe Glu			
	110	115	120
aat gat tgc att ttg gag caa aca ccg gtt tct gat tgt aag agg gca			
556			
Asn Asp Cys Ile Leu Glu Gln Thr Pro Val Ser Asp Cys Lys Arg Ala			
125	130	135	140
tct ggt ttg aag tcc ctg gta ggg agc atc act gag gag aca tgt gtt			
604			
Ser Gly Leu Lys Ser Leu Val Gly Ser Ile Thr Glu Glu Thr Cys Val			
	145	150	155
gtt aat gag gat gcc gga tct gaa caa ggt gct aat act ttc agc tta			
652			
Val Asn Glu Asp Ala Gly Ser Glu Gln Gly Ala Asn Thr Phe Ser Leu			
	160	165	170
aag gat cca agt caa tta cat tcg cag tct cca gaa tcg gtc ctt ctg			
700			
Lys Asp Pro Ser Gln Leu His Ser Gln Ser Pro Glu Ser Val Leu Leu			
	175	180	185
gat ggc gat gtg aaa tta gca cca tgc acg gat caa gtc cct aat gat			
748			
Asp Gly Asp Val Lys Leu Ala Pro Cys Thr Asp Gln Val Pro Asn Asp			
	190	195	200
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796			
Ser Phe Lys Gly Tyr Arg Asn His Ser Lys Leu Val Cys Arg Asp Asp			
205	210	215	220
gac gaa aac tat tgt aag tat tat aaa ttt agt gac aaa tgt aag tca			
844			
Asp Glu Asn Tyr Cys Lys Tyr Tyr Lys Phe Ser Asp Lys Cys Lys Ser			
	225	230	235
tat agg cct ctc tcc cgg gtt ggc aat aga aga ata atg cag tcg gtg			
892			
Tyr Arg Pro Leu Ser Arg Val Gly Asn Arg Arg Ile Met Gln Ser Val			
	240	245	250

aga gca atc tcc aag ttg aag tgt ttt gaa gac act aga aca gat ggt
 940
 Arg Ala Ile Ser Lys Leu Lys Cys Phe Glu Asp Thr Arg Thr Asp Gly
 255 260 265
 cgt ttg aag gct ctc tac cgc aag aga aaa tta tgt tat ggt tac aac
 988
 Arg Leu Lys Ala Leu Tyr Arg Lys Arg Lys Leu Cys Tyr Gly Tyr Asn
 270 275 280
 cca tgg aag cgt gag acc att cat agg aag aga aga ttg tct gac aaa
 1036
 Pro Trp Lys Arg Glu Thr Ile His Arg Lys Arg Arg Leu Ser Asp Lys
 285 290 295 300
 ggt ttg gtc gta aat tat gat ggt ggg ctc agt agt gaa agt gtt tcc
 1084
 Gly Leu Val Val Asn Tyr Asp Gly Gly Leu Ser Ser Glu Ser Val Ser
 305 310 315
 aat tca cct gaa aag gga gaa tca gaa aat ggt gat ttc tct gct gca
 1132
 Asn Ser Pro Glu Lys Gly Glu Ser Glu Asn Gly Asp Phe Ser Ala Ala
 320 325 330
 aaa ata ggt ctt ctt tcg aaa gac tcc cgt gta aag ttc agc atc aag
 1180
 Lys Ile Gly Leu Leu Ser Lys Asp Ser Arg Val Lys Phe Ser Ile Lys
 335 340 345
 tcc ctt agg att ccg gag ctt gta att gaa gtt cca gaa aca gca aca
 1228
 Ser Leu Arg Ile Pro Glu Leu Val Ile Glu Val Pro Glu Thr Ala Thr
 350 355 360
 gta ggc tta ctg aag agg acg gtg aag gag gcg gtt act gct tta ctc
 1276
 Val Gly Leu Leu Lys Arg Thr Val Lys Glu Ala Val Thr Ala Leu Leu
 365 370 375 380
 ggt ggt gga ata cgt att ggg gtg tta gtc caa ggg aaa aaa gtt aga
 1324
 Gly Gly Gly Ile Arg Ile Gly Val Leu Val Gln Gly Lys Lys Val Arg
 385 390 395
 gat gac aac aac act cta tca cag act ggt ctt tcg tgt aga gaa aat
 1372
 Asp Asp Asn Asn Thr Leu Ser Gln Thr Gly Leu Ser Cys Arg Glu Asn
 400 405 410
 ctt ggc aac ctt ggc ttc acc tta gag cct ggt ttg gaa aca ctg cct
 1420
 Leu Gly Asn Leu Gly Phe Thr Leu Glu Pro Gly Leu Glu Thr Leu Pro
 415 420 425
 gta cct ctt tgt tct gaa act cct gtc ctt tct ctg cca act gac tct
 1468
 Val Pro Leu Cys Ser Glu Thr Pro Val Leu Ser Leu Pro Thr Asp Ser
 430 435 440

aca aag ttg tca gaa agg tcc gca gct tct cca gcg tta gag act gga
 1516
 Thr Lys Leu Ser Glu Arg Ser Ala Ala Ser Pro Ala Leu Glu Thr Gly
 445 450 455 460

att cct ctc cct ccc caa gat gaa gat tac ttg att aat ttg gga aat
 1564
 Ile Pro Leu Pro Pro Gln Asp Glu Asp Tyr Leu Ile Asn Leu Gly Asn
 465 470 475

agt gtg gag aac aat gat gaa tta gtc cca cat ctg agt gac ata cca
 1612
 Ser Val Glu Asn Asn Asp Glu Leu Val Pro His Leu Ser Asp Ile Pro
 480 485 490

gct gat gaa caa cct tca tca gat tca aga gcg ctg gtt cca gtt ttg
 1660
 Ala Asp Glu Gln Pro Ser Ser Asp Ser Arg Ala Leu Val Pro Val Leu
 495 500 505

gcc ttg gag tcc gac gct ctt gca ctt gtt cca gtt aac gag aaa cct
 1708
 Ala Leu Glu Ser Asp Ala Leu Ala Leu Val Pro Val Asn Glu Lys Pro
 510 515 520

aag cgt aca gag ctt tca caa cgc aga acc agg aga cca ttc tct gtt
 1756
 Lys Arg Thr Glu Leu Ser Gln Arg Arg Thr Arg Arg Pro Phe Ser Val
 525 530 535 540

aca gag gta gaa gct cta gta agc gca gtt gaa gaa gtt ggg act gga
 1804
 Thr Glu Val Glu Ala Leu Val Ser Ala Val Glu Glu Val Gly Thr Gly
 545 550 555

aga tgg cgt gat gtg aag ttg cgt tct ttt gag aat gca agt cat cga
 1852
 Arg Trp Arg Asp Val Lys Leu Arg Ser Phe Glu Asn Ala Ser His Arg
 560 565 570

acc tat gtg gac ttg aag gac aaa tgg aaa acg ttg gtt cac aca gca
 1900
 Thr Tyr Val Asp Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr Ala
 575 580 585

agt ata tca cca cag caa cga aga gga gaa cca gtg cct caa gaa ctg
 1948
 Ser Ile Ser Pro Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu Leu
 590 595 600

cta gac aga gtc tta gga gca cat agg tac tgg aca cag cac caa atg
 1996
 Leu Asp Arg Val Leu Gly Ala His Arg Tyr Trp Thr Gln His Gln Met
 605 610 615 620

aaa cag aac ggg aaa cat cag gtg gct aca aca atg gtg gtt gaa gca
 2044
 Lys Gln Asn Gly Lys His Gln Val Ala Thr Thr Met Val Val Glu Ala
 625 630 635

ggt tcg tcc atg taa agaaggagaa tggtaataac aataactttc acttgacgac
2099

Gly Ser Ser Met
640

taaggaacca aagtgggcaa ctgtacaaag ggaaacaaca aaatacagaa acataacttaa
2159

tttctgaaaa gaagagtcta tttttttatt ttttttaaata catagccggt agaaacaaga
2219

cgttccttga cacttttggt tacttttatg gtaggtctgt tcattccaaa tttctaattg
2279

atttgattat gtaatttggt ggtaggacca tg
2311

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Phe Pro Asn Ile Pro Lys Ala Pro Arg Ser Ser Arg Arg Lys Val Ser
20 25 30

Gly Lys Arg Ser Asp Asp Glu Ser Glu Ile Cys Ala Ile Asp Leu Leu
35 40 45

Ala Ser Leu Ala Gly Lys Leu Leu Glu Glu Ser Glu Ser Ser Ser Thr
50 55 60

Ser Thr Tyr Ala Ser Glu Ala Asp Asn Leu Asp His Leu Gly Gly Leu
65 70 75 80

Ile Lys Gln Glu Leu Glu Asp Gly Tyr Thr Thr Lys Pro Cys Lys Ser
85 90 95

Glu Phe Phe Asp Pro Gly Asn Pro Ala Ser Lys Ser Thr Ser Glu Asn
100 105 110

Thr Ser Val Thr Cys Leu Pro Phe Ser Ser Phe Glu Asn Asp Cys Ile
115 120 125

Leu Glu Gln Thr Pro Val Ser Asp Cys Lys Arg Ala Ser Gly Leu Lys
130 135 140

Ser Leu Val Gly Ser Ile Thr Glu Glu Thr Cys Val Val Asn Glu Asp
145 150 155 160

Ala Gly Ser Glu Gln Gly Ala Asn Thr Phe Ser Leu Lys Asp Pro Ser
165 170 175

Gln Leu His Ser Gln Ser Pro Glu Ser Val Leu Leu Asp Gly Asp Val
180 185 190

Lys Leu Ala Pro Cys Thr Asp Gln Val Pro Asn Asp Ser Phe Lys Gly
195 200 205

Tyr Arg Asn His Ser Lys Leu Val Cys Arg Asp Asp Asp Glu Asn Tyr
210 215 220

Cys Lys Tyr Tyr Lys Phe Ser Asp Lys Cys Lys Ser Tyr Arg Pro Leu
225 230 235 240

Ser Arg Val Gly Asn Arg Arg Ile Met Gln Ser Val Arg Ala Ile Ser
245 250 255

Lys Leu Lys Cys Phe Glu Asp Thr Arg Thr Asp Gly Arg Leu Lys Ala
260 265 270

Leu Tyr Arg Lys Arg Lys Leu Cys Tyr Gly Tyr Asn Pro Trp Lys Arg
275 280 285

Glu Thr Ile His Arg Lys Arg Arg Leu Ser Asp Lys Gly Leu Val Val
290 295 300

Asn Tyr Asp Gly Gly Leu Ser Ser Glu Ser Val Ser Asn Ser Pro Glu
305 310 315 320

Lys Gly Glu Ser Glu Asn Gly Asp Phe Ser Ala Ala Lys Ile Gly Leu
325 330 335

Leu Ser Lys Asp Ser Arg Val Lys Phe Ser Ile Lys Ser Leu Arg Ile
340 345 350

Pro Glu Leu Val Ile Glu Val Pro Glu Thr Ala Thr Val Gly Leu Leu
355 360 365

Lys Arg Thr Val Lys Glu Ala Val Thr Ala Leu Leu Gly Gly Gly Ile
370 375 380

Arg Ile Gly Val Leu Val Gln Gly Lys Lys Val Arg Asp Asp Asn Asn
385 390 395 400

Thr Leu Ser Gln Thr Gly Leu Ser Cys Arg Glu Asn Leu Gly Asn Leu

405 410 415
 Gly Phe Thr Leu Glu Pro Gly Leu Glu Thr Leu Pro Val Pro Leu Cys
 420 425 430
 Ser Glu Thr Pro Val Leu Ser Leu Pro Thr Asp Ser Thr Lys Leu Ser
 435 440 445
 Glu Arg Ser Ala Ala Ser Pro Ala Leu Glu Thr Gly Ile Pro Leu Pro
 450 455 460
 Pro Gln Asp Glu Asp Tyr Leu Ile Asn Leu Gly Asn Ser Val Glu Asn
 465 470 475 480
 Asn Asp Glu Leu Val Pro His Leu Ser Asp Ile Pro Ala Asp Glu Gln
 485 490 495
 Pro Ser Ser Asp Ser Arg Ala Leu Val Pro Val Leu Ala Leu Glu Ser
 500 505 510
 Asp Ala Leu Ala Leu Val Pro Val Asn Glu Lys Pro Lys Arg Thr Glu
 515 520 525
 Leu Ser Gln Arg Arg Thr Arg Arg Pro Phe Ser Val Thr Glu Val Glu
 530 535 540
 Ala Leu Val Ser Ala Val Glu Glu Val Gly Thr Gly Arg Trp Arg Asp
 545 550 555 560
 Val Lys Leu Arg Ser Phe Glu Asn Ala Ser His Arg Thr Tyr Val Asp
 565 570 575
 Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr Ala Ser Ile Ser Pro
 580 585 590
 Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu Leu Leu Asp Arg Val
 595 600 605
 Leu Gly Ala His Arg Tyr Trp Thr Gln His Gln Met Lys Gln Asn Gly
 610 615 620
 Lys His Gln Val Ala Thr Thr Met Val Val Glu Ala Gly Ser Ser Met
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106
Met Arg Ser Gly Glu Cys Asp Glu Glu Glu Ile Gln Ala Lys Gln Glu
1 5 10 15

aga gat caa aat caa aat cat caa gta aac tta aac cac atg ttg caa
154
Arg Asp Gln Asn Gln Asn His Gln Val Asn Leu Asn His Met Leu Gln
20 25 30

caa caa cag ccg agt tcg gta tca tct tca agg caa tgg act tca gct
202
Gln Gln Gln Pro Ser Ser Val Ser Ser Ser Arg Gln Trp Thr Ser Ala
35 40 45

ttt agg aat cca aga atc gtt cga gtc tca aga aca ttc ggt ggc aaa
250
Phe Arg Asn Pro Arg Ile Val Arg Val Ser Arg Thr Phe Gly Gly Lys
50 55 60

gac aga cac agc aaa gta tgt aca gtc cgt ggt ctt cga gac cgg agg
298
Asp Arg His Ser Lys Val Cys Thr Val Arg Gly Leu Arg Asp Arg Arg
65 70 75 80

ata agg ttg tcc gta cct aca gct att caa ctc tac gac ctt caa gat
346
Ile Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Asp
85 90 95

cga tta ggg ctg agt cag cca agc aaa gtc att gat tgg tta ctc gaa
394
Arg Leu Gly Leu Ser Gln Pro Ser Lys Val Ile Asp Trp Leu Leu Glu
100 105 110

gca gca aaa gat gac gta gac aag cta cct cct cta caa ttc cca cat
442
Ala Ala Lys Asp Asp Val Asp Lys Leu Pro Pro Leu Gln Phe Pro His
115 120 125

gga ttt aac cag atg tat cca aat ctc atc ttc gga aac tcc ggg ttt
490
Gly Phe Asn Gln Met Tyr Pro Asn Leu Ile Phe Gly Asn Ser Gly Phe
130 135 140

gga gaa tct cca tct tca act aca tca aca acg ttt cca gga acc aat
538
Gly Glu Ser Pro Ser Ser Thr Thr Ser Thr Thr Phe Pro Gly Thr Asn
145 150 155 160

ctc ggg ttc ttg gaa aat tgg gat ctt ggt ggt tct tca aga aca aga
586
Leu Gly Phe Leu Glu Asn Trp Asp Leu Gly Gly Ser Ser Arg Thr Arg
165 170 175

gca aga tta acc gat aca act acg acc caa aga gaa agt ttt gat ctt
 634
 Ala Arg Leu Thr Asp Thr Thr Thr Thr Gln Arg Glu Ser Phe Asp Leu
 180 185 190

gat aaa gga aaa tgg atc aaa aac gac gag aat agt aat caa gat cat
 682
 Asp Lys Gly Lys Trp Ile Lys Asn Asp Glu Asn Ser Asn Gln Asp His
 195 200 205

caa ggg ttt aac acc aat cat caa caa caa ttt cct ctg acc aat ccg
 730
 Gln Gly Phe Asn Thr Asn His Gln Gln Gln Phe Pro Leu Thr Asn Pro
 210 215 220

tac aac aac act tca gct tat tac aac ctt gga cat ctt caa caa tcg
 778
 Tyr Asn Asn Thr Ser Ala Tyr Tyr Asn Leu Gly His Leu Gln Gln Ser
 225 230 235 240

tta gac caa tct ggt aat aac gtt act gtc gca ata tct aat gtt gct
 826
 Leu Asp Gln Ser Gly Asn Asn Val Thr Val Ala Ile Ser Asn Val Ala
 245 250 255

gct aat aat aac aat aat ctc aat ttg cat cct cct tcc tcg tct gcc
 874
 Ala Asn Asn Asn Asn Asn Leu Asn Leu His Pro Pro Ser Ser Ser Ala
 260 265 270

gga gat gga tct cag ctt ttt ttc ggt cct act cct ccg gca atg agc
 922
 Gly Asp Gly Ser Gln Leu Phe Phe Gly Pro Thr Pro Pro Ala Met Ser
 275 280 285

tct cta ttc ccg aca tac cct tcg ttt ctt gga gct tct cat cat cat
 970
 Ser Leu Phe Pro Thr Tyr Pro Ser Phe Leu Gly Ala Ser His His His
 290 295 300

cat gtc gtc gat gga gcc ggt cat ctt cag ctc ttt agc tcg aat tca
 1018
 His Val Val Asp Gly Ala Gly His Leu Gln Leu Phe Ser Ser Asn Ser
 305 310 315 320

aat acc gca tcg cag caa cac atg atg ccg ggt aat acg agt ttg att
 1066
 Asn Thr Ala Ser Gln Gln His Met Met Pro Gly Asn Thr Ser Leu Ile
 325 330 335

aga cca ttt cat cat ttg atg agc tcg aat cat gat acg gat cat cat
 1114
 Arg Pro Phe His His Leu Met Ser Ser Asn His Asp Thr Asp His His
 340 345 350

agt agc gat aat gaa tca gat tct tga atgattttat atatctacac
 1161
 Ser Ser Asp Asn Glu Ser Asp Ser
 355 360

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1221

gttggattgg tttatgtatc t
1242

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Arg Asp Gln Asn Gln Asn His Gln Val Asn Leu Asn His Met Leu Gln
20 25 30

Gln Gln Gln Pro Ser Ser Val Ser Ser Ser Arg Gln Trp Thr Ser Ala
35 40 45

Phe Arg Asn Pro Arg Ile Val Arg Val Ser Arg Thr Phe Gly Gly Lys
50 55 60

Asp Arg His Ser Lys Val Cys Thr Val Arg Gly Leu Arg Asp Arg Arg
65 70 75 80

Ile Arg Leu Ser Val Pro Thr Ala Ile Gln Leu Tyr Asp Leu Gln Asp
85 90 95

Arg Leu Gly Leu Ser Gln Pro Ser Lys Val Ile Asp Trp Leu Leu Glu
100 105 110

Ala Ala Lys Asp Asp Val Asp Lys Leu Pro Pro Leu Gln Phe Pro His
115 120 125

Gly Phe Asn Gln Met Tyr Pro Asn Leu Ile Phe Gly Asn Ser Gly Phe
130 135 140

Gly Glu Ser Pro Ser Ser Thr Thr Ser Thr Thr Phe Pro Gly Thr Asn
145 150 155 160

Leu Gly Phe Leu Glu Asn Trp Asp Leu Gly Gly Ser Ser Arg Thr Arg
165 170 175

Ala Arg Leu Thr Asp Thr Thr Thr Thr Gln Arg Glu Ser Phe Asp Leu
180 185 190

Asp Lys Gly Lys Trp Ile Lys Asn Asp Glu Asn Ser Asn Gln Asp His
195 200 205

Gln Gly Phe Asn Thr Asn His Gln Gln Gln Phe Pro Leu Thr Asn Pro
 210 215 220

Tyr Asn Asn Thr Ser Ala Tyr Tyr Asn Leu Gly His Leu Gln Gln Ser
 225 230 235 240

Leu Asp Gln Ser Gly Asn Asn Val Thr Val Ala Ile Ser Asn Val Ala
 245 250 255

Ala Asn Asn Asn Asn Asn Leu Asn Leu His Pro Pro Ser Ser Ser Ala
 260 265 270

Gly Asp Gly Ser Gln Leu Phe Phe Gly Pro Thr Pro Pro Ala Met Ser
 275 280 285

Ser Leu Phe Pro Thr Tyr Pro Ser Phe Leu Gly Ala Ser His His His
 290 295 300

His Val Val Asp Gly Ala Gly His Leu Gln Leu Phe Ser Ser Asn Ser
 305 310 315 320

Asn Thr Ala Ser Gln Gln His Met Met Pro Gly Asn Thr Ser Leu Ile
 325 330 335

Arg Pro Phe His His Leu Met Ser Ser Asn His Asp Thr Asp His His
 340 345 350

Ser Ser Asp Asn Glu Ser Asp Ser
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 aac cgt tta tcc ggt tta ccc gat caa cct tct tcg cat agc ttc act
 96
 Asn Arg Leu Ser Gly Leu Pro Asp Gln Pro Ser Ser His Ser Phe Thr
 20 25 30
 ccg gta aca cta tac gac ggt ttc aat tac aat ctc tcc tcc gat cat
 144
 Pro Val Thr Leu Tyr Asp Gly Phe Asn Tyr Asn Leu Ser Ser Asp His
 35 40 45

ata aac acc gtt gta gca gcg ccg gag aat tca gtt ttt atc cgg gaa
 192
 Ile Asn Thr Val Val Ala Ala Pro Glu Asn Ser Val Phe Ile Arg Glu
 50 55 60

gaa gaa gaa gaa gag gat cca gct gat gat ttc gat ttc tct gac gct
 240
 Glu Glu Glu Glu Glu Asp Pro Ala Asp Asp Phe Asp Phe Ser Asp Ala
 65 70 75 80

gtt tta gga tac att agt cag atg ttg aat gag gaa gac atg gat gat
 288
 Val Leu Gly Tyr Ile Ser Gln Met Leu Asn Glu Glu Asp Met Asp Asp
 85 90 95

aaa gtc tgc atg ctt caa gag tct cta gat ctc gaa gct gct gag aga
 336
 Lys Val Cys Met Leu Gln Glu Ser Leu Asp Leu Glu Ala Ala Glu Arg
 100 105 110

tcg tta tac gaa gct att ggt aag aag tat cct cca tct cca gaa cga
 384
 Ser Leu Tyr Glu Ala Ile Gly Lys Lys Tyr Pro Pro Ser Pro Glu Arg
 115 120 125

aac tta gct ttc gct gaa cga aac agc gag aat ctt gac cgt gtg gtt
 432
 Asn Leu Ala Phe Ala Glu Arg Asn Ser Glu Asn Leu Asp Arg Val Val
 130 135 140

cca gga aac tac act gga gga gat tgt ata ggt ttt ggg aac ggt gga
 480
 Pro Gly Asn Tyr Thr Gly Gly Asp Cys Ile Gly Phe Gly Asn Gly Gly
 145 150 155 160

atc aag cct ttg agt agt ggt ttt act ttg gat ttt cga aat cct cag
 528
 Ile Lys Pro Leu Ser Ser Gly Phe Thr Leu Asp Phe Arg Asn Pro Gln
 165 170 175

agt tgt tct tcg att cta agt gtt cca caa tct aat ggt tta att act
 576
 Ser Cys Ser Ser Ile Leu Ser Val Pro Gln Ser Asn Gly Leu Ile Thr
 180 185 190

atc tac gga gat gga att gat gaa tcg tcg aag aac aat cgg gag aat
 624
 Ile Tyr Gly Asp Gly Ile Asp Glu Ser Ser Lys Asn Asn Arg Glu Asn
 195 200 205

cat caa tct gtt tgg ttg ttt agg cgt gag att gaa gaa gct aat agg
 672
 His Gln Ser Val Trp Leu Phe Arg Arg Glu Ile Glu Glu Ala Asn Arg
 210 215 220

ttt aat cct gaa gaa aac gag ttg att gtg aat ttc aga gag gag aat
 720
 Phe Asn Pro Glu Glu Asn Glu Leu Ile Val Asn Phe Arg Glu Glu Asn
 225 230 235 240

tgt gtg agc aaa gca agg aag aac tct agc cgt gat gag att tgt gtt
 768
 Cys Val Ser Lys Ala Arg Lys Asn Ser Ser Arg Asp Glu Ile Cys Val
 245 250 255

gaa gaa gag agg agt agt aaa tta cct gca gtg ttt ggt gag gat att
 816
 Glu Glu Glu Arg Ser Ser Lys Leu Pro Ala Val Phe Gly Glu Asp Ile
 260 265 270

ttg agg tca gat gtt gta gat aag atc ttg gtt cat gta cca gga gga
 864
 Leu Arg Ser Asp Val Val Asp Lys Ile Leu Val His Val Pro Gly Gly
 275 280 285

gag agc atg aag gag ttt aat gcg ttg cgt gac gtt ttg aag aaa gga
 912
 Glu Ser Met Lys Glu Phe Asn Ala Leu Arg Asp Val Leu Lys Lys Gly
 290 295 300

gtg gag aag aag aaa gct tca gat gct caa ggt ggg aag aga cga gcc
 960
 Val Glu Lys Lys Lys Ala Ser Asp Ala Gln Gly Gly Lys Arg Arg Ala
 305 310 315 320

aga gga aga gga cgt gga aga gga aga gga gga gga gga gga gga gga
 1008
 Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Gly Gly Gly Gly Gln Asn
 325 330 335

ggg aaa aaa gaa gtt gtg gat ttg aga agt tta ttg ata cat tgt gct
 1056
 Gly Lys Lys Glu Val Val Asp Leu Arg Ser Leu Leu Ile His Cys Ala
 340 345 350

caa gct gtt gca gct gat gat cgt agg tgt gca ggt cag ttg tta aaa
 1104
 Gln Ala Val Ala Ala Asp Asp Arg Arg Cys Ala Gly Gln Leu Leu Lys
 355 360 365

cag ata aga ttg cat tct acg ccg ttt ggt gat ggg aat cag agg ttg
 1152
 Gln Ile Arg Leu His Ser Thr Pro Phe Gly Asp Gly Asn Gln Arg Leu
 370 375 380

gct cat tgt ttt gct aat ggt ctc gag gcg agg tta gcc ggt act gga
 1200
 Ala His Cys Phe Ala Asn Gly Leu Glu Ala Arg Leu Ala Gly Thr Gly
 385 390 395 400

agc cag att tac aaa ggg att gtg agt aaa ccg aga tcc gct gca gct
 1248
 Ser Gln Ile Tyr Lys Gly Ile Val Ser Lys Pro Arg Ser Ala Ala Ala
 405 410 415

gtg ttg aag gct cac cag ctt ttt ctt gcg tgt tgt cct ttt aga aag
 1296
 Val Leu Lys Ala His Gln Leu Phe Leu Ala Cys Cys Pro Phe Arg Lys
 420 425 430

ctc tct tat ttc ata act aat aag acg ata cgt gat ctt gtt ggg aac
 1344
 Leu Ser Tyr Phe Ile Thr Asn Lys Thr Ile Arg Asp Leu Val Gly Asn
 435 440 445
 tct cag cgc gtt cat gtt att gat ttt ggt att ctt tac ggt ttc caa
 1392
 Ser Gln Arg Val His Val Ile Asp Phe Gly Ile Leu Tyr Gly Phe Gln
 450 455 460
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 1440
 Trp Pro Thr Leu Ile His Arg Phe Ser Met Tyr Gly Ser Pro Lys Val
 465 470 475 480
 agg atc acc ggg att gag ttt ccg cag ccc ggg ttt cgt ccg gca cag
 1488
 Arg Ile Thr Gly Ile Glu Phe Pro Gln Pro Gly Phe Arg Pro Ala Gln
 485 490 495
 cgg gtt gaa gaa act ggt caa agg tta gca gcg tat gcc aaa ctc ttt
 1536
 Arg Val Glu Glu Thr Gly Gln Arg Leu Ala Ala Tyr Ala Lys Leu Phe
 500 505 510
 ggg gtg cca ttt gag tat aaa gca att gct aag aag tgg gat gca att
 1584
 Gly Val Pro Phe Glu Tyr Lys Ala Ile Ala Lys Lys Trp Asp Ala Ile
 515 520 525
 caa ctt gaa gat ctt gat atc gac agg gat gag att act gtt gtt aat
 1632
 Gln Leu Glu Asp Leu Asp Ile Asp Arg Asp Glu Ile Thr Val Val Asn
 530 535 540
 tgc ctg tac cgg gct gag aat ttg cat gat gag tca gtc aaa gta gaa
 1680
 Cys Leu Tyr Arg Ala Glu Asn Leu His Asp Glu Ser Val Lys Val Glu
 545 550 555 560
 agt tgt aga gac act gtt ctc aat ttg atc ggg aag atc aat cct gat
 1728
 Ser Cys Arg Asp Thr Val Leu Asn Leu Ile Gly Lys Ile Asn Pro Asp
 565 570 575
 ctc ttt gtc ttt ggc att gtg aat ggt gca tac aac gca ccg ttt ttc
 1776
 Leu Phe Val Phe Gly Ile Val Asn Gly Ala Tyr Asn Ala Pro Phe Phe
 580 585 590
 gta aca cgg ttt cgc gaa gct cta ttt cat ttc tcc tcg att ttt gac
 1824
 Val Thr Arg Phe Arg Glu Ala Leu Phe His Phe Ser Ser Ile Phe Asp
 595 600 605
 atg ctt gag aca att gtg cca cga gaa gac gaa gag agg atg ttc ctt
 1872
 Met Leu Glu Thr Ile Val Pro Arg Glu Asp Glu Glu Arg Met Phe Leu
 610 615 620

gag atg gag gtc ttt ggg aga gag gca ctg aat gtg att gct tgc gaa
1920

Glu Met Glu Val Phe Gly Arg Glu Ala Leu Asn Val Ile Ala Cys Glu
625 630 635 640

ggt tgg gaa aga gtg gag agg cct gag aca tac aag cag tgg cac gta
1968

Gly Trp Glu Arg Val Glu Arg Pro Glu Thr Tyr Lys Gln Trp His Val
645 650 655

cgg gct atg agg tca ggg ttg gtg cag gtt cca ttt gac cca agc att
2016

Arg Ala Met Arg Ser Gly Leu Val Gln Val Pro Phe Asp Pro Ser Ile
660 665 670

atg aag aca tcg ctg cat aag gtc cac aca ttc tac cac aag gat ttt
2064

Met Lys Thr Ser Leu His Lys Val His Thr Phe Tyr His Lys Asp Phe
675 680 685

gtg atc gat caa gat aac cgg tgg ctc ttg caa ggc tgg aag gga aga
2112

Val Ile Asp Gln Asp Asn Arg Trp Leu Leu Gln Gly Trp Lys Gly Arg
690 695 700

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2157

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705 710 715

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336

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Asn Arg Leu Ser Gly Leu Pro Asp Gln Pro Ser Ser His Ser Phe Thr
20 25 30

Pro Val Thr Leu Tyr Asp Gly Phe Asn Tyr Asn Leu Ser Ser Asp His
35 40 45

Ile Asn Thr Val Val Ala Ala Pro Glu Asn Ser Val Phe Ile Arg Glu
50 55 60

Glu Glu Glu Glu Glu Asp Pro Ala Asp Asp Phe Asp Phe Ser Asp Ala
65 70 75 80

Val Leu Gly Tyr Ile Ser Gln Met Leu Asn Glu Glu Asp Met Asp Asp
85 90 95

Lys Val Cys Met Leu Gln Glu Ser Leu Asp Leu Glu Ala Ala Glu Arg
100 105 110

Ser Leu Tyr Glu Ala Ile Gly Lys Lys Tyr Pro Pro Ser Pro Glu Arg
 115 120 125

Asn Leu Ala Phe Ala Glu Arg Asn Ser Glu Asn Leu Asp Arg Val Val
 130 135 140

Pro Gly Asn Tyr Thr Gly Gly Asp Cys Ile Gly Phe Gly Asn Gly Gly
 145 150 155 160

Ile Lys Pro Leu Ser Ser Gly Phe Thr Leu Asp Phe Arg Asn Pro Gln
 165 170 175

Ser Cys Ser Ser Ile Leu Ser Val Pro Gln Ser Asn Gly Leu Ile Thr
 180 185 190

Ile Tyr Gly Asp Gly Ile Asp Glu Ser Ser Lys Asn Asn Arg Glu Asn
 195 200 205

His Gln Ser Val Trp Leu Phe Arg Arg, Glu Ile Glu Glu Ala Asn Arg
 210 215 220

Phe Asn Pro Glu Glu Asn Glu Leu Ile Val Asn Phe Arg Glu Glu Asn
 225 230 235 240

Cys Val Ser Lys Ala Arg Lys Asn Ser Ser Arg Asp Glu Ile Cys Val
 245 250 255

Glu Glu Glu Arg Ser Ser Lys Leu Pro Ala Val Phe Gly Glu Asp Ile
 260 265 270

Leu Arg Ser Asp Val Val Asp Lys Ile Leu Val His Val Pro Gly Gly
 275 280 285

Glu Ser Met Lys Glu Phe Asn Ala Leu Arg Asp Val Leu Lys Lys Gly
 290 295 300

Val Glu Lys Lys Lys Ala Ser Asp Ala Gln Gly Gly Lys Arg Arg Ala
 305 310 315 320

Arg Gly Arg Gly Arg Gly Arg Gly Gly Gly Gly Gly Gln Asn
 325 330 335

Gly Lys Lys Glu Val Val Asp Leu Arg Ser Leu Leu Ile His Cys Ala
 340 345 350

Gln Ala Val Ala Ala Asp Asp Arg Arg Cys Ala Gly Gln Leu Leu Lys
 355 360 365

Gln Ile Arg Leu His Ser Thr Pro Phe Gly Asp Gly Asn Gln Arg Leu
 370 375 380

Ala His Cys Phe Ala Asn Gly Leu Glu Ala Arg Leu Ala Gly Thr Gly
 385 390 395 400

Ser Gln Ile Tyr Lys Gly Ile Val Ser Lys Pro Arg Ser Ala Ala Ala
 405 410 415

Val Leu Lys Ala His Gln Leu Phe Leu Ala Cys Cys Pro Phe Arg Lys
 420 425 430

Leu Ser Tyr Phe Ile Thr Asn Lys Thr Ile Arg Asp Leu Val Gly Asn
 435 440 445

Ser Gln Arg Val His Val Ile Asp Phe Gly Ile Leu Tyr Gly Phe Gln
 450 455 460

Trp Pro Thr Leu Ile His Arg Phe Ser Met Tyr Gly Ser Pro Lys Val
 465 470 475 480

Arg Ile Thr Gly Ile Glu Phe Pro Gln Pro Gly Phe Arg Pro Ala Gln
 485 490 495

Arg Val Glu Glu Thr Gly Gln Arg Leu Ala Ala Tyr Ala Lys Leu Phe
 500 505 510

Gly Val Pro Phe Glu Tyr Lys Ala Ile Ala Lys Lys Trp Asp Ala Ile
 515 520 525

Gln Leu Glu Asp Leu Asp Ile Asp Arg Asp Glu Ile Thr Val Val Asn
 530 535 540

Cys Leu Tyr Arg Ala Glu Asn Leu His Asp Glu Ser Val Lys Val Glu
 545 550 555 560

Ser Cys Arg Asp Thr Val Leu Asn Leu Ile Gly Lys Ile Asn Pro Asp
 565 570 575

Leu Phe Val Phe Gly Ile Val Asn Gly Ala Tyr Asn Ala Pro Phe Phe
 580 585 590

Val Thr Arg Phe Arg Glu Ala Leu Phe His Phe Ser Ser Ile Phe Asp

595 600 605

Met Leu Glu Thr Ile Val Pro Arg Glu Asp Glu Glu Arg Met Phe Leu
610 615 620

Glu Met Glu Val Phe Gly Arg Glu Ala Leu Asn Val Ile Ala Cys Glu
625 630 635 640

Gly Trp Glu Arg Val Glu Arg Pro Glu Thr Tyr Lys Gln Trp His Val
645 650 655

Arg Ala Met Arg Ser Gly Leu Val Gln Val Pro Phe Asp Pro Ser Ile
660 665 670

Met Lys Thr Ser Leu His Lys Val His Thr Phe Tyr His Lys Asp Phe
675 680 685

Val Ile Asp Gln Asp Asn Arg Trp Leu Leu Gln Gly Trp Lys Gly Arg
690 695 700

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705 710 715

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aag aaa ggt ttg tgg aca gta gaa gaa gac aaa atc ctc atg gat tat
96
Lys Lys Gly Leu Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr
20 25 30
gtc aaa gct cat ggc aaa ggt cac tgg aat cgt att gcc aaa aag act
144
Val Lys Ala His Gly Lys Gly His Trp Asn Arg Ile Ala Lys Lys Thr
35 40 45
ggt tta aag aga tgt gga aag agt tgt aga ttg agg tgg atg aat tat
192
Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr
50 55 60
ctc agc cct aat gtg aaa aga ggc aat ttc acc gag caa gaa gag gat
240
Leu Ser Pro Asn Val Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Asp
65 70 75 80

ctt atc att agg ctc cac aag ttg ctt ggt aat agg tgg tct tta att
288

Leu Ile Ile Arg Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile
85 90 95

gct aaa aga gtg ccg ggt cga acg gat aat caa gtg aag aac tat tgg
336

Ala Lys Arg Val Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp
100 105 110

aac acg cat ctt agt aag aaa ctc gga atc aaa gat cag aaa acc aaa
384

Asn Thr His Leu Ser Lys Lys Leu Gly Ile Lys Asp Gln Lys Thr Lys
115 120 125

cag agc aat ggt gat att gtt tat caa atc aat ctc ccg aat cct acc
432

Gln Ser Asn Gly Asp Ile Val Tyr Gln Ile Asn Leu Pro Asn Pro Thr
130 135 140

gaa aca tca gaa gaa acg aaa atc tcg aat att gtc gat aac aat aat
480

Glu Thr Ser Glu Glu Thr Lys Ile Ser Asn Ile Val Asp Asn Asn Asn
145 150 155 160

atc ctc gga gat gaa att caa gaa gat cat caa gga agt aac tac ttg
528

Ile Leu Gly Asp Glu Ile Gln Glu Asp His Gln Gly Ser Asn Tyr Leu
165 170 175

agt tca ctt tgg gtt cat gag gat gag ttt gag ctt agc aca ctc acc
576

Ser Ser Leu Trp Val His Glu Asp Glu Phe Glu Leu Ser Thr Leu Thr
180 185 190

aac atg atg gac ttt ata gat gga cac tgt ttt tga
612

Asn Met Met Asp Phe Ile Asp Gly His Cys Phe
195 200

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Lys Lys Gly Leu Trp Thr Val Glu Glu Asp Lys Ile Leu Met Asp Tyr
20 25 30

Val Lys Ala His Gly Lys Gly His Trp Asn Arg Ile Ala Lys Lys Thr
35 40 45

Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr
50 55 60

Leu Ser Pro Asn Val Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Asp

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cct cca cca cct gga acc acc atc tcc gcc gca gga gga gga gct tct
96
Pro Pro Pro Gly Thr Thr Ile Ser Ala Ala Gly Gly Gly Ala Ser
20 25 30
tac cac cac ctt ctc caa caa caa caa caa cag ctc caa cta ttc tgg
144
Tyr His His Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Leu Phe Trp
35 40 45
acc tac caa cgc caa gag atc gaa caa gtt aac gat ttc aaa aac cat
192
Thr Tyr Gln Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn His
50 55 60
cag ctt cca cta gct agg ata aaa aag atc atg aaa gcc gat gaa gat
240

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Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp
 65 70 75 80
 gtt cgt atg atc tcc gca gaa gca ccg att ctc ttc gcg aaa gct tgt
 288
 Val Arg Met Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys Ala Cys
 85 90 95
 gag ctt ttc att ctc gag ctc acg atc aga tct tgg ctt cac gct gag
 336
 Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala Glu
 100 105 110
 gag aat aaa cgt cgt acg ctt cag aaa aac gat atc gct gct gcg att
 384
 Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Ile
 115 120 125
 act agg act gat atc ttc gat ttc ctt gtt gat att gtt cct aga gat
 432
 Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Asp
 130 135 140
 gag att aag gac gaa gcc gca gtc ctc ggt ggt gga atg gtg gtg gct
 480
 Glu Ile Lys Asp Glu Ala Ala Val Leu Gly Gly Gly Met Val Val Ala
 145 150 155 160
 cct acc gcg agc ggc gtg cct tac tat tat ccg ccg atg gga caa cca
 528
 Pro Thr Ala Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro
 165 170 175
 gct ggt cct gga ggg atg atg att ggg aga cca gct atg gat ccg aat
 576
 Ala Gly Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Asn
 180 185 190
 ggt gtt tat gtc cag cct ccg tct cag gcg tgg cag agt gtt tgg cag
 624
 Gly Val Tyr Val Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln
 195 200 205
 act tcg acg ggg acg gga gat gat gtc tct tat ggt agt ggt gga agt
 672
 Thr Ser Thr Gly Thr Gly Asp Asp Val Ser Tyr Gly Ser Gly Gly Ser
 210 215 220
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 225 230
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Pro Pro Pro Pro Gly Thr Thr Ile Ser Ala Ala Gly Gly Gly Ala Ser
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Tyr His His Leu Leu Gln Gln Gln Gln Gln Gln Leu Gln Leu Phe Trp
35 40 45

Thr Tyr Gln Arg Gln Glu Ile Glu Gln Val Asn Asp Phe Lys Asn His
50 55 60

Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp
65 70 75 80

Val Arg Met Ile Ser Ala Glu Ala Pro Ile Leu Phe Ala Lys Ala Cys
85 90 95

Glu Leu Phe Ile Leu Glu Leu Thr Ile Arg Ser Trp Leu His Ala Glu
100 105 110

Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile Ala Ala Ala Ile
115 120 125

Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile Val Pro Arg Asp
130 135 140

Glu Ile Lys Asp Glu Ala Ala Val Leu Gly Gly Gly Met Val Val Ala
145 150 155 160

Pro Thr Ala Ser Gly Val Pro Tyr Tyr Tyr Pro Pro Met Gly Gln Pro
165 170 175

Ala Gly Pro Gly Gly Met Met Ile Gly Arg Pro Ala Met Asp Pro Asn
180 185 190

Gly Val Tyr Val Gln Pro Pro Ser Gln Ala Trp Gln Ser Val Trp Gln
195 200 205

Thr Ser Thr Gly Thr Gly Asp Asp Val Ser Tyr Gly Ser Gly Gly Ser
210 215 220

Ser Gly Gln Gly Asn Leu Asp Gly Gln Gly
225 230

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atgattgata gggaaagaga gagagatgaa agaaagtaaa atatataata gattattagg
120

acacgagtgt catcttttga tttgtgtctt gtgtgctctc tctttcttct cttcctcgaa
180

tgatcatctt tatataaccc tactctcttt ctcttttccc attctttcat atcattctcc
240

ctttctctct cgggacttga tctctctttc cagtaacctt ttcccaggga gcactgtcaa
300

atcttgtcca ctctttgatc ttatctcgat ctctttctct ttctagtctt gtgtagtctt
360

caaacttggt atgttatcta tatagtaatc acgagagaga atcatacaat agctgaaaca
420

taaagctttc ttagaagctt taaaaaggtc tcactctggat tatcctgttt aatttctaga
480

gtttcttcag gcagattatt aaccgatcaa gaagacaaac atg aat tca ttt tcc
535

Met Asn Ser Phe Ser
1 5

cac gtc cct ccg ggt ttt aga ttt cac ccg aca gat gaa gaa ctt gta
583

His Val Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val
10 15 20

gac tac tac ctg agg aaa aaa gtc gca tcg aag aga ata gaa att gat
631

Asp Tyr Tyr Leu Arg Lys Lys Val Ala Ser Lys Arg Ile Glu Ile Asp
25 30 35

ttc ata aag gac att gat ctt tac aag att gag cca tgg gac ctt caa
679

Phe Ile Lys Asp Ile Asp Leu Tyr Lys Ile Glu Pro Trp Asp Leu Gln
40 45 50

gag ttg tgc aaa att ggg cat gaa gag cag agt gat tgg tac ttc ttt
727

Glu Leu Cys Lys Ile Gly His Glu Glu Gln Ser Asp Trp Tyr Phe Phe
55 60 65

agc cat aaa gac aag aag tat ccc aca ggg act cga acc aat aga gca
775

Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr Arg Thr Asn Arg Ala
70 75 80 85

aca aaa gca ggg ttt tgg aaa gcc acc gga aga gat aag gct atc tat
823

Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg Asp Lys Ala Ile Tyr
90 95 100

ttg agg cat agt cta att ggc atg agg aaa aca ctt gtg ttt tac aag
871

Leu Arg His Ser Leu Ile Gly Met Arg Lys Thr Leu Val Phe Tyr Lys
 105 110 115
 gga aga gcc cca aat gga caa aag tct gat tgg atc atg cac gaa tac
 919
 Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp Ile Met His Glu Tyr
 120 125 130
 cgc tta gaa acc gat gaa aac gga act cct cag gaa gaa gga tgg gtt
 967
 Arg Leu Glu Thr Asp Glu Asn Gly Thr Pro Gln Glu Glu Gly Trp Val
 135 140 145
 gtg tgt agg gtt ttc aag aag aga ttg gct gca gtt aga cga atg gga
 1015
 Val Cys Arg Val Phe Lys Lys Arg Leu Ala Ala Val Arg Arg Met Gly
 150 155 160 165
 gat tac gac tca tcc cct tca cat tgg tac gat gat caa ctt tct ttt
 1063
 Asp Tyr Asp Ser Ser Pro Ser His Trp Tyr Asp Asp Gln Leu Ser Phe
 170 175 180
 atg gcc tcc gag ctc gag aca aac ggt caa cga cgg att ctc ccc aat
 1111
 Met Ala Ser Glu Leu Glu Thr Asn Gly Gln Arg Arg Ile Leu Pro Asn
 185 190 195
 cat cat cag cag cag cag cac gag cac caa caa cat atg cca tat ggc
 1159
 His His Gln Gln Gln Gln His Glu His Gln Gln His Met Pro Tyr Gly
 200 205 210
 ctc aat gca tct gct tac gct ctc aac aac cct aac ttg caa tgc aag
 1207
 Leu Asn Ala Ser Ala Tyr Ala Leu Asn Asn Pro Asn Leu Gln Cys Lys
 215 220 225
 caa gag cta gaa cta cac tac aac cac ctg caa tca aat atc gcg cat
 1255
 Gln Glu Leu Glu Leu His Tyr Asn His Leu Gln Ser Asn Ile Ala His
 230 235 240 245
 gag gaa caa ttg aat caa gga aat cag aac ttc agc tct cta tac atg
 1303
 Glu Glu Gln Leu Asn Gln Gly Asn Gln Asn Phe Ser Ser Leu Tyr Met
 250 255 260
 aac agc ggc aac gag caa gtg atg gac caa gtc aca gac tgg aga gtt
 1351
 Asn Ser Gly Asn Glu Gln Val Met Asp Gln Val Thr Asp Trp Arg Val
 265 270 275
 ctc gat aaa ttt gtt gct tct cag cta agc aac gag gag gct gcc aca
 1399
 Leu Asp Lys Phe Val Ala Ser Gln Leu Ser Asn Glu Glu Ala Ala Thr
 280 285 290
 gct tct gca tct ata cag aat aat gcc aag gac aca agc aat gct gag
 1447
 Ala Ser Ala Ser Ile Gln Asn Asn Ala Lys Asp Thr Ser Asn Ala Glu

295 300 305
 tac caa gtt gat gaa gaa aaa gat ccg aaa agg gct tca gac atg gga
 1495
 Tyr Gln Val Asp Glu Glu Lys Asp Pro Lys Arg Ala Ser Asp Met Gly
 310 315 320 325
 gaa gaa tat act gct tct act tct tcg agt tgt cag att gat cta tgg
 1543
 Glu Glu Tyr Thr Ala Ser Thr Ser Ser Ser Cys Gln Ile Asp Leu Trp
 330 335 340
 aag tga gctgaaagag aagacatata aatgcatata tacatatata tatatacgta
 1599
 Lys
 cacacgaaca ctaatcaagt gtagatgatg atgatggtac agatttatat ttgctttgat
 1659
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 1719
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 Arg Ile Glu Ile Asp Phe Ile Lys Asp Ile Asp Leu Tyr Lys Ile Glu
 35 40 45
 Pro Trp Asp Leu Gln Glu Leu Cys Lys Ile Gly His Glu Glu Gln Ser
 50 55 60
 Asp Trp Tyr Phe Phe Ser His Lys Asp Lys Lys Tyr Pro Thr Gly Thr
 65 70 75 80
 Arg Thr Asn Arg Ala Thr Lys Ala Gly Phe Trp Lys Ala Thr Gly Arg
 85 90 95
 Asp Lys Ala Ile Tyr Leu Arg His Ser Leu Ile Gly Met Arg Lys Thr
 100 105 110

Leu Val Phe Tyr Lys Gly Arg Ala Pro Asn Gly Gln Lys Ser Asp Trp
 115 120 125

Ile Met His Glu Tyr Arg Leu Glu Thr Asp Glu Asn Gly Thr Pro Gln
 130 135 140

Glu Glu Gly Trp Val Val Cys Arg Val Phe Lys Lys Arg Leu Ala Ala
 145 150 155 160

Val Arg Arg Met Gly Asp Tyr Asp Ser Ser Pro Ser His Trp Tyr Asp
 165 170 175

Asp Gln Leu Ser Phe Met Ala Ser Glu Leu Glu Thr Asn Gly Gln Arg
 180 185 190

Arg Ile Leu Pro Asn His His Gln Gln Gln Gln His Glu His Gln Gln
 195 200 205

His Met Pro Tyr Gly Leu Asn Ala Ser Ala Tyr Ala Leu Asn Asn Pro
 210 215 220

Asn Leu Gln Cys Lys Gln Glu Leu Glu Leu His Tyr Asn His Leu Gln
 225 230 235 240

Ser Asn Ile Ala His Glu Glu Gln Leu Asn Gln Gly Asn Gln Asn Phe
 245 250 255

Ser Ser Leu Tyr Met Asn Ser Gly Asn Glu Gln Val Met Asp Gln Val
 260 265 270

Thr Asp Trp Arg Val Leu Asp Lys Phe Val Ala Ser Gln Leu Ser Asn
 275 280 285

Glu Glu Ala Ala Thr Ala Ser Ala Ser Ile Gln Asn Asn Ala Lys Asp
 290 295 300

Thr Ser Asn Ala Glu Tyr Gln Val Asp Glu Glu Lys Asp Pro Lys Arg
 305 310 315 320

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 325 330 335

Gln Ile Asp Leu Trp Lys
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tttgttttca aaagaaacga ttttttagtag ccgccgggga atcaggaga atg gtg tct
 118

Met Val Ser
 1

ccg gag aat acg aac tgg.ctt agt gat tac cct ttg att gaa ggt gct
 166

Pro Glu Asn Thr Asn Trp Leu Ser Asp Tyr Pro Leu Ile Glu Gly Ala
 5 10 15

ttc tct gat cag aac ccc act ttc cct tgg cag ata gat ggc tca gct
 214

Phe Ser Asp Gln Asn Pro Thr Phe Pro Trp Gln Ile Asp Gly Ser Ala
 20 25 30 35

act gtc agt gtt gaa gtg gat ggc ttc ctt tgt gat gca gat gtg atc
 262

Thr Val Ser Val Glu Val Asp Gly Phe Leu Cys Asp Ala Asp Val Ile
 40 45 50

aaa gaa cca agt tca agg aag agg atc aaa act gaa tct tgc act ggt
 310

Lys Glu Pro Ser Ser Arg Lys Arg Ile Lys Thr Glu Ser Cys Thr Gly
 55 60 65

tct aac tgc aaa gct tgt agg gag aaa caa aga cgt gat aga cta aat
 358

Ser Asn Ser Lys Ala Cys Arg Glu Lys Gln Arg Arg Asp Arg Leu Asn
 70 75 80

gac aag ttt acg gag ttg agt tcc gta ttg gaa cct ggg aga act cca
 406

Asp Lys Phe Thr Glu Leu Ser Ser Val Leu Glu Pro Gly Arg Thr Pro
 85 90 95

aaa aca gac aag gtt gct att atc aat gat gca att cgc atg gtg aat
 454

Lys Thr Asp Lys Val Ala Ile Ile Asn Asp Ala Ile Arg Met Val Asn
 100 105 110 115

caa gca aga gat gaa gcg cag aaa cta aag gac ttg aac tca agc ctc
 502

Gln Ala Arg Asp Glu Ala Gln Lys Leu Lys Asp Leu Asn Ser Ser Leu
 120 125 130

cag gag aaa atc aag gag ttg aag gat gag aag aac gag ctg cgt gat
 550

Gln Glu Lys Ile Lys Glu Leu Lys Asp Glu Lys Asn Glu Leu Arg Asp
 135 140 145

gag aaa cag aag ctt aag gtc gag aag gag aga atc gat cag caa ctg
 598

Glu Lys Gln Lys Leu Lys Val Glu Lys Glu Arg Ile Asp Gln Gln Leu
 150 155 160

aaa gct att aag aca cag cct cag cct caa cct tgt ttc tta cca aat
646

Lys Ala Ile Lys Thr Gln Pro Gln Pro Gln Pro Cys Phe Leu Pro Asn
165 170 175

ccg caa aca ctc tct caa gct caa gct cct gga agc aag ctt gtc cct
694

Pro Gln Thr Leu Ser Gln Ala Gln Ala Pro Gly Ser Lys Leu Val Pro
180 185 190 195

ttc aca act tat ccc ggc ttt gca atg tgg caa ttc atg cct cct gct
742

Phe Thr Thr Tyr Pro Gly Phe Ala Met Trp Gln Phe Met Pro Pro Ala
200 205 210

gct gtt gat acc tca cag gac cat gtc ctt cgt cct cca gtt gct taa
790

Ala Val Asp Thr Ser Gln Asp His Val Leu Arg Pro Pro Val Ala
215 220 225

agctgctgct tctctctact actattaacg gttctgtaag attacttctt acgcgctttt
850

ttctgatgta atgattctca cattctgtga ttggtgacat agtcactgc aacttaaaat
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gtaaaattga aataagcttg cactaaaaat caaatctcat tgtgcaaaaa gttggataat
970

ttggaaatca ttgttttaca aaaaaaaaaac cccccgag
1008

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20 25 30

Gly Ser Ala Thr Val Ser Val Glu Val Asp Gly Phe Leu Cys Asp Ala
35 40 45

Asp Val Ile Lys Glu Pro Ser Ser Arg Lys Arg Ile Lys Thr Glu Ser
50 55 60

Cys Thr Gly Ser Asn Ser Lys Ala Cys Arg Glu Lys Gln Arg Arg Asp
65 70 75 80

Arg Leu Asn Asp Lys Phe Thr Glu Leu Ser Ser Val Leu Glu Pro Gly
85 90 95

Arg Thr Pro Lys Thr Asp Lys Val Ala Ile Ile Asn Asp Ala Ile Arg
 100 105 110

Met Val Asn Gln Ala Arg Asp Glu Ala Gln Lys Leu Lys Asp Leu Asn
 115 120 125

Ser Ser Leu Gln Glu Lys Ile Lys Glu Leu Lys Asp Glu Lys Asn Glu
 130 135 140

Leu Arg Asp Glu Lys Gln Lys Leu Lys Val Glu Lys Glu Arg Ile Asp
 145 150 155 160

Gln Gln Leu Lys Ala Ile Lys Thr Gln Pro Gln Pro Gln Pro Cys Phe
 165 170 175

Leu Pro Asn Pro Gln Thr Leu Ser Gln Ala Gln Ala Pro Gly Ser Lys
 180 185 190

Leu Val Pro Phe Thr Thr Tyr Pro Gly Phe Ala Met Trp Gln Phe Met
 195 200 205

Pro Pro Ala Ala Val Asp Thr Ser Gln Asp His Val Leu Arg Pro Pro
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Val Ala
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 112

Met Asn Leu Phe Thr Arg Ile
 1 5

tca tct cgg act aag aag gcc aat ctt tac tac gta acc cta gtt gct
 160

Ser Ser Arg Thr Lys Lys Ala Asn Leu Tyr Tyr Val Thr Leu Val Ala
 10 15 20

ctt ctc tgc atc gct agc tac ctt ctc ggt att tgg caa aac acg gcg
 208

Leu Leu Cys Ile Ala Ser Tyr Leu Leu Gly Ile Trp Gln Asn Thr Ala
 25 30 35

gtt aat cca cgc gcc gcc ttc gat gat tca gac ggt aca ccg tgc gag
 256

Val Asn Pro Arg Ala Ala Phe Asp Asp Ser Asp Gly Thr Pro Cys Glu

40 45 50 55
 gga ttc acc aga cct aat tct acg aaa gat ctc gac ttc gac gcg cat
 304
 Gly Phe Thr Arg Pro Asn Ser Thr Lys Asp Leu Asp Phe Asp Ala His
 60 65 70
 cac aac att caa gat cca cct ccg gtg acg gaa acc gcc gtt agt ttc
 352
 His Asn Ile Gln Asp Pro Pro Pro Val Thr Glu Thr Ala Val Ser Phe
 75 80 85
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 Pro Ser Cys Ala Ala Ala Leu Ser Glu His Thr Pro Cys Glu Asp Ala
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 448
 Lys Arg Ser Leu Lys Phe Ser Arg Glu Arg Leu Glu Tyr Arg Gln Arg
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 496
 His Cys Pro Glu Arg Glu Glu Ile Leu Lys Cys Arg Ile Pro Ala Pro
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 Tyr Gly Tyr Lys Thr Pro Phe Arg Trp Pro Ala Ser Arg Asp Val Ala
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 Trp Phe Ala Asn Val Pro His Thr Glu Leu Thr Val Glu Lys Lys Asn
 155 160 165
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 Gln Asn Trp Val Arg Tyr Glu Asn Asp Arg Phe Trp Phe Pro Gly Gly
 170 175 180
 ggt acg atg ttt cca cgt ggc gct gat gct tac att gat gat atc gga
 688
 Gly Thr Met Phe Pro Arg Gly Ala Asp Ala Tyr Ile Asp Asp Ile Gly
 185 190 195
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 736
 Arg Leu Ile Asp Leu Ser Asp Gly Ser Ile Arg Thr Ala Ile Asp Thr
 200 205 210 215
 ggt tgc ggg gtg gct agc ttc ggt gca tat ctt tta tca aga aac att
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 Gly Cys Gly Val Ala Ser Phe Gly Ala Tyr Leu Leu Ser Arg Asn Ile
 220 225 230
 aca acg atg tca ttt gca cca aga gac aca cac gaa gct caa gtc cag
 832
 Thr Thr Met Ser Phe Ala Pro Arg Asp Thr His Glu Ala Gln Val Gln
 235 240 245

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 Phe Ala Leu Glu Arg Gly Val Pro Ala Met Ile Gly Ile Met Ala Thr
 250 255 260

atc cgc cta ccg tac cct tct aga gcc ttt gat tta gca cat tgc tct
 928
 Ile Arg Leu Pro Tyr Pro Ser Arg Ala Phe Asp Leu Ala His Cys Ser
 265 270 275

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 976
 Arg Cys Leu Ile Pro Trp Gly Gln Asn Asp Gly Ala Tyr Leu Met Glu
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 1024
 Val Asp Arg Val Leu Arg Pro Gly Gly Tyr Trp Ile Leu Ser Gly Pro
 300 305 310

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 Pro Ile Asn Trp Gln Lys Arg Trp Lys Gly Trp Glu Arg Thr Met Asp
 315 320 325

gat ttg aat gca gag cag act cag atc gag cag gtc gcg aga agc ttg
 1120
 Asp Leu Asn Ala Glu Gln Thr Gln Ile Glu Gln Val Ala Arg Ser Leu
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 Cys Trp Lys Lys Val Val Gln Arg Asp Asp Leu Ala Ile Trp Gln Lys
 345 350 355

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 Pro Phe Asn His Ile Asp Cys Lys Lys Thr Arg Glu Val Leu Lys Asn
 360 365 370 375

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 1264
 Pro Glu Phe Cys Arg His Asp Gln Asp Pro Asp Met Ala Trp Tyr Thr
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 Lys Met Asp Ser Cys Leu Thr Pro Leu Pro Glu Val Asp Asp Ala Glu
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 Asp Leu Lys Thr Val Ala Gly Gly Lys Val Glu Lys Trp Pro Ala Arg
 410 415 420

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 1408
 Leu Asn Ala Ile Pro Pro Arg Val Asn Lys Gly Ala Leu Glu Glu Ile
 425 430 435

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 Thr Pro Glu Ala Phe Leu Glu Asn Thr Lys Leu Trp Lys Gln Arg Val
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 1504
 Ser Tyr Tyr Lys Lys Leu Asp Tyr Gln Leu Gly Glu Thr Gly Arg Tyr
 460 465 470
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 1552
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 475 480 485
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 490 495 500
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 Lys Leu Asn Thr Leu Gly Val Ile Tyr Glu Arg Gly Leu Ile Gly Thr
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 1744
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 1792
 Pro Glu Glu Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Gly Gly
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 Gly Val Ile Ile Arg Asp Asp Val Asp Val Leu Ile Lys Val Lys Glu
 570 575 580
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 1888
 Leu Thr Lys Gly Leu Glu Trp Glu Gly Arg Ile Ala Asp His Glu Lys
 585 590 595
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 1936
 Gly Pro His Glu Arg Glu Lys Ile Tyr Tyr Ala Val Lys Gln Tyr Trp
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 acc gtt cct gcg cct gat gaa gat aaa aac aac act agt gct ctc tcc
 1984
 Thr Val Pro Ala Pro Asp Glu Asp Lys Asn Asn Thr Ser Ala Leu Ser
 620 625 630

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2079

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35 40 45

Ser Asp Gly Thr Pro Cys Glu Gly Phe Thr Arg Pro Asn Ser Thr Lys
50 55 60

Asp Leu Asp Phe Asp Ala His His Asn Ile Gln Asp Pro Pro Pro Val
65 70 75 80

Thr Glu Thr Ala Val Ser Phe Pro Ser Cys Ala Ala Ala Leu Ser Glu
85 90 95

His Thr Pro Cys Glu Asp Ala Lys Arg Ser Leu Lys Phe Ser Arg Glu
100 105 110

Arg Leu Glu Tyr Arg Gln Arg His Cys Pro Glu Arg Glu Glu Ile Leu
115 120 125

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130 135 140

Pro Ala Ser Arg Asp Val Ala Trp Phe Ala Asn Val Pro His Thr Glu
145 150 155 160

Leu Thr Val Glu Lys Lys Asn Gln Asn Trp Val Arg Tyr Glu Asn Asp
165 170 175

Arg Phe Trp Phe Pro Gly Gly Gly Thr Met Phe Pro Arg Gly Ala Asp
180 185 190

Ala Tyr Ile Asp Asp Ile Gly Arg Leu Ile Asp Leu Ser Asp Gly Ser
195 200 205

Ile Arg Thr Ala Ile Asp Thr Gly Cys Gly Val Ala Ser Phe Gly Ala
 210 215 220

Tyr Leu Leu Ser Arg Asn Ile Thr Thr Met Ser Phe Ala Pro Arg Asp
 225 230 235 240

Thr His Glu Ala Gln Val Gln Phe Ala Leu Glu Arg Gly Val Pro Ala
 245 250 255

Met Ile Gly Ile Met Ala Thr Ile Arg Leu Pro Tyr Pro Ser Arg Ala
 260 265 270

Phe Asp Leu Ala His Cys Ser Arg Cys Leu Ile Pro Trp Gly Gln Asn
 275 280 285

Asp Gly Ala Tyr Leu Met Glu Val Asp Arg Val Leu Arg Pro Gly Gly
 290 295 300

Tyr Trp Ile Leu Ser Gly Pro Pro Ile Asn Trp Gln Lys Arg Trp Lys
 305 310 315 320

Gly Trp Glu Arg Thr Met Asp Asp Leu Asn Ala Glu Gln Thr Gln Ile
 325 330 335

Glu Gln Val Ala Arg Ser Leu Cys Trp Lys Lys Val Val Gln Arg Asp
 340 345 350

Asp Leu Ala Ile Trp Gln Lys Pro Phe Asn His Ile Asp Cys Lys Lys
 355 360 365

Thr Arg Glu Val Leu Lys Asn Pro Glu Phe Cys Arg His Asp Gln Asp
 370 375 380

Pro Asp Met Ala Trp Tyr Thr Lys Met Asp Ser Cys Leu Thr Pro Leu
 385 390 395 400

Pro Glu Val Asp Asp Ala Glu Asp Leu Lys Thr Val Ala Gly Gly Lys
 405 410 415

Val Glu Lys Trp Pro Ala Arg Leu Asn Ala Ile Pro Pro Arg Val Asn
 420 425 430

Lys Gly Ala Leu Glu Glu Ile Thr Pro Glu Ala Phe Leu Glu Asn Thr
 435 440 445

Lys Leu Trp Lys Gln Arg Val Ser Tyr Tyr Lys Lys Leu Asp Tyr Gln
 450 455 460

Leu Gly Glu Thr Gly Arg Tyr Arg Asn Leu Val Asp Met Asn Ala Tyr
 465 470 475 480

Leu Gly Gly Phe Ala Ala Ala Leu Ala Asp Asp Pro Val Trp Val Met
 485 490 495

Asn Val Val Pro Val Glu Ala Lys Leu Asn Thr Leu Gly Val Ile Tyr
 500 505 510

Glu Arg Gly Leu Ile Gly Thr Tyr Gln Asn Trp Cys Glu Ala Met Ser
 515 520 525

Thr Tyr Pro Arg Thr Tyr Asp Phe Ile His Ala Asp Ser Val Phe Thr
 530 535 540

Leu Tyr Gln Gly Gln Cys Glu Pro Glu Glu Ile Leu Leu Glu Met Asp
 545 550 555 560

Arg Ile Leu Arg Pro Gly Gly Gly Val Ile Ile Arg Asp Asp Val Asp
 565 570 575

Val Leu Ile Lys Val Lys Glu Leu Thr Lys Gly Leu Glu Trp Glu Gly
 580 585 590

Arg Ile Ala Asp His Glu Lys Gly Pro His Glu Arg Glu Lys Ile Tyr
 595 600 605

Tyr Ala Val Lys Gln Tyr Trp Thr Val Pro Ala Pro Asp Glu Asp Lys
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 120

cogtcatcat catttttccc accgacaaca atctctcgga gtttggtat tattacttct
 180

ctcatcaacc aattgtacca ctgatctcc cagattcctt cattatctct atcaata
237

atg gcg ttg aag tct agt tct gct gat ggt aaa acc aga agc tct gtt
285
Met Ala Leu Lys Ser Ser Ser Ala Asp Gly Lys Thr Arg Ser Ser Val
1 5 10 15

cag atc ttc att gtg ttt agt tta tgt tgc ttc ttt tac att ttg gga
333
Gln Ile Phe Ile Val Phe Ser Leu Cys Cys Phe Phe Tyr Ile Leu Gly
20 25 30

gca tgg caa cga agt ggt ttt ggt aaa gga gac agt att gct ctt gag
381
Ala Trp Gln Arg Ser Gly Phe Gly Lys Gly Asp Ser Ile Ala Leu Glu
35 40 45

atg acc aac agt gga gct gat tgc aac att gtt cct agc ttg aat ttc
429
Met Thr Asn Ser Gly Ala Asp Cys Asn Ile Val Pro Ser Leu Asn Phe
50 55 60

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477
Glu Thr His His Ala Gly Glu Ser Ser Leu Val Gly Ala Ser Glu Ala
65 70 75 80

gca aag gtc aag gct ttc gag ccc tgt gat ggt cgt tac acg gat tac
525
Ala Lys Val Lys Ala Phe Glu Pro Cys Asp Gly Arg Tyr Thr Asp Tyr
85 90 95

act cct tgt caa gat cag aga cgt gcc atg act ttc ccg aga gat agt
573
Thr Pro Cys Gln Asp Gln Arg Arg Ala Met Thr Phe Pro Arg Asp Ser
100 105 110

atg att tac cga gaa agg cat tgc gct cct gag aat gag aag ctc cat
621
Met Ile Tyr Arg Glu Arg His Cys Ala Pro Glu Asn Glu Lys Leu His
115 120 125

tgt ctt ata ccg gct cct aaa gga tat gtg aca cct ttc tct tgg cct
669
Cys Leu Ile Pro Ala Pro Lys Gly Tyr Val Thr Pro Phe Ser Trp Pro
130 135 140

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717
Lys Ser Arg Asp Tyr Val Pro Tyr Ala Asn Ala Pro Tyr Lys Ala Leu
145 150 155 160

act gtt gag aag gct att cag aat tgg att cag tat gag gga gac gtt
765
Thr Val Glu Lys Ala Ile Gln Asn Trp Ile Gln Tyr Glu Gly Asp Val
165 170 175

ttt aga ttc cct ggt ggt gga act cag ttc cct caa ggt gct gat aag
813
Phe Arg Phe Pro Gly Gly Gly Thr Gln Phe Pro Gln Gly Ala Asp Lys

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861		
Tyr Ile Asp Gln Leu Ala Ser Val Ile Pro Met Glu Asn Gly Thr Val		
195	200	205
agg act gct ttg gac act ggt tgt ggg gtt gca agt tgg gga gcg tac		
909		
Arg Thr Ala Leu Asp Thr Gly Cys Gly Val Ala Ser Trp Gly Ala Tyr		
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957		
Leu Trp Ser Arg Asn Val Arg Ala Met Ser Phe Ala Pro Arg Asp Ser		
225	230	235 240
cac gag gct cag gtc cag ttt gct ctc gag aga ggt gtt ccc gct gtt		
1005		
His Glu Ala Gln Val Gln Phe Ala Leu Glu Arg Gly Val Pro Ala Val		
	245	250 255
att ggt gtt ctt ggt acc ata aag ttg cca tac cca aca cgt gct ttc		
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Ile Gly Val Leu Gly Thr Ile Lys Leu Pro Tyr Pro Thr Arg Ala Phe		
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gac atg gct cat tgc tct cgg tgt ttg att cca tgg gga gca aat gat		
1101		
Asp Met Ala His Cys Ser Arg Cys Leu Ile Pro Trp Gly Ala Asn Asp		
	275	280 285
ggg atg tac ttg atg gaa gtt gac cgt gtg ctt aga cct ggt ggg tac		
1149		
Gly Met Tyr Leu Met Glu Val Asp Arg Val Leu Arg Pro Gly Gly Tyr		
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tgg att ctg tct ggt cct cca atc aac tgg aaa gtc aac tac aag gca		
1197		
Trp Ile Leu Ser Gly Pro Pro Ile Asn Trp Lys Val Asn Tyr Lys Ala		
305	310	315 320
tgg caa cgt ccc aag gag gac ctt caa gag gaa caa aga aag att gag		
1245		
Trp Gln Arg Pro Lys Glu Asp Leu Gln Glu Glu Gln Arg Lys Ile Glu		
	325	330 335
gaa gct gct aaa ctt ctt tgt tgg gag aaa aag tat gaa cac ggt gag		
1293		
Glu Ala Ala Lys Leu Leu Cys Trp Glu Lys Lys Tyr Glu His Gly Glu		
	340	345 350
att gca att tgg cag aag aga gtc aat gat gag gca tgc cga tca aga		
1341		
Ile Ala Ile Trp Gln Lys Arg Val Asn Asp Glu Ala Cys Arg Ser Arg		
	355	360 365
caa gat gat cct aga gcc aat ttc tgc aaa acc gat gat acc gat gat		
1389		
Gln Asp Asp Pro Arg Ala Asn Phe Cys Lys Thr Asp Asp Thr Asp Asp		
	370	375 380

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 Val Trp Tyr Lys Lys Met Glu Ala Cys Ile Thr Pro Tyr Pro Glu Thr
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 1485
 Ser Ser Ser Asp Glu Val Ala Gly Gly Glu Leu Gln Ala Phe Pro Asp
 405 410 415
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 1533
 Arg Leu Asn Ala Val Pro Pro Arg Ile Ser Ser Gly Ser Ile Ser Gly
 420 425 430
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 1581
 Val Thr Val Asp Ala Tyr Glu Asp Asp Asn Arg Gln Trp Lys Lys His
 435 440 445
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 1629
 Val Lys Ala Tyr Lys Arg Ile Asn Ser Leu Leu Asp Thr Gly Arg Tyr
 450 455 460
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 1677
 Arg Asn Ile Met Asp Met Asn Ala Gly Phe Gly Gly Phe Ala Ala Ala
 465 470 475 480
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 1725
 Leu Glu Ser Gln Lys Leu Trp Val Met Asn Val Val Pro Thr Ile Ala
 485 490 495
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 1773
 Glu Lys Asn Arg Leu Gly Val Val Tyr Glu Arg Gly Leu Ile Gly Ile
 500 505 510
 tac cat gac tgg tgt gag gct ttc tct aca tat cca aga aca tat gac
 1821
 Tyr His Asp Trp Cys Glu Ala Phe Ser Thr Tyr Pro Arg Thr Tyr Asp
 515 520 525
 ctg atc cac gcg aac cac ctc ttc agt cta tac aag aac aag tgc aat
 1869
 Leu Ile His Ala Asn His Leu Phe Ser Leu Tyr Lys Asn Lys Cys Asn
 530 535 540
 gcg gat gat att ctt cta gag atg gat aga att ctc cga cca gaa gga
 1917
 Ala Asp Asp Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Glu Gly
 545 550 555 560
 gcg gtt ata atc cgg gat gat gtg gat aca ttg atc aag gtg aag aga
 1965
 Ala Val Ile Ile Arg Asp Asp Val Asp Thr Leu Ile Lys Val Lys Arg
 565 570 575

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2010

Ile Ile Ala Trp Asn Glu Met Gly Cys Glu Ala Cys Arg Ser
580 585 590

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2070

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2190

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2276

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Ala Trp Gln Arg Ser Gly Phe Gly Lys Gly Asp Ser Ile Ala Leu Glu
35 40 45

Met Thr Asn Ser Gly Ala Asp Cys Asn Ile Val Pro Ser Leu Asn Phe
50 55 60

Glu Thr His His Ala Gly Glu Ser Ser Leu Val Gly Ala Ser Glu Ala
65 70 75 80

Ala Lys Val Lys Ala Phe Glu Pro Cys Asp Gly Arg Tyr Thr Asp Tyr
85 90 95

Thr Pro Cys Gln Asp Gln Arg Arg Ala Met Thr Phe Pro Arg Asp Ser
100 105 110

Met Ile Tyr Arg Glu Arg His Cys Ala Pro Glu Asn Glu Lys Leu His
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Cys Leu Ile Pro Ala Pro Lys Gly Tyr Val Thr Pro Phe Ser Trp Pro
130 135 140

Lys Ser Arg Asp Tyr Val Pro Tyr Ala Asn Ala Pro Tyr Lys Ala Leu

145 150 155 160
 Thr Val Glu Lys Ala Ile Gln Asn Trp Ile Gln Tyr Glu Gly Asp Val
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 Phe Arg Phe Pro Gly Gly Gly Thr Gln Phe Pro Gln Gly Ala Asp Lys
 180 185 190
 Tyr Ile Asp Gln Leu Ala Ser Val Ile Pro Met Glu Asn Gly Thr Val
 195 200 205
 Arg Thr Ala Leu Asp Thr Gly Cys Gly Val Ala Ser Trp Gly Ala Tyr
 210 215 220
 Leu Trp Ser Arg Asn Val Arg Ala Met Ser Phe Ala Pro Arg Asp Ser
 225 230 235 240
 His Glu Ala Gln Val Gln Phe Ala Leu Glu Arg Gly Val Pro Ala Val
 245 250 255
 Ile Gly Val Leu Gly Thr Ile Lys Leu Pro Tyr Pro Thr Arg Ala Phe
 260 265 270
 Asp Met Ala His Cys Ser Arg Cys Leu Ile Pro Trp Gly Ala Asn Asp
 275 280 285
 Gly Met Tyr Leu Met Glu Val Asp Arg Val Leu Arg Pro Gly Gly Tyr
 290 295 300
 Trp Ile Leu Ser Gly Pro Pro Ile Asn Trp Lys Val Asn Tyr Lys Ala
 305 310 315 320
 Trp Gln Arg Pro Lys Glu Asp Leu Gln Glu Glu Gln Arg Lys Ile Glu
 325 330 335
 Glu Ala Ala Lys Leu Leu Cys Trp Glu Lys Lys Tyr Glu His Gly Glu
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 Ile Ala Ile Trp Gln Lys Arg Val Asn Asp Glu Ala Cys Arg Ser Arg
 355 360 365
 Gln Asp Asp Pro Arg Ala Asn Phe Cys Lys Thr Asp Asp Thr Asp Asp
 370 375 380
 Val Trp Tyr Lys Lys Met Glu Ala Cys Ile Thr Pro Tyr Pro Glu Thr
 385 390 395 400

Ser Ser Ser Asp Glu Val Ala Gly Gly Glu Leu Gln Ala Phe Pro Asp
 405 410 415

Arg Leu Asn Ala Val Pro Pro Arg Ile Ser Ser Gly Ser Ile Ser Gly
 420 425 430

Val Thr Val Asp Ala Tyr Glu Asp Asp Asn Arg Gln Trp Lys Lys His
 435 440 445

Val Lys Ala Tyr Lys Arg Ile Asn Ser Leu Leu Asp Thr Gly Arg Tyr
 450 455 460

Arg Asn Ile Met Asp Met Asn Ala Gly Phe Gly Gly Phe Ala Ala Ala
 465 470 475 480

Leu Glu Ser Gln Lys Leu Trp Val Met Asn Val Val Pro Thr Ile Ala
 485 490 495

Glu Lys Asn Arg Leu Gly Val Val Tyr Glu Arg Gly Leu Ile Gly Ile
 500 505 510

Tyr His Asp Trp Cys Glu Ala Phe Ser Thr Tyr Pro Arg Thr Tyr Asp
 515 520 525

Leu Ile His Ala Asn His Leu Phe Ser Leu Tyr Lys Asn Lys Cys Asn
 530 535 540

Ala Asp Asp Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro Glu Gly
 545 550 555 560

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180

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240

ttggttctgg gtttggttga ttccttgta gaaatgtaaa tttagggctt ttgtatctga
300

aaccgatctt cagacttggtg taatcttctt gatcttcatg caagattgat aattctacaa
360

gaagaagaag aagagaaa atg gct act ttg act gag cca tca tca tct ttg
411

Met Ala Thr Leu Thr Glu Pro Ser Ser Ser Leu
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459

Ser Phe Thr Ser Ser His Phe Ser Tyr Gly Ser Ile Gly Ser Asn His
15 20 25

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507

Phe Ser Ser Ser Ser Ala Ser Asn Pro Glu Val Val Ser Leu Thr Lys
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555

Leu Ser Ser Asn Leu Glu Gln Leu Leu Ser Asn Ser Asp Cys Asp Tyr
45 50 55

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603

Ser Asp Ala Glu Ile Ile Val Asp Gly Val Pro Val Gly Val His Arg
60 65 70 75

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651

Cys Ile Leu Ala Ala Arg Ser Lys Phe Phe Gln Asp Leu Phe Lys Lys
80 85 90

gaa aag aaa att tcg aaa act gag aaa cca aag tat cag ttg aga gag
699

Glu Lys Lys Ile Ser Lys Thr Glu Lys Pro Lys Tyr Gln Leu Arg Glu
95 100 105

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747

Met Leu Pro Tyr Gly Ala Val Ala His Glu Ala Phe Leu Tyr Phe Leu
110 115 120

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795

Ser Tyr Ile Tyr Thr Gly Arg Leu Lys Pro Phe Pro Leu Glu Val Ser
125 130 135

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843

Thr Cys Val Asp Pro Val Cys Ser His Asp Cys Cys Arg Pro Ala Ile
140 145 150 155

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 160 165 170

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 939
 Glu Leu Val Ser Ser Phe Gln Arg Arg Leu Cys Asn Phe Val Glu Lys
 175 180 185

acc ctt gtt gag aat gtt ctt ccc att ctt atg gtt gct ttc aat tgt
 987
 Thr Leu Val Glu Asn Val Leu Pro Ile Leu Met Val Ala Phe Asn Cys
 190 195 200

aag ttg act cag ctt ctt gat cag tgt att gag aga gtg gcg agg tca
 1035
 Lys Leu Thr Gln Leu Leu Asp Gln Cys Ile Glu Arg Val Ala Arg Ser
 205 210 215

gat ctt tac agg ttc tgt att gaa aag gaa gtt cct ccc gaa gta gca
 1083
 Asp Leu Tyr Arg Phe Cys Ile Glu Lys Glu Val Pro Pro Glu Val Ala
 220 225 230 235

gag aag att aaa cag ctt cga ctt ata tcc ccg caa gac gaa gaa acc
 1131
 Glu Lys Ile Lys Gln Leu Arg Leu Ile Ser Pro Gln Asp Glu Glu Thr
 240 245 250

agt ccc aag att tcg gag aaa ttg ctt gaa aga atc ggt aaa att ctc
 1179
 Ser Pro Lys Ile Ser Glu Lys Leu Leu Glu Arg Ile Gly Lys Ile Leu
 255 260 265

aag gcc ttg gat tca tat gat gtt ctt cat ttt gct gcg atg cgt aga
 1227
 Lys Ala Leu Asp Ser Tyr Asp Val Leu His Phe Ala Ala Met Arg Arg
 270 275 280

gag cca tcg atc att ata tcg ctt atc gat aaa ggc gcc aat gca tct
 1275
 Glu Pro Ser Ile Ile Ile Ser Leu Ile Asp Lys Gly Ala Asn Ala Ser
 285 290 295

gag ttt aca tct gac gga cgt agc gca gtt aat ata tta aga aga ctg
 1323
 Glu Phe Thr Ser Asp Gly Arg Ser Ala Val Asn Ile Leu Arg Arg Leu
 300 305 310 315

aca aat cca aag gat tat cat acc aaa aca gct aaa ggg cgt gaa tct
 1371
 Thr Asn Pro Lys Asp Tyr His Thr Lys Thr Ala Lys Gly Arg Glu Ser
 320 325 330

agt aaa gcc agg tta tgc atc gat atc ttg gaa aga gaa atc agg aag
 1419
 Ser Lys Ala Arg Leu Cys Ile Asp Ile Leu Glu Arg Glu Ile Arg Lys
 335 340 345

aac ccc atg gtt cta gat aca cca atg tgt tcc att tct atg cct gaa
 1467
 Asn Pro Met Val Leu Asp Thr Pro Met Cys Ser Ile Ser Met Pro Glu
 350 355 360

gat ctc cag atg aga ctg ttg tac cta gaa aag aga gtg ggg ctt gct
 1515
 Asp Leu Gln Met Arg Leu Leu Tyr Leu Glu Lys Arg Val Gly Leu Ala
 365 370 375

cag ttg ttc ttt cca acg gaa gct aaa gtt gct atg gac att ggt aac
 1563
 Gln Leu Phe Phe Pro Thr Glu Ala Lys Val Ala Met Asp Ile Gly Asn
 380 385 390 395

gta gaa ggt aca agt gag ttc acg ggt ttg tca cct cct tcg agt ggg
 1611
 Val Glu Gly Thr Ser Glu Phe Thr Gly Leu Ser Pro Pro Ser Ser Gly
 400 405 410

tta acc gga aac ttg agt cag gtt gat tta aac gaa act cct cat atg
 1659
 Leu Thr Gly Asn Leu Ser Gln Val Asp Leu Asn Glu Thr Pro His Met
 415 420 425

caa acc caa aga ctt ctt act cgt atg gtg gct cta atg aaa aca gtt
 1707
 Gln Thr Gln Arg Leu Leu Thr Arg Met Val Ala Leu Met Lys Thr Val
 430 435 440

gag act ggt cga agg ttt ttt cca tat ggt tca gag gtt cta gat aag
 1755
 Glu Thr Gly Arg Arg Phe Phe Pro Tyr Gly Ser Glu Val Leu Asp Lys
 445 450 455

tac atg gct gag tat ata gac gac gac atc ctc gac gat ttc cat ttt
 1803
 Tyr Met Ala Glu Tyr Ile Asp Asp Asp Ile Leu Asp Asp Phe His Phe
 460 465 470 475

gag aag gga tct aca cat gaa aga aga ttg aaa aga atg aga tat aga
 1851
 Glu Lys Gly Ser Thr His Glu Arg Arg Leu Lys Arg Met Arg Tyr Arg
 480 485 490

gag ctt aag gat gat gtc caa aag gca tat agc aaa gac aaa gag tct
 1899
 Glu Leu Lys Asp Asp Val Gln Lys Ala Tyr Ser Lys Asp Lys Glu Ser
 495 500 505

aag att gcg cgg tct tgt ctt tct gct tca tct tct cct tct tct tct
 1947
 Lys Ile Ala Arg Ser Cys Leu Ser Ala Ser Ser Ser Pro Ser Ser Ser
 510 515 520

tcc ata aga gat gac ctg cac aac aca aca tga aactgcacca taagtcaaat
 2000
 Ser Ile Arg Asp Asp Leu His Asn Thr Thr
 525 530

gtaattagat atcttttgta aaagggtttt ttctttatgg atgttactca gattttatac
2060

agatgcttta ggttcagttt caataaagag agatggatag atagatgtac aagattagga
2120

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2196

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His Phe Ser Tyr Gly Ser Ile Gly Ser Asn His Phe Ser Ser Ser Ser
20 25 30

Ala Ser Asn Pro Glu Val Val Ser Leu Thr Lys Leu Ser Ser Asn Leu
35 40 45

Glu Gln Leu Leu Ser Asn Ser Asp Cys Asp Tyr Ser Asp Ala Glu Ile
50 55 60

Ile Val Asp Gly Val Pro Val Gly Val His Arg Cys Ile Leu Ala Ala
65 70 75 80

Arg Ser Lys Phe Phe Gln Asp Leu Phe Lys Lys Glu Lys Lys Ile Ser
85 90 95

Lys Thr Glu Lys Pro Lys Tyr Gln Leu Arg Glu Met Leu Pro Tyr Gly
100 105 110

Ala Val Ala His Glu Ala Phe Leu Tyr Phe Leu Ser Tyr Ile Tyr Thr
115 120 125

Gly Arg Leu Lys Pro Phe Pro Leu Glu Val Ser Thr Cys Val Asp Pro
130 135 140

Val Cys Ser His Asp Cys Cys Arg Pro Ala Ile Asp Phe Val Val Gln
145 150 155 160

Leu Met Tyr Ala Ser Ser Val Leu Gln Val Pro Glu Leu Val Ser Ser
165 170 175

Phe Gln Arg Arg Leu Cys Asn Phe Val Glu Lys Thr Leu Val Glu Asn

180					185					190					
Val	Leu	Pro	Ile	Leu	Met	Val	Ala	Phe	Asn	Cys	Lys	Leu	Thr	Gln	Leu
		195					200						205		
Leu	Asp	Gln	Cys	Ile	Glu	Arg	Val	Ala	Arg	Ser	Asp	Leu	Tyr	Arg	Phe
	210						215				220				
Cys	Ile	Glu	Lys	Glu	Val	Pro	Pro	Glu	Val	Ala	Glu	Lys	Ile	Lys	Gln
	225				230					235					240
Leu	Arg	Leu	Ile	Ser	Pro	Gln	Asp	Glu	Glu	Thr	Ser	Pro	Lys	Ile	Ser
				245					250						255
Glu	Lys	Leu	Leu	Glu	Arg	Ile	Gly	Lys	Ile	Leu	Lys	Ala	Leu	Asp	Ser
			260					265					270		
Tyr	Asp	Val	Leu	His	Phe	Ala	Ala	Met	Arg	Arg	Glu	Pro	Ser	Ile	Ile
		275					280						285		
Ile	Ser	Leu	Ile	Asp	Lys	Gly	Ala	Asn	Ala	Ser	Glu	Phe	Thr	Ser	Asp
	290						295				300				
Gly	Arg	Ser	Ala	Val	Asn	Ile	Leu	Arg	Arg	Leu	Thr	Asn	Pro	Lys	Asp
	305				310					315					320
Tyr	His	Thr	Lys	Thr	Ala	Lys	Gly	Arg	Glu	Ser	Ser	Lys	Ala	Arg	Leu
				325					330					335	
Cys	Ile	Asp	Ile	Leu	Glu	Arg	Glu	Ile	Arg	Lys	Asn	Pro	Met	Val	Leu
			340					345					350		
Asp	Thr	Pro	Met	Cys	Ser	Ile	Ser	Met	Pro	Glu	Asp	Leu	Gln	Met	Arg
		355					360					365			
Leu	Leu	Tyr	Leu	Glu	Lys	Arg	Val	Gly	Leu	Ala	Gln	Leu	Phe	Phe	Pro
		370					375				380				
Thr	Glu	Ala	Lys	Val	Ala	Met	Asp	Ile	Gly	Asn	Val	Glu	Gly	Thr	Ser
					390					395					400
Glu	Phe	Thr	Gly	Leu	Ser	Pro	Pro	Ser	Ser	Gly	Leu	Thr	Gly	Asn	Leu
				405					410					415	
Ser	Gln	Val	Asp	Leu	Asn	Glu	Thr	Pro	His	Met	Gln	Thr	Gln	Arg	Leu
			420					425					430		

Leu Thr Arg Met Val Ala Leu Met Lys Thr Val Glu Thr Gly Arg Arg
 435 440 445

Phe Phe Pro Tyr Gly Ser Glu Val Leu Asp Lys Tyr Met Ala Glu Tyr
 450 455 460

Ile Asp Asp Asp Ile Leu Asp Asp Phe His Phe Glu Lys Gly Ser Thr
 465 470 475 480

His Glu Arg Arg Leu Lys Arg Met Arg Tyr Arg Glu Leu Lys Asp Asp
 485 490 495

Val Gln Lys Ala Tyr Ser Lys Asp Lys Glu Ser Lys Ile Ala Arg Ser
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Cys Leu Ser Ala Ser Ser Ser Pro Ser Ser Ser Ser Ile Arg Asp Asp
 515 520 525

Leu His Asn Thr Thr
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ccagatctcg ttccccgca tctagtttat tctttgaaaa agtgatagaa gcagaa atg
 119

Met
 1

gga agg ggc aag atc gcg att aag agg atc aat aac tct acg agc cgt
 167

Gly Arg Gly Lys Ile Ala Ile Lys Arg Ile Asn Asn Ser Thr Ser Arg
 5 10 15

cag gtt acg ttc tcg aag cga agg aat gga ttg ttg aag aaa gct aag
 215

Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Lys
 20 25 30

gag ctt gcg att ctc tgc gat gct gag gtt ggt gtc atc atc ttc tcc
 263

Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe Ser
 35 40 45

agc acc ggt agg ctc tac gat ttc tcc agc tcc agc atg aaa tcg gtc
 311

Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Ser Met Lys Ser Val
 50 55 60 65

ata gag aga tac agc gat gcc aaa gga gaa acc agt tca gaa aat gat
 359
 Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn Asp
 70 75 80
 ccc gct tca gaa att cag ttc tgg caa aag gag gct gcg att cta aag
 407
 Pro Ala Ser Glu Ile Gln Phe Trp Gln Lys Glu Ala Ala Ile Leu Lys
 85 90 95
 cgt cag cta cat aac ttg caa gaa aac cac cgg caa atg atg ggg gag
 455
 Arg Gln Leu His Asn Leu Gln Glu Asn His Arg Gln Met Met Gly Glu
 100 105 110
 gag ctc tct gga cta agt gta gaa gct tta cag aat ttg gaa aat cag
 503
 Glu Leu Ser Gly Leu Ser Val Glu Ala Leu Gln Asn Leu Glu Asn Gln
 115 120 125
 ctt gaa ttg agc ctt cgt ggc gtt cga atg aaa aag gat caa atg tta
 551
 Leu Glu Leu Ser Leu Arg Gly Val Arg Met Lys Lys Asp Gln Met Leu
 130 135 140 145
 atc gaa gaa ata caa gta ctt aac cga gag ggg aat ctc gtt cac caa
 599
 Ile Glu Glu Ile Gln Val Leu Asn Arg Glu Gly Asn Leu Val His Gln
 150 155 160
 gag aat tta gac ctc cac aag aaa gta aac cta atg cac caa cag aac
 647
 Glu Asn Leu Asp Leu His Lys Lys Val Asn Leu Met His Gln Gln Asn
 165 170 175
 atg gaa cta cat gaa aag gtt tca gag gtc gag ggt gtg aaa atc gca
 695
 Met Glu Leu His Glu Lys Val Ser Glu Val Glu Gly Val Lys Ile Ala
 180 185 190
 aac aag aat tct ctt ctc aca aat ggt cta gac atg aga gat acc tcg
 743
 Asn Lys Asn Ser Leu Leu Thr Asn Gly Leu Asp Met Arg Asp Thr Ser
 195 200 205
 aac gaa cat gtc cat ctt cag ctc agc caa ccg cag cat gat cat gag
 791
 Asn Glu His Val His Leu Gln Leu Ser Gln Pro Gln His Asp His Glu
 210 215 220 225
 acg cat tca aaa gct atc caa ctc aac tat ttt tcc ttc att gca taa
 839
 Thr His Ser Lys Ala Ile Gln Leu Asn Tyr Phe Ser Phe Ile Ala
 230 235 240
 tataattcgg tgtgcccaaca cacttatggt gacctcgtcg gaatcatatc acaattcact
 899
 gtgtcagctt gcctctgcat aagcgaaaat aaaaacataa acatgatcag ttgtcattcc
 959

atatctatca aacaccagct ttgtaacttt taaaactttt tctccgtgca aagacctttg
1019

gtttggcgct taagcatgta gtttgatgat caaaggaaat ggggtgttta gcataaagtt
1079

gtcacccttc cgttgcatth tagcttccca tccaaatcaa tttgtaaaat gtgagttagt
1139

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1199

aaaaaaaaa a
1210

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Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
20 25 30

Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe
35 40 45

Ser Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Ser Met Lys Ser
50 55 60

Val Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn
65 70 75 80

Asp Pro Ala Ser Glu Ile Gln Phe Trp Gln Lys Glu Ala Ala Ile Leu
85 90 95

Lys Arg Gln Leu His Asn Leu Gln Glu Asn His Arg Gln Met Met Gly
100 105 110

Glu Glu Leu Ser Gly Leu Ser Val Glu Ala Leu Gln Asn Leu Glu Asn
115 120 125

Gln Leu Glu Leu Ser Leu Arg Gly Val Arg Met Lys Lys Asp Gln Met
130 135 140

Leu Ile Glu Glu Ile Gln Val Leu Asn Arg Glu Gly Asn Leu Val His
145 150 155 160

Gln Glu Asn Leu Asp Leu His Lys Lys Val Asn Leu Met His Gln Gln

165 170 175

Asn Met Glu Leu His Glu Lys Val Ser Glu Val Glu Gly Val Lys Ile
180 185 190

Ala Asn Lys Asn Ser Leu Leu Thr Asn Gly Leu Asp Met Arg Asp Thr
195 200 205

Ser Asn Glu His Val His Leu Gln Leu Ser Gln Pro Gln His Asp His
210 215 220

Glu Thr His Ser Lys Ala Ile Gln Leu Asn Tyr Phe Ser Phe Ile Ala
225 230 235 240

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106
Met Phe Arg Phe Pro Val Ser Leu Gly Gly Gly Pro Arg Glu Asn Leu
1 5 10 15

aag cca tca gat gag cag cat caa cgt gcg gtg gtg aat gag gtt gac
154
Lys Pro Ser Asp Glu Gln His Gln Arg Ala Val Val Asn Glu Val Asp
20 25 30

ttt ttc cga tca gcg gag aag aga gat agg gtt tca cgt gaa gaa caa
202
Phe Phe Arg Ser Ala Glu Lys Arg Asp Arg Val Ser Arg Glu Glu Gln
35 40 45

aac att atc gcc gat gag act cat agg gtt cat gtc aaa agg gag aat
250
Asn Ile Ile Ala Asp Glu Thr His Arg Val His Val Lys Arg Glu Asn
50 55 60

tca cgt gtt gat gat cat gac gat cgt tct act gat cac atc aat att
298
Ser Arg Val Asp Asp His Asp Asp Arg Ser Thr Asp His Ile Asn Ile
65 70 75 80

gga ctt aat ctt ctc act gcg aat acg gga agc gac gag tca atg gtg
346
Gly Leu Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Met Val
85 90 95

gat gat gga ttg tct gtg gat atg gaa gag aaa cgt aca aag tgt gag
394
Asp Asp Gly Leu Ser Val Asp Met Glu Glu Lys Arg Thr Lys Cys Glu
100 105 110

aat gca caa ctt cgc gaa gag cta aag aag gcg agt gaa gat aat caa
 442
 Asn Ala Gln Leu Arg Glu Glu Leu Lys Lys Ala Ser Glu Asp Asn Gln
 115 120 125
 aga cta aag caa atg cta agt caa aca acc aac aac ttc aat tcc ttg
 490
 Arg Leu Lys Gln Met Leu Ser Gln Thr Thr Asn Asn Phe Asn Ser Leu
 130 135 140
 cag atg caa ctt gtt gct gtc atg agg caa caa gaa gat cat cat cac
 538
 Gln Met Gln Leu Val Ala Val Met Arg Gln Gln Glu Asp His His His
 145 150 155 160
 cta gct acg acc gag aac aat gac aat gta aag aac cga cat gaa gtg
 586
 Leu Ala Thr Thr Glu Asn Asn Asp Asn Val Lys Asn Arg His Glu Val
 165 170 175
 cct gaa atg gtt cca aga cag ttc atc gat ttg gga ccg cat tct gac
 634
 Pro Glu Met Val Pro Arg Gln Phe Ile Asp Leu Gly Pro His Ser Asp
 180 185 190
 gaa gtg tcg tcc gag gag agg acg acg gtt cgg tcg gga tct cct ccc
 682
 Glu Val Ser Ser Glu Glu Arg Thr Thr Val Arg Ser Gly Ser Pro Pro
 195 200 205
 tcg ctt cta gag aaa tct agc tca cgt caa aac gga aag aga gtg ctt
 730
 Ser Leu Leu Glu Lys Ser Ser Ser Arg Gln Asn Gly Lys Arg Val Leu
 210 215 220
 gta aga gaa gaa agc ccg gaa acc gaa tcc aac ggc tgg aga aac cct
 778
 Val Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Gly Trp Arg Asn Pro
 225 230 235 240
 aac aaa gtt cct aaa cac cat gca tca tcc agc att tgc ggt ggc aat
 826
 Asn Lys Val Pro Lys His His Ala Ser Ser Ser Ile Cys Gly Gly Asn
 245 250 255
 ggc agt gaa aat gca agt agc aag gtc att gag caa gcg gcc gcc gaa
 874
 Gly Ser Glu Asn Ala Ser Ser Lys Val Ile Glu Gln Ala Ala Ala Glu
 260 265 270
 gcc acc atg cgt aaa gcc cgt gtc tcg gtt cgt gct cga tcc gaa gct
 922
 Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg Ser Glu Ala
 275 280 285
 ccc atg tta agc gat gga tgt caa tgg aga aaa tac gga caa aaa atg
 970
 Pro Met Leu Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met
 290 295 300

gcg aaa gga aac ccg tgc cct cga gct tat tac cgt tgc aca atg gct
 1018
 Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala
 305 310 315 320

gtt gga tgt cct gtt cgc aag caa gtg caa cgt tgc gcg gaa gat aga
 1066
 Val Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Arg
 325 330 335

acc att ctc ata aca acc tac gaa gga aac cat aac cat cca tta cct
 1114
 Thr Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro
 340 345 350

cct gcg gct atg aac atg gct tca act aca aca gca gcc gca agc atg
 1162
 Pro Ala Ala Met Asn Met Ala Ser Thr Thr Thr Ala Ala Ala Ser Met
 355 360 365

ctt ctc tca ggc tcc acc atg tcg aac caa gac ggt tta atg aac cca
 1210
 Leu Leu Ser Gly Ser Thr Met Ser Asn Gln Asp Gly Leu Met Asn Pro
 370 375 380

aca aat ctc ttg gct cga acc ata tta ccg tgt tcc tca agc atg gct
 1258
 Thr Asn Leu Leu Ala Arg Thr Ile Leu Pro Cys Ser Ser Ser Met Ala
 385 390 395 400

act atc tca gcc tct gca cca ttc cca acc att aca tta gac ctc aca
 1306
 Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp Leu Thr
 405 410 415

gag tca ccc aac ggg aac aat cca acc aat aac ccg ctg atg caa ttc
 1354
 Glu Ser Pro Asn Gly Asn Asn Pro Thr Asn Asn Pro Leu Met Gln Phe
 420 425 430

tct caa cgg tct ggt ttg gtg gag ttg aac caa tcg gtt ttg cct cat
 1402
 Ser Gln Arg Ser Gly Leu Val Glu Leu Asn Gln Ser Val Leu Pro His
 435 440 445

atg atg ggt cag gct ttg tac tac aac caa cag tct aag ttt tcg ggt
 1450
 Met Met Gly Gln Ala Leu Tyr Tyr Asn Gln Gln Ser Lys Phe Ser Gly
 450 455 460

tta cat atg ccg tct cag ccg cta aac gct ggt gag agt gtt agc gcc
 1498
 Leu His Met Pro Ser Gln Pro Leu Asn Ala Gly Glu Ser Val Ser Ala
 465 470 475 480

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 1546
 Ala Thr Ala Ala Ile Ala Ser Asn Pro Asn Phe Ala Ala Ala Leu Ala
 485 490 495

gca gcc ata act tcg att atc aac ggt tcg aac aat cag cag aat ggg
1594

Ala Ala Ile Thr Ser Ile Ile Asn Gly Ser Asn Asn Gln Gln Asn Gly
500 505 510

aac aac aat aac agt aat gtt aca acg agc aac gtt gac aat agg caa
1642

Asn Asn Asn Asn Ser Asn Val Thr Thr Ser Asn Val Asp Asn Arg Gln
515 520 525

taa cttttttta taagtttttag ttagggactt tttatcggtc gattttgttt
1695

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1755

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1797

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20 25 30

Phe Phe Arg Ser Ala Glu Lys Arg Asp Arg Val Ser Arg Glu Glu Gln
35 40 45

Asn Ile Ile Ala Asp Glu Thr His Arg Val His Val Lys Arg Glu Asn
50 55 60

Ser Arg Val Asp Asp His Asp Asp Arg Ser Thr Asp His Ile Asn Ile
65 70 75 80

Gly Leu Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Met Val
85 90 95

Asp Asp Gly Leu Ser Val Asp Met Glu Glu Lys Arg Thr Lys Cys Glu
100 105 110

Asn Ala Gln Leu Arg Glu Glu Leu Lys Lys Ala Ser Glu Asp Asn Gln
115 120 125

Arg Leu Lys Gln Met Leu Ser Gln Thr Thr Asn Asn Phe Asn Ser Leu
130 135 140

Gln Met Gln Leu Val Ala Val Met Arg Gln Gln Glu Asp His His His
145 150 155 160

Leu Ala Thr Thr Glu Asn Asn Asp Asn Val Lys Asn Arg His Glu Val
 165 170 175

Pro Glu Met Val Pro Arg Gln Phe Ile Asp Leu Gly Pro His Ser Asp
 180 185 190

Glu Val Ser Ser Glu Glu Arg Thr Thr Val Arg Ser Gly Ser Pro Pro
 195 200 205

Ser Leu Leu Glu Lys Ser Ser Ser Arg Gln Asn Gly Lys Arg Val Leu
 210 215 220

Val Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Gly Trp Arg Asn Pro
 225 230 235 240

Asn Lys Val Pro Lys His His Ala Ser Ser Ser Ile Cys Gly Gly Asn
 245 250 255

Gly Ser Glu Asn Ala Ser Ser Lys Val Ile Glu Gln Ala Ala Ala Glu
 260 265 270

Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg Ser Glu Ala
 275 280 285

Pro Met Leu Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met
 290 295 300

Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala
 305 310 315 320

Val Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Arg
 325 330 335

Thr Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro
 340 345 350

Pro Ala Ala Met Asn Met Ala Ser Thr Thr Thr Ala Ala Ala Ser Met
 355 360 365

Leu Leu Ser Gly Ser Thr Met Ser Asn Gln Asp Gly Leu Met Asn Pro
 370 375 380

Thr Asn Leu Leu Ala Arg Thr Ile Leu Pro Cys Ser Ser Ser Met Ala
 385 390 395 400

Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp Leu Thr
405 410 415

Glu Ser Pro Asn Gly Asn Asn Pro Thr Asn Asn Pro Leu Met Gln Phe
420 425 430

Ser Gln Arg Ser Gly Leu Val Glu Leu Asn Gln Ser Val Leu Pro His
435 440 445

Met Met Gly Gln Ala Leu Tyr Tyr Asn Gln Gln Ser Lys Phe Ser Gly
450 455 460

Leu His Met Pro Ser Gln Pro Leu Asn Ala Gly Glu Ser Val Ser Ala
465 470 475 480

Ala Thr Ala Ala Ile Ala Ser Asn Pro Asn Phe Ala Ala Ala Leu Ala
485 490 495

Ala Ala Ile Thr Ser Ile Ile Asn Gly Ser Asn Asn Gln Gln Asn Gly
500 505 510

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515 520 525

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tct tcc tcc aca tct ctc gat gtg tgt cca tta cca caa gct gaa caa
96
Ser Ser Ser Thr Ser Leu Asp Val Cys Pro Leu Pro Gln Ala Glu Gln
20 25 30
gaa cct gta gtt gaa gat gtc gac tac acc gat gat gag atg gat gtg
144
Glu Pro Val Val Glu Asp Val Asp Tyr Thr Asp Asp Glu Met Asp Val
35 40 45
gat gag ctt gag aag agg atg tgg aga gac aaa atg cgt ttg aaa cgt
192
Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
50 55 60
ctc aag gag caa cag agt aag tgt aaa gaa ggc gtc gat ggt tcg aaa
240
Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys
65 70 75 80

cag agg cag tcg caa gag caa gct agg agg aag aaa atg tct aga gcc
 288
 Gln Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala
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 caa gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa
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 Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys
 100 105 110
 gct caa ggc ttt gtt tat ggt att att cct gag aag ggt aag cct gtg
 384
 Ala Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro Val
 115 120 125
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 432
 Thr Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg
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 Phe Asp Arg Asn Gly Pro Ala Ala Ile Ala Lys Tyr Gln Ser Glu Asn
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 Asn Ile Ser Gly Gly Ser Asn Asp Cys Asn Ser Leu Val Gly Pro Thr
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 Pro His Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu
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 624
 Ser Ala Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu
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 672
 Glu Lys Gly Val Ser Pro Pro Trp Trp Pro Asn Gly Asn Glu Glu Trp
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 720
 Trp Pro Gln Leu Gly Leu Pro Asn Glu Gln Gly Pro Pro Pro Tyr Lys
 225 230 235 240
 aag cct cat gat ttg aag aaa gct tgg aaa gtc ggt gtt tta act gcg
 768
 Lys Pro His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala
 245 250 255
 gtg atc aag cat atg tcg ccg gat att gcg aag atc cgt aag ctt gtg
 816
 Val Ile Lys His Met Ser Pro Asp Ile Ala Lys Ile Arg Lys Leu Val
 260 265 270

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 Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala
 275 280 285
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 Thr Trp Leu Ala Ile Ile Asn Gln Glu Glu Val Val Ala Arg Glu Leu
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 Tyr Pro Glu Ser Cys Pro Pro Leu Ser Ser Ser Ser Ser Leu Gly Ser
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 Gly Ser Leu Leu Ile Asn Asp Cys Ser Glu Tyr Asp Val Glu Gly Phe
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 Glu Lys Glu Gln His Gly Phe Asp Val Glu Glu Arg Lys Pro Glu Ile
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 Val Met Met His Pro Leu Ala Ser Phe Gly Val Ala Lys Met Gln His
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 1296
 Asn Leu Gly Phe Gln Asp Arg Ser Ser Arg Asp Asn His Gln Met Val
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 1344
 Cys Pro Tyr Arg Asp Asn Arg Leu Ala Tyr Gly Ala Ser Lys Phe His
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 atg ggt gga atg aaa cta gta gtt cct cag caa cca gtc caa ccg atc
 1392
 Met Gly Gly Met Lys Leu Val Val Pro Gln Gln Pro Val Gln Pro Ile
 450 455 460

gac cta tcg ggc gtt gga gtt ccg gaa aac ggg cag aag atg atc acc
1440

Asp Leu Ser Gly Val Gly Val Pro Glu Asn Gly Gln Lys Met Ile Thr
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1488

Glu Leu Met Ala Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Pro
485 490 495

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1536

Pro Thr Leu Met Glu Asn Gln Ser Met Val Ile Asp Ala Lys Ala Ala
500 505 510

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1584

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515 520 525

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1632

Gln Gly Thr Asn Asn Gly Val Asn Asn Arg Phe Gln Met Val Phe Asp
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1680

Ser Thr Pro Phe Asp Met Ala Ala Phe Asp Tyr Arg Asp Asp Trp Gln
545 550 555 560

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1728

Thr Gly Ala Met Glu Gly Met Gly Lys Gln Gln Gln Gln Gln Gln
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1755

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35 40 45

Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
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Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys

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Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys						
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Thr Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg						
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Phe Asp Arg Asn Gly Pro Ala Ala Ile Ala Lys Tyr Gln Ser Glu Asn						
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Asn Ile Ser Gly Gly Ser Asn Asp Cys Asn Ser Leu Val Gly Pro Thr						
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Pro His Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu						
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Ser Ala Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu						
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Glu Lys Gly Val Ser Pro Pro Trp Trp Pro Asn Gly Asn Glu Glu Trp						
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Trp Pro Gln Leu Gly Leu Pro Asn Glu Gln Gly Pro Pro Pro Tyr Lys						
			225			230
Lys Pro His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala						
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Val Ile Lys His Met Ser Pro Asp Ile Ala Lys Ile Arg Lys Leu Val						
			260			265
Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala						
			275			280
Thr Trp Leu Ala Ile Ile Asn Gln Glu Glu Val Val Ala Arg Glu Leu						
			290			295
Tyr Pro Glu Ser Cys Pro Pro Leu Ser Ser Ser Ser Ser Leu Gly Ser						
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						315
						320

Gly Ser Leu Leu Ile Asn Asp Cys Ser Glu Tyr Asp Val Glu Gly Phe
 325 330 335

Glu Lys Glu Gln His Gly Phe Asp Val Glu Glu Arg Lys Pro Glu Ile
 340 345, 350

Val Met Met His Pro Leu Ala Ser Phe Gly Val Ala Lys Met Gln His
 355 360 365

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 370 375 380

Arg Lys Arg Lys Gln Asn Asn Asp Met Asn Val Met Val Met Asp Arg
 385 390 395 400

Ser Ala Gly Tyr Thr Cys Glu Asn Gly Gln Cys Pro His Ser Lys Met
 405 410 415

Asn Leu Gly Phe Gln Asp Arg Ser Ser Arg Asp Asn His Gln Met Val
 420 425 430

Cys Pro Tyr Arg Asp Asn Arg Leu Ala Tyr Gly Ala Ser Lys Phe His
 435 440 445

Met Gly Gly Met Lys Leu Val Val Pro Gln Gln Pro Val Gln Pro Ile
 450 455 460

Asp Leu Ser Gly Val Gly Val Pro Glu Asn Gly Gln Lys Met Ile Thr
 465 470 475 480

Glu Leu Met Ala Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Pro
 485 490 495

Pro Thr Leu Met Glu Asn Gln Ser Met Val Ile Asp Ala Lys Ala Ala
 500 505 510

Gln Asn Gln Gln Leu Asn Phe Asn Ser Gly Asn Gln Met Phe Met Gln
 515 520 525

Gln Gly Thr Asn Asn Gly Val Asn Asn Arg Phe Gln Met Val Phe Asp
 530 535 540

Ser Thr Pro Phe Asp Met Ala Ala Phe Asp Tyr Arg Asp Asp Trp Gln
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Gln Gln Asp Val Ser Ile Trp Phe
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 120

ttttcttca tcatttttat tctccttctt cttctgctgt tcatttctcc aggttaca
 178

atg atg ttt aat gag atg gga atg tgt gga aac atg gat ttc ttc tct
 226
 Met Met Phe Asn Glu Met Gly Met Cys Gly Asn Met Asp Phe Phe Ser
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 274
 Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu
 20 25 30

cct gat tcc att gtt gaa gat gac tat act gat gat gag att gat gtt
 322
 Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val
 35 40 45

gat gaa ttg gag agg agg atg tgg aga gac aaa atg cgg ctt aaa cgt
 370
 Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
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ctc aag gag cag gat aag ggt aaa gaa ggt gtt gat gct gct aaa cag
 418
 Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
 65 70 75 80

agg cag tct caa gag caa gct agg agg aag aaa atg tct aga gct caa
 466
 Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
 85 90 95

gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa gct
 514
 Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
 100 105 110

caa ggc ttt gtt tat ggg att att ccg gag aat ggg aag cct gtg act
 562
 Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
 115 120 125

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 610
 Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
 130 135 140
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 658
 Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
 145 150 155 160
 atc ccg ggg att cat gaa ggt aat aac ccg att gga ccg act cct cat
 706
 Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
 165 170 175
 acc ttg caa gag ctt caa gac acg act ctt gga tcg ctt ttg tct gcg
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 802
 Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
 195 200 205
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 Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
 210 215 220
 caa ctt ggt ttg cct aaa gat caa ggt cct gca cct tac aag aag cct
 898
 Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
 225 230 235 240
 cat gat ttg aag aag gcg tgg aaa gtc ggc gtt ttg act gcg gtt atc
 946
 His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
 245 250 255
 aag cat atg ttt cct gat att gct aag atc cgt aag ctc gtg agg caa
 994
 Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
 260 265 270
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 1042
 Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
 275 280 285
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 1090
 Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
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 gag tca tgt cca cct ctt tct ctg tct ggt gga agt tgc tcg ctt ctg
 1138
 Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
 305 310 315 320

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 1186
 Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
 325 330 335

cac tat gaa gtg gaa gag ctc aag cca gaa aaa gtt atg aat tct tca
 1234
 His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
 340 345 350

aac ttt ggg atg gtt gct aaa atg cat gac ttt cct gtc aaa gaa gaa
 1282
 Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
 355 360 365

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 1330
 Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
 370 375 380

gat ctg aac act att atg gac aga acc gtt ttc acc tgc gag aat ctt
 1378
 Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
 385 390 395 400

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 Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
 405 410 415

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 1474
 Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
 420 425 430

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 1522
 Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
 435 440 445

gtt gga ttt cct cag cca agg cca gtg aac tca gta gcc caa cca att
 1570
 Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
 450 455 460

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 Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
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 1666
 Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met
 485 490 495

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 1714
 Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
 500 505 510

cat caa gaa cat ctc cag ttc cca gga aac atg gtg gaa gga agt ttc
1762

His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
515 520 525

ttt gaa gac ttg aac atc cca aac aga gca aac aac aac aac agc agc
1810

Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser
530 535 540

aac aat caa acg ttt ttt caa ggg aac aac aac aac aat gtg ttt
1858

Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Asn Val Phe
545 550 555 560

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1906

Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
565 570 575

aac aat aac agt agc ggc aac agg ttc cag ctt gtg ttt gat tcc aca
1954

Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
580 585 590

ccg ttc gac atg gcg tca ttc gat tac aga gat gat atg tcg atg cca
2002

Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
595 600 605

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2050

Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val
610 615 620

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2105

Ser Ile Trp Phe
625

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2165

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Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln	65		70		75	80
Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln		85		90		95
Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala		100		105		110
Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr		115		120		125
Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe		130		135		140
Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn	145		150		155	160
Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His		165		170		175
Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala		180		185		190
Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys		195		200		205
Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro	210		215		220	
Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro	225		230		235	240
His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile		245		250		255
Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln		260		265		270

Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
 275 280 285

Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
 290 295 300

Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
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Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
 325 330 335

His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
 340 345 350

Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
 355 360 365

Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
 370 375 380

Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
 385 390 395 400

Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
 405 410 415

Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
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Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
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Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
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Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
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Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met
 485 490 495

Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
 500 505 510

His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
515 520 525

Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser
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Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
565 570 575

Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
580 585 590

Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
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Ser Ile Trp Phe
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Met Ala Asp Pro Asn Asn Pro Ile Thr Glu Pro Lys Ala Ile
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158

Ile Gln Ser Ser Thr Ser Ser Ser Val Thr Ile Val Pro Val Pro Thr
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206

Cys Gly Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys Pro
35 40 45

ctt gat act atc act act act act act act gtt tgt ttt gcg gct cct
254

Leu Asp Thr Ile Thr Thr Thr Thr Thr Thr Val Cys Phe Ala Ala Pro
50 55 60

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 Cys Arg Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Thr
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 Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu Leu
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 Asn Phe Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Leu Ser Ser Ser
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 638
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 686
 Tyr Asp Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu
 195 200 205
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 734
 Leu Leu Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met Met
 210 215 220
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 782
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 225 230 235
 aat tct gat gga gag agc ttg tgg agc tat tga tcgattgaaa gcagtttaat
 835
 Asn Ser Asp Gly Glu Ser Leu Trp Ser Tyr
 240 245

atcttttttg gatcctttgt tcacgtttat gctagtcac tttgtttcct tctcctatga
895

ttgttagaga tgatttgta aatatataat cgtaatgatt ttcacttttt tttattcaaa
955

aaaaaaaa
963

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20 25 30

Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys Pro Leu Asp
35 40 45

Thr Ile Thr Thr Thr Thr Thr Thr Val Cys Phe Ala Ala Pro Ser Ser
50 55 60

Thr Ala Ser Gly Asn Asp Ile Asn Thr Leu Met Ala Thr Asp Thr Asp
65 70 75 80

Ile Ser Arg Arg Lys Lys Asn Pro Val Tyr Arg Gly Ile Arg Cys Arg
85 90 95

Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Thr Thr Arg
100 105 110

Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala Ala Tyr
115 120 125

Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu Leu Asn Phe
130 135 140

Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Leu Ser Ser Ser Ala Ala
145 150 155 160

His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg Gly Ala Ala
165 170 175

Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys Val Tyr Asp
180 185 190

Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu Leu Leu
 195 200 205

Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met Met Val Ala
 210 215 220

Pro Pro Trp Met Gly Ser Pro Pro Ser Asp Asp Ser Pro Glu Asn Ser
 225 230 235 240

Asp Gly Glu Ser Leu Trp Ser Tyr
 245

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ctc tcc atc tct act act cca aag ccg aca acg acg acg gag aag aaa
 98
 Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys
 20 25 30

ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc
 146
 Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser
 35 40 45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag
 194
 Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu
 50 55 60

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct
 242
 Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
 65 70 75

aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg
 290
 Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp
 80 85 90 95

ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc
 338
 Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile
 100 105 110

gcc gtg agg aga ttc cgc ggc cgc gac gcc gtc act aac ttc aaa tct
 386
 Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser
 115 120 125

caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct
 434
 Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser
 130 135 140
 aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag
 482
 Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu
 145 150 155
 ttt gag cag agt aga cgg aag ttt gtt aac ggc gac gga aaa cgc tct
 530
 Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser
 160 165 170 175
 ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gcg cgt
 578
 Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg
 180 185 190
 gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg
 626
 Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
 195 200 205
 aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta
 674
 Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu
 210 215 220
 ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc
 722
 Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly
 225 230 235
 gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt
 770
 Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg
 240 245 250 255
 tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag ggc tgg
 818
 Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp
 260 265 270
 agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt
 866
 Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys
 275 280 285
 ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa
 914
 Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys
 290 295 300
 gtc cgg tct agt ccg gtt cag act gtg gtt agg cta ttc gga gtc aac
 962
 Val Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn
 305 310 315

att ttc aat gtg agt aac gag aaa cca aac gac gtc gca gta gag tgt
 1010
 Ile Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys
 320 325 330 335
 gtt ggc aag aag aga tct cgg gaa gat gat ttg ttt tcg tta ggg tgt
 1058
 Val Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys
 340 345 350
 tcc aag aag cag gcg att atc aac atc ttg tga caaattcttt ttttttggtt
 1111
 Ser Lys Lys Gln Ala Ile Ile Asn Ile Leu
 355 360
 tttttcttca atttgtttct cctttttcaa ttttttgtat tgaaatgaca agttgtaaat
 1171
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 1239

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 Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys Leu
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 Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser Gly
 35 40 45
 Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu Ser
 50 55 60
 Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro Asn
 65 70 75 80
 Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp Leu
 85 90 95
 Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile Ala
 100 105 110
 Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser Gln
 115 120 125
 Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser Lys

130 135 140
 Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
 145 150 155 160
 Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
 165 170 175
 Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
 180 185 190
 Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
 195 200 205
 Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
 210 215 220
 Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
 225 230 235 240
 Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
 245 250 255
 Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
 260 265 270
 Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
 275 280 285
 Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
 290 295 300
 Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
 305 310 315 320
 Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
 325 330 335
 Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
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 Lys Lys Gln Ala Ile Ile Asn Ile Leu
 355 360

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57 Met Tyr
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gga cag tgc aat ata gaa tcc gac tac gct ttg ttg gag tcg ata aca
105
Gly Gln Cys Asn Ile Glu Ser Asp Tyr Ala Leu Leu Glu Ser Ile Thr
5 10 15

cgt cac ttg cta gga gga gga gga gag aac gag ctg cga ctc aat gag
153
Arg His Leu Leu Gly Gly Gly Glu Asn Glu Leu Arg Leu Asn Glu
20 25 30

tca aca ccg agt tcg tgt ttc aca gag agt tgg gga ggt ttg cca ttg
201
Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu Pro Leu
35 40 45 50

aaa gag aat gat tca gag gac atg ttg gtg tac gga ctc ctc aaa gat
249
Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu Lys Asp
55 60 65

gcc ttc cat ttt gac acg tca tca tcg gac ttg agc tgt ctt ttt gat
297
Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu Phe Asp
70 75 80

ttt ccg gcg gtt aaa gtc gag cca act gag aac ttt acg gcg atg gag
345
Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala Met Glu
85 90 95

gag aaa cca aag aaa gcg ata ccg gtt acg gag acg gca gtg aag gcg
393
Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val Lys Ala
100 105 110

aag cat tac aga gga gtg agg cag aga ccg tgg ggg aaa ttc gcg gcg
441
Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala Ala
115 120 125 130

gag ata cgt gat ccg gcg aag aat gga gct agg gtt tgg tta ggg acg
489
Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu Gly Thr
135 140 145

ttt gag acg gcg gaa gat gcg gct tta gct tac gat ata gct gct ttt
537
Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala Ala Phe
150 155 160

agg atg cgt ggt tcc cgc gct tta ttg aat ttt ccg ttg agg gtt aat
585
Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg Val Asn
165 170 175

tcc ggt gaa cct gac ccg gtt cgg atc acg tct aag aga tct tct tcg
633

Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser Ser Ser
180 185 190

tcg tcg tcg tcg tcg tcc tct tct acg tcg tcg tct gaa aac ggg aag
681

Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn Gly Lys
195 200 205 210

ttg aaa cga agg aga aaa gca gag aat ctg acg tcg gag gtg gtg cag
729

Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val Val Gln
215 220 225

gtg aag tgt gag gtt ggt gat gag aca cgt gtt gat gag tta ttg gtt
777

Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu Leu Val
230 235 240

tca taa gtttgatcct gtgtgttttg tagttgaata gttttgctat aaatgttgag
833

Ser

gcaccaagta aaagtgttcc cgtgatgtaa attagttact aaacagagcc atatatcttc
893

aatcaaaaaa aaaaaaaaaa
913

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364

Met Tyr Gly Gln Cys Asn Ile Glu Ser Asp Tyr Ala Leu Leu Glu Ser
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Ile Thr Arg His Leu Leu Gly Gly Gly Glu Asn Glu Leu Arg Leu
20 25 30

Asn Glu Ser Thr Pro Ser Ser Cys Phe Thr Glu Ser Trp Gly Gly Leu
35 40 45

Pro Leu Lys Glu Asn Asp Ser Glu Asp Met Leu Val Tyr Gly Leu Leu
50 55 60

Lys Asp Ala Phe His Phe Asp Thr Ser Ser Ser Asp Leu Ser Cys Leu
65 70 75 80

Phe Asp Phe Pro Ala Val Lys Val Glu Pro Thr Glu Asn Phe Thr Ala
85 90 95

Met Glu Glu Lys Pro Lys Lys Ala Ile Pro Val Thr Glu Thr Ala Val

100 105 110
 Lys Ala Lys His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe
 115 120 125
 Ala Ala Glu Ile Arg Asp Pro Ala Lys Asn Gly Ala Arg Val Trp Leu
 130 135 140
 Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Leu Ala Tyr Asp Ile Ala
 145 150 155 160
 Ala Phe Arg Met Arg Gly Ser Arg Ala Leu Leu Asn Phe Pro Leu Arg
 165 170 175
 Val Asn Ser Gly Glu Pro Asp Pro Val Arg Ile Thr Ser Lys Arg Ser
 180 185 190
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Glu Asn
 195 200 205
 Gly Lys Leu Lys Arg Arg Arg Lys Ala Glu Asn Leu Thr Ser Glu Val
 210 215 220
 Val Gln Val Lys Cys Glu Val Gly Asp Glu Thr Arg Val Asp Glu Leu
 225 230 235 240
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 110

Met Ala Gln Leu Pro Pro Lys Ile Pro Asn Met Thr Gln His Trp
 1 5 10 15

cct gat ttc tct tcc caa aag ctc tct cct ttc tct acc cca acc gca
 158

Pro Asp Phe Ser Ser Gln Lys Leu Ser Pro Phe Ser Thr Pro Thr Ala
 20 25 30

acc gct gtc gcc acc gct aca acc acc gta caa aac ccc tca tgg gtc
 206

Thr Ala Val Ala Thr Ala Thr Thr Thr Val Gln Asn Pro Ser Trp Val
 35 40 45

gac gaa ttc ctc gac ttc tca gcg tct cgc cgt ggc aac cac cgt cgt
 254
 Asp Glu Phe Leu Asp Phe Ser Ala Ser Arg Arg Gly Asn His Arg Arg
 50 55 60
 tcc atc agc gac tct atc gca ttc ctc gaa gct cca aca gtc agc atc
 302
 Ser Ile Ser Asp Ser Ile Ala Phe Leu Glu Ala Pro Thr Val Ser Ile
 65 70 75
 gaa gac cac caa ttc gac agg ttc gat gac gaa cag ttc atg tcg atg
 350
 Glu Asp His Gln Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met
 80 85 90 95
 ttc acc gac gac gac aac ctt cat agc aat cct tcc cat atc aac aac
 398
 Phe Thr Asp Asp Asp Asn Leu His Ser Asn Pro Ser His Ile Asn Asn
 100 105 110
 aaa aat aac aat gtg ggg ccc acg gga tct tcc tcg aac aca tcc acg
 446
 Lys Asn Asn Asn Val Gly Pro Thr Gly Ser Ser Ser Asn Thr Ser Thr
 115 120 125
 ccg tcc aat agc ttc aac gac gat aac aaa gaa tta cca ccg tcc gat
 494
 Pro Ser Asn Ser Phe Asn Asp Asp Asn Lys Glu Leu Pro Pro Ser Asp
 130 135 140
 cat aac atg aac aat aat atc aac aac aac tat aac gat gaa gtc caa
 542
 His Asn Met Asn Asn Asn Ile Asn Asn Asn Tyr Asn Asp Glu Val Gln
 145 150 155
 agc caa tgc aag atg gag cca gaa gat ggt acg gcg tcg aat aac aat
 590
 Ser Gln Cys Lys Met Glu Pro Glu Asp Gly Thr Ala Ser Asn Asn Asn
 160 165 170 175
 tcc ggt gat agc tcc ggc aac cgg att ctc gat ccc aaa agg gtt aag
 638
 Ser Gly Asp Ser Ser Gly Asn Arg Ile Leu Asp Pro Lys Arg Val Lys
 180 185 190
 aga ata tta gca aat cgg caa tca gca cag aga tca agg gtg agg aaa
 686
 Arg Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys
 195 200 205
 ctg caa tac ata tca gag ctc gaa cgt agc gtc act tcg ttg cag gcg
 734
 Leu Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Ala
 210 215 220
 gaa gtg tca gtg tta tcg cca aga gtt gca ttc ttg gat cat caa cgt
 782
 Glu Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg
 225 230 235

ttg ctt ctt aac gtt gac aac agc gct ctc aag caa cga atc gct gct
830

Leu Leu Leu Asn Val Asp Asn Ser Ala Leu Lys Gln Arg Ile Ala Ala
240 245 250 255

tta tct caa gac aag ctt ttc aaa gac gca cat caa gaa gca ttg aag
878

Leu Ser Gln Asp Lys Leu Phe Lys Asp Ala His Gln Glu Ala Leu Lys
260 265 270

aga gaa ata gag aga ctt cga caa gtg tat aat caa caa agc ctc acg
926

Arg Glu Ile Glu Arg Leu Arg Gln Val Tyr Asn Gln Gln Ser Leu Thr
275 280 285

aat gtg gaa aat gca aat cat tta tcg gcg acc gga gcc ggt gct act
974

Asn Val Glu Asn Ala Asn His Leu Ser Ala Thr Gly Ala Gly Ala Thr
290 295 300

ccg gcc gtc gac atc aag tcg tcc gtt gaa aca gag cag ctc ctc aat
1022

Pro Ala Val Asp Ile Lys Ser Ser Val Glu Thr Glu Gln Leu Leu Asn
305 310 315

gtc tca taa attaaccatc atgcatcatc atcaacattt ctctctttta
1071

Val Ser
320

gcttcttgcc aaaagttctt gactataaaa tctcttttcgg gtaagaaatt caggagatat
1131

acatttttta ttctaatacac attgttttta agttgtgatg aattcagttt gatgtatctt
1191

atttattttg tttatgtcgt ctttttttct tgggggttgat ggaaggaat catcaattgt
1251

tgtttgtaca aagaactagt tgaatttttt tttttttttt
1291

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366

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1 5 10 15

Asp Phe Ser Ser Gln Lys Leu Ser Pro Phe Ser Thr Pro Thr Ala Thr
20 25 30

Ala Val Ala Thr Ala Thr Thr Thr Val Gln Asn Pro Ser Trp Val Asp
35 40 45

Glu Phe Leu Asp Phe Ser Ala Ser Arg Arg Gly Asn His Arg Arg Ser
50 55 60

Ile Ser Asp Ser Ile Ala Phe Leu Glu Ala Pro Thr Val Ser Ile Glu
 65 70 75 80
 Asp His Gln Phe Asp Arg Phe Asp Asp Glu Gln Phe Met Ser Met Phe
 85 90 95
 Thr Asp Asp Asp Asn Leu His Ser Asn Pro Ser His Ile Asn Asn Lys
 100 105 110
 Asn Asn Asn Val Gly Pro Thr Gly Ser Ser Ser Asn Thr Ser Thr Pro
 115 120 125
 Ser Asn Ser Phe Asn Asp Asp Asn Lys Glu Leu Pro Pro Ser Asp His
 130 135 140
 Asn Met Asn Asn Asn Ile Asn Asn Asn Tyr Asn Asp Glu Val Gln Ser
 145 150 155 160
 Gln Cys Lys Met Glu Pro Glu Asp Gly Thr Ala Ser Asn Asn Asn Ser
 165 170 175
 Gly Asp Ser Ser Gly Asn Arg Ile Leu Asp Pro Lys Arg Val Lys Arg
 180 185 190
 Ile Leu Ala Asn Arg Gln Ser Ala Gln Arg Ser Arg Val Arg Lys Leu
 195 200 205
 Gln Tyr Ile Ser Glu Leu Glu Arg Ser Val Thr Ser Leu Gln Ala Glu
 210 215 220
 Val Ser Val Leu Ser Pro Arg Val Ala Phe Leu Asp His Gln Arg Leu
 225 230 235 240
 Leu Leu Asn Val Asp Asn Ser Ala Leu Lys Gln Arg Ile Ala Ala Leu
 245 250 255
 Ser Gln Asp Lys Leu Phe Lys Asp Ala His Gln Glu Ala Leu Lys Arg
 260 265 270
 Glu Ile Glu Arg Leu Arg Gln Val Tyr Asn Gln Gln Ser Leu Thr Asn
 275 280 285
 Val Glu Asn Ala Asn His Leu Ser Ala Thr Gly Ala Gly Ala Thr Pro
 290 295 300

Ala Val Asp Ile Lys Ser Ser Val Glu Thr Glu Gln Leu Leu Asn Val
 305 310 315 320

Ser

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tttcaataaa atagaaaaaa acatatacaa atctacagag aagagaagct ttattttaat
 120

cttggtgtgtg tgtgtgtgtt ttatataatt tttatttttt ttcaaattaa aatctcttct
 180

ttgcttttga tgtgggc atg gct ggt ctt gat cta ggc aca gct ttt cgt
 230

Met Ala Gly Leu Asp Leu Gly Thr Ala Phe Arg
 1 5 10

tac gtt aat cac cag ctc cat cgt ccc gat ctc cac ctt cac cac aat
 278

Tyr Val Asn His Gln Leu His Arg Pro Asp Leu His Leu His His Asn
 15 20 25

tcc tcc tcc gat gac gtc act ccc gga gcc ggg atg ggt cat ttc acc
 326

Ser Ser Ser Asp Asp Val Thr Pro Gly Ala Gly Met Gly His Phe Thr
 30 35 40

gtc gac gac gaa gac aac aac aac aac cat caa ggt ctt gac tta gcc
 374

Val Asp Asp Glu Asp Asn Asn Asn Asn His Gln Gly Leu Asp Leu Ala
 45 50 55

tct ggt gga gga tca gga agc tct gga gga gga gga ggt cac ggc ggg
 422

Ser Gly Gly Gly Ser Gly Ser Ser Gly Gly Gly Gly Gly His Gly Gly
 60 65 70 75

gga gga gac gtc gtt ggt cgt cgt cca cgt ggc aga cca ccg gga tcc
 470

Gly Gly Asp Val Val Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser
 80 85 90

aag aac aaa ccg aaa cct ccg gta att atc acg cgc gag agc gca aac
 518

Lys Asn Lys Pro Lys Pro Pro Val Ile Ile Thr Arg Glu Ser Ala Asn
 95 100 105

act cta aga gct cac att ctt gaa gta aca aac ggc tgc gat gtt ttc
 566

Thr Leu Arg Ala His Ile Leu Glu Val Thr Asn Gly Cys Asp Val Phe
 110 115 120

gac tgc gtt gcg act tat gct cgt cgg aga cag cga ggg atc tgc gtt
 614
 Asp Cys Val Ala Thr Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val
 125 130 135
 ctg agc ggt agc gga acg gtc acg aac gtc agc ata cgt cag cca tct
 662
 Leu Ser Gly Ser Gly Thr Val Thr Asn Val Ser Ile Arg Gln Pro Ser
 140 145 150 155
 gcg gct gga gcg gtt gtg acg cta caa gga acg ttc gag att ctt tct
 710
 Ala Ala Gly Ala Val Val Thr Leu Gln Gly Thr Phe Glu Ile Leu Ser
 160 165 170
 ctc tcc gga tcg ttt ctt cct cct ccg gca cct ccc gga gca acg agt
 758
 Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser
 175 180 185
 ttg aca att ttc tta gcc gga gga caa ggt cag gtg gtt gga gga agc
 806
 Leu Thr Ile Phe Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser
 190 195 200
 gtt gtg ggt gag ctt acg gcg gct gga ccg gtg att gtg att gca gct
 854
 Val Val Gly Glu Leu Thr Ala Ala Gly Pro Val Ile Val Ile Ala Ala
 205 210 215
 tcg ttt act aat gtt gct tat gag aga ctt cct tta gaa gaa gat gag
 902
 Ser Phe Thr Asn Val Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu
 220 225 230 235
 cag cag caa cag ctt gga gga gga tct aac ggc gga ggt aat ttg ttt
 950
 Gln Gln Gln Gln Leu Gly Gly Gly Ser Asn Gly Gly Gly Asn Leu Phe
 240 245 250
 ccg gag gtg gca gct gga gga gga gga gga ctt ccg ttc ttt aat tta
 998
 Pro Glu Val Ala Ala Gly Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu
 255 260 265
 ccg atg aat atg caa cca aat gtg caa ctt ccg gtg gaa ggt tgg ccg
 1046
 Pro Met Asn Met Gln Pro Asn Val Gln Leu Pro Val Glu Gly Trp Pro
 270 275 280
 ggg aat tcc ggt gga aga ggt cct ttc tga tgtgtatata ttgataatca
 1096
 Gly Asn Ser Gly Gly Arg Gly Pro Phe
 285 290
 ttatatatat accggcggag aagcttttcc ggcgaagaat ttgcgagagt gaagaaaggt
 1156
 tagaaaagct tttaatggac taatgaatctt caaattatca tcgtgatttc ggacattgtc
 1216

ttgttcacatca tgtaagctt aggtttatatt tttgtcgttt gtagaatttt atgtttgaat
1276

cctttttttt ttctgtgaaa ctctattgtg ttcgtctgcg aaggaaaaaa aaattctcaa
1336

aaaaaa
1342

<210> 368 <211> 292 <212> PRT <213> Arabidopsis thaliana <400>
368

Met Ala Gly Leu Asp Leu Gly Thr Ala Phe Arg Tyr Val Asn His Gln
1 5 10 15

Leu His Arg Pro Asp Leu His Leu His His Asn Ser Ser Ser Asp Asp
20 25 30

Val Thr Pro Gly Ala Gly Met Gly His Phe Thr Val Asp Asp Glu Asp
35 40 45

Asn Asn Asn Asn His Gln Gly Leu Asp Leu Ala Ser Gly Gly Gly Ser
50 55 60

Gly Ser Ser Gly Gly Gly Gly Gly His Gly Gly Gly Gly Asp Val Val
65 70 75 80

Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys
85 90 95

Pro Pro Val Ile Ile Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His
100 105 110

Ile Leu Glu Val Thr Asn Gly Cys Asp Val Phe Asp Cys Val Ala Thr
115 120 125

Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Ser Gly
130 135 140

Thr Val Thr Asn Val Ser Ile Arg Gln Pro Ser Ala Ala Gly Ala Val
145 150 155 160

Val Thr Leu Gln Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe
165 170 175

Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe Leu
180 185 190

Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Glu Leu
195 200 205

Thr Ala Ala Gly Pro Val Ile Val Ile Ala Ala Ser Phe Thr Asn Val
210 215 220

Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu Gln Gln Gln Gln Leu
225 230 235 240

Gly Gly Gly Ser Asn Gly Gly Gly Asn Leu Phe Pro Glu Val Ala Ala
245 250 255

Gly Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu Pro Met Asn Met Gln
260 265 270

Pro Asn Val Gln Leu Pro Val Glu Gly Trp Pro Gly Asn Ser Gly Gly
275 280 285

Arg Gly Pro Phe
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Met Glu Glu Arg Glu Gly Thr Asn Ile Asn Asn Ile Pro Thr Ser Phe
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ggt ctg aaa caa cat gaa act cct ctt cct cct cct ggt tac cca cca
96
Gly Leu Lys Gln His Glu Thr Pro Leu Pro Pro Pro Gly Tyr Pro Pro
20 25 30
cgg tct gaa aac cct aat ctt ttt ccg gtg ggt caa tcc agc act tcc
144
Arg Ser Glu Asn Pro Asn Leu Phe Pro Val Gly Gln Ser Ser Thr Ser
35 40 45
tcc gcc gcc gcc gcg gtg aaa cct tct gag aat gtt gct cct cct ttt
192
Ser Ala Ala Ala Ala Val Lys Pro Ser Glu Asn Val Ala Pro Pro Phe
50 55 60
agc tta aca atg ccg gtg gag aat tct tct tct gag ttg aag aag aag
240
Ser Leu Thr Met Pro Val Glu Asn Ser Ser Ser Glu Leu Lys Lys Lys
65 70 75 80
aga ggg aga cca aga aag tat aac cct gac ggc tca ctc gct gtg act
288
Arg Gly Arg Pro Arg Lys Tyr Asn Pro Asp Gly Ser Leu Ala Val Thr
85 90 95

ctc tct cct atg cct atc tca tcc tcc gtt ccg ttg acg tcg gag ttt
 336
 Leu Ser Pro Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe
 100 105 110

ggt tct cgg aaa cga gga aga ggt cga gga aga ggc aga gga aga gga
 384
 Gly Ser Arg Lys Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly
 115 120 125

cga gga cgt gga caa gga caa gga agc aga gag ccc aat aac aac aac
 432
 Arg Gly Arg Gly Gln Gly Gln Gly Ser Arg Glu Pro Asn Asn Asn Asn
 130 135 140

aac gac aac aat tgg ctc aag aat cct cag atg ttc gaa ttt aac aac
 480
 Asn Asp Asn Asn Trp Leu Lys Asn Pro Gln Met Phe Glu Phe Asn Asn
 145 150 155 160

aac act cct act tct ggt gga gga gga cct gct gaa att gtc agt cca
 528
 Asn Thr Pro Thr Ser Gly Gly Gly Gly Pro Ala Glu Ile Val Ser Pro
 165 170 175

agt ttt aca cct cat gtg ctc aca gta aat gcc ggt gag gat gtg aca
 576
 Ser Phe Thr Pro His Val Leu Thr Val Asn Ala Gly Glu Asp Val Thr
 180 185 190

atg aag ata atg aca ttc tct caa caa ggc tcg cgt gct att tgt att
 624
 Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg Ala Ile Cys Ile
 195 200 205

ctt tca gcg aac ggt ccc ata tcc aat gtt aca ctt cgt caa tct atg
 672
 Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu Arg Gln Ser Met
 210 215 220

aca tct ggt ggt act ctc act tat gag ggt cat ttt gag att ctt tct
 720
 Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly His Phe Glu Ile Leu Ser
 225 230 235 240

ttg acg ggt tcg ttt ata cca agc gag agt gga gga acc cga agc aga
 768
 Leu Thr Gly Ser Phe Ile Pro Ser Glu Ser Gly Gly Thr Arg Ser Arg
 245 250 255

gct ggt ggg atg agt gtc tct ctt gca gga caa gat ggt cgt gtc ttt
 816
 Ala Gly Gly Met Ser Val Ser Leu Ala Gly Gln Asp Gly Arg Val Phe
 260 265 270

ggt ggt gga ctt gct ggt ctc ttt att gcc gct ggt cct gtt cag gta
 864
 Gly Gly Gly Leu Ala Gly Leu Phe Ile Ala Ala Gly Pro Val Gln Val
 275 280 285

atg gta ggg agt ttt ata gcg ggt cag gag gaa tcg cag cag cag cag
 912
 Met Val Gly Ser Phe Ile Ala Gly Gln Glu Glu Ser Gln Gln Gln Gln
 290 295 300
 cag cag ata aag aag caa aga agg gaa aga ctc ggg atc ccg aca aca
 960
 Gln Gln Ile Lys Lys Gln Arg Arg Glu Arg Leu Gly Ile Pro Thr Thr
 305 310 315 320
 aca caa gct tct aat atc tca ttc ggt ggc tca gcg gaa gat cct aag
 1008
 Thr Gln Ala Ser Asn Ile Ser Phe Gly Gly Ser Ala Glu Asp Pro Lys
 325 330 335
 gct aga tac ggg ctc aac aag cct gtt gtt att cag cca cca ccg gtg
 1056
 Ala Arg Tyr Gly Leu Asn Lys Pro Val Val Ile Gln Pro Pro Pro Val
 340 345 350
 tct gca cca cct gtg tcc ttt tcg cat gaa cca agt act aac acc gtc
 1104
 Ser Ala Pro Pro Val Ser Phe Ser His Glu Pro Ser Thr Asn Thr Val
 355 360 365
 cat ggt tac tat gca aat aac aca gct aac cat atc aag gat ctc ttc
 1152
 His Gly Tyr Tyr Ala Asn Asn Thr Ala Asn His Ile Lys Asp Leu Phe
 370 375 380
 tct tcc ctc cct gga gaa gat agg gaa gaa gat gag gat gat tta gaa
 1200
 Ser Ser Leu Pro Gly Glu Asp Arg Glu Glu Asp Glu Asp Asp Leu Glu
 385 390 395 400
 ggt gaa gat gat gaa gaa ttc gga ggc cat agc gaa tct gac acc gag
 1248
 Gly Glu Asp Asp Glu Glu Phe Gly Gly His Ser Glu Ser Asp Thr Glu
 405 410 415
 gtt cca agc tga tgatcgatgg aaagaatccg acatatatgt gttatgaatc
 1300
 Val Pro Ser
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 1360
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 1420
 tagaggatgt aatcttttagg gttctttgac ttgtgtcttt cttttaatcc tcagatgggt
 1480
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 1556

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20 25 30

Arg Ser Glu Asn Pro Asn Leu Phe Pro Val Gly Gln Ser Ser Thr Ser
35 40 45

Ser Ala Ala Ala Ala Val Lys Pro Ser Glu Asn Val Ala Pro Pro Phe
50 55 60

Ser Leu Thr Met Pro Val Glu Asn Ser Ser Ser Glu Leu Lys Lys Lys
65 70 75 80

Arg Gly Arg Pro Arg Lys Tyr Asn Pro Asp Gly Ser Leu Ala Val Thr
85 90 95

Leu Ser Pro Met Pro Ile Ser Ser Ser Val Pro Leu Thr Ser Glu Phe
100 105 110

Gly Ser Arg Lys Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly
115 120 125

Arg Gly Arg Gly Gln Gly Gln Gly Ser Arg Glu Pro Asn Asn Asn Asn
130 135 140

Asn Asp Asn Asn Trp Leu Lys Asn Pro Gln Met Phe Glu Phe Asn Asn
145 150 155 160

Asn Thr Pro Thr Ser Gly Gly Gly Gly Pro Ala Glu Ile Val Ser Pro
165 170 175

Ser Phe Thr Pro His Val Leu Thr Val Asn Ala Gly Glu Asp Val Thr
180 185 190

Met Lys Ile Met Thr Phe Ser Gln Gln Gly Ser Arg Ala Ile Cys Ile
195 200 205

Leu Ser Ala Asn Gly Pro Ile Ser Asn Val Thr Leu Arg Gln Ser Met
210 215 220

Thr Ser Gly Gly Thr Leu Thr Tyr Glu Gly His Phe Glu Ile Leu Ser
225 230 235 240

Leu Thr Gly Ser Phe Ile Pro Ser Glu Ser Gly Gly Thr Arg Ser Arg
 245 250 255

Ala Gly Gly Met Ser Val Ser Leu Ala Gly Gln Asp Gly Arg Val Phe
 260 265 270

Gly Gly Gly Leu Ala Gly Leu Phe Ile Ala Ala Gly Pro Val Gln Val
 275 280 285

Met Val Gly Ser Phe Ile Ala Gly Gln Glu Glu Ser Gln Gln Gln Gln
 290 295 300

Gln Gln Ile Lys Lys Gln Arg Arg Glu Arg Leu Gly Ile Pro Thr Thr
 305 310 315 320

Thr Gln Ala Ser Asn Ile Ser Phe Gly Gly Ser Ala Glu Asp Pro Lys
 325 330 335

Ala Arg Tyr Gly Leu Asn Lys Pro Val Val Ile Gln Pro Pro Pro Val
 340 345 350

Ser Ala Pro Pro Val Ser Phe Ser His Glu Pro Ser Thr Asn Thr Val
 355 360 365

His Gly Tyr Tyr Ala Asn Asn Thr Ala Asn His Ile Lys Asp Leu Phe
 370 375 380

Ser Ser Leu Pro Gly Glu Asp Arg Glu Glu Asp Glu Asp Asp Leu Glu
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Gly Glu Asp Asp Glu Glu Phe Gly Gly His Ser Glu Ser Asp Thr Glu
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Val Pro Ser

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 115

Met, Pro Leu Asp
 1

acc aaa cag cag aaa tgg ttg cca tta ggc tta aat cct caa gct tgt
 163
 Thr Lys Gln Gln Lys Trp Leu Pro Leu Gly Leu Asn Pro Gln Ala Cys
 5 10 15 20
 gtc cag gac aag gcg act gag tat ttc cgt cct gga att cct ttt ccg
 211
 Val Gln Asp Lys Ala Thr Glu Tyr Phe Arg Pro Gly Ile Pro Phe Pro
 25 30 35
 gaa ctc ggt aaa gtt tat gca gct gag cat cag ttt cgc tat ttg cag
 259
 Glu Leu Gly Lys Val Tyr Ala Ala Glu His Gln Phe Arg Tyr Leu Gln
 40 45 50
 cca ccg ttc caa gcc tta ttg tct aga tat gat cag cag tct tgt gga
 307
 Pro Pro Phe Gln Ala Leu Leu Ser Arg Tyr Asp Gln Gln Ser Cys Gly
 55 60 65
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 355
 Lys Gln Val Ser Cys Leu Asn Gly Arg Ser Ser Asn Gly Ala Ala Pro
 70 75 80
 gag ggg gca ctc aag tct tct cgg aaa aga ttt ata gta ttc gat cag
 403
 Glu Gly Ala Leu Lys Ser Ser Arg Lys Arg Phe Ile Val Phe Asp Gln
 85 90 95 100
 tcg gga gag cag act cgt ttg tta caa tgt gga ttt cct ctg cgg ttt
 451
 Ser Gly Glu Gln Thr Arg Leu Leu Gln Cys Gly Phe Pro Leu Arg Phe
 105 110 115
 cct tct tct atg gat gca gag cga ggg aac att ctc ggt gcc cta cac
 499
 Pro Ser Ser Met Asp Ala Glu Arg Gly Asn Ile Leu Gly Ala Leu His
 120 125 130
 cca gag aaa ggg ttt agt aaa gat cat gcc att caa gaa aag ata ttg
 547
 Pro Glu Lys Gly Phe Ser Lys Asp His Ala Ile Gln Glu Lys Ile Leu
 135 140 145
 caa cat gaa gat cat gaa aat ggc gaa gaa gac tcg gaa atg cac gaa
 595
 Gln His Glu Asp His Glu Asn Gly Glu Glu Asp Ser Glu Met His Glu
 150 155 160
 gac act gag gaa atc aac gcg tta ctg tat tct gat gat gac gat aat
 643
 Asp Thr Glu Glu Ile Asn Ala Leu Leu Tyr Ser Asp Asp Asp Asp Asn
 165 170 175 180
 gat gat tgg gaa agt gat gat gaa gta atg agc act ggt cac tct cca
 691
 Asp Asp Trp Glu Ser Asp Asp Glu Val Met Ser Thr Gly His Ser Pro
 185 190 195

ttc aca gtt gaa caa caa gcg tgc aac ata aca aca gaa gag ctg gat
 739
 Phe Thr Val Glu Gln Gln Ala Cys Asn Ile Thr Thr Glu Glu Leu Asp
 200 205 210
 gaa act gaa agc act gtt gat ggt cca ctt ctt aaa aga cag aaa cta
 787
 Glu Thr Glu Ser Thr Val Asp Gly Pro Leu Leu Lys Arg Gln Lys Leu
 215 220 225
 ctg gac cat tcg tac aga gac tca tca cca tcc ctt gtg ggc acc act
 835
 Leu Asp His Ser Tyr Arg Asp Ser Ser Pro Ser Leu Val Gly Thr Thr
 230 235 240
 aaa gtc aaa ggc tta tca gat gaa aac ctt cct gaa tca aac att tca
 883
 Lys Val Lys Gly Leu Ser Asp Glu Asn Leu Pro Glu Ser Asn Ile Ser
 245 250 255 260
 agc aaa caa gaa acg ggt tct ggt ttg agc gac gag cag tca aga aaa
 931
 Ser Lys Gln Glu Thr Gly Ser Gly Leu Ser Asp Glu Gln Ser Arg Lys
 265 270 275
 gac aag att cac acc gct ctg aga atc ctg gag agt gta gtt cca ggg
 979
 Asp Lys Ile His Thr Ala Leu Arg Ile Leu Glu Ser Val Val Pro Gly
 280 285 290
 gca aag gga aaa gaa gct ctt tta cta cta gac gaa gcc att gat tac
 1027
 Ala Lys Gly Lys Glu Ala Leu Leu Leu Leu Asp Glu Ala Ile Asp Tyr
 295 300 305
 ctc aag ttg ctg aag caa agc tta aac tca tca aag ggt ttg aat aac
 1075
 Leu Lys Leu Leu Lys Gln Ser Leu Asn Ser Ser Lys Gly Leu Asn Asn
 310 315 320
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 1124
 His Trp
 325
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 1184
 gaagattctc tcaaattcat taacgtgggt ttgaaacaat tagaacacgc ctggtgaccc
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 1322

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 Ile Pro Phe Pro Glu Leu Gly Lys Val Tyr Ala Ala Glu His Gln Phe
 35 40 45
 Arg Tyr Leu Gln Pro Pro Phe Gln Ala Leu Leu Ser Arg Tyr Asp Gln
 50 55 60
 Gln Ser Cys Gly Lys Gln Val Ser Cys Leu Asn Gly Arg Ser Ser Asn
 65 70 75 80
 Gly Ala Ala Pro Glu Gly Ala Leu Lys Ser Ser Arg Lys Arg Phe Ile
 85 90 95
 Val Phe Asp Gln Ser Gly Glu Gln Thr Arg Leu Leu Gln Cys Gly Phe
 100 105 110
 Pro Leu Arg Phe Pro Ser Ser Met Asp Ala Glu Arg Gly Asn Ile Leu
 115 120 125
 Gly Ala Leu His Pro Glu Lys Gly Phe Ser Lys Asp His Ala Ile Gln
 130 135 140
 Glu Lys Ile Leu Gln His Glu Asp His Glu Asn Gly Glu Glu Asp Ser
 145 150 155 160
 Glu Met His Glu Asp Thr Glu Glu Ile Asn Ala Leu Leu Tyr Ser Asp
 165 170 175
 Asp Asp Asp Asn Asp Asp Trp Glu Ser Asp Asp Glu Val Met Ser Thr
 180 185 190
 Gly His Ser Pro Phe Thr Val Glu Gln Gln Ala Cys Asn Ile Thr Thr
 195 200 205
 Glu Glu Leu Asp Glu Thr Glu Ser Thr Val Asp Gly Pro Leu Leu Lys
 210 215 220
 Arg Gln Lys Leu Leu Asp His Ser Tyr Arg Asp Ser Ser Pro Ser Leu
 225 230 235 240
 Val Gly Thr Thr Lys Val Lys Gly Leu Ser Asp Glu Asn Leu Pro Glu

245 250 255

Ser Asn Ile Ser Ser Lys Gln Glu Thr Gly Ser Gly Leu Ser Asp Glu
260 265 270

Gln Ser Arg Lys Asp Lys Ile His Thr Ala Leu Arg Ile Leu Glu Ser
275 280 285

Val Val Pro Gly Ala Lys Gly Lys Glu Ala Leu Leu Leu Leu Asp Glu
290 295 300

Ala Ile Asp Tyr Leu Lys Leu Leu Lys Gln Ser Leu Asn Ser Ser Lys
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Gly Leu Asn Asn His Trp
325

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112
Met Ala Lys Glu Asn Ser Ser His
1 5
agc ctt gca gaa gca aag aga aag aga ctc act tgg att ctt tgt gta
160
Ser Leu Ala Glu Ala Lys Arg Lys Arg Leu Thr Trp Ile Leu Cys Val
10 15 20
agt gga ctt tgc ata ttg tct tat gtt ctt gga tct tgg caa acc aac
208
Ser Gly Leu Cys Ile Leu Ser Tyr Val Leu Gly Ser Trp Gln Thr Asn
25 30 35 40
act gtc cca act tct tcc tct gag gct tac tca aga atg gga tgt gat
256
Thr Val Pro Thr Ser Ser Ser Glu Ala Tyr Ser Arg Met Gly Cys Asp
45 50 55
gaa aca tca aca acc act cgg gct cag act act cag act caa aca aat
304
Glu Thr Ser Thr Thr Thr Arg Ala Gln Thr Thr Gln Thr Gln Thr Asn
60 65 70
cct tct tct gac gat act tct tcc tct ttg tct tcc tca gaa cca gtt
352
Pro Ser Ser Asp Asp Thr Ser Ser Ser Leu Ser Ser Ser Glu Pro Val
75 80 85

gag tta gat ttc gaa agc cat cac aaa ctc gag ctg aag att acg aat
 400
 Glu Leu Asp Phe Glu Ser His His Lys Leu Glu Leu Lys Ile Thr Asn
 90 95 100

caa acc gta aag tac ttt gag cca tgt gac atg tct ttg agt gag tac
 448
 Gln Thr Val Lys Tyr Phe Glu Pro Cys Asp Met Ser Leu Ser Glu Tyr
 105 110 115 120

act cca tgt gaa gat cga gag aga gga aga aga ttt gat agg aac atg
 496
 Thr Pro Cys Glu Asp Arg Glu Arg Gly Arg Arg Phe Asp Arg Asn Met
 125 130 135

atg aag tac aga gag aga cat tgt cct tct aaa gat gag ctt ctt tat
 544
 Met Lys Tyr Arg Glu Arg His Cys Pro Ser Lys Asp Glu Leu Leu Tyr
 140 145 150

tgt ctg att cct cct cca cca aac tac aag att cca ttc aag tgg cct
 592
 Cys Leu Ile Pro Pro Pro Pro Asn Tyr Lys Ile Pro Phe Lys Trp Pro
 155 160 165

caa agt aga gat tat gct tgg tac gac aac att cca cac aag gag ctt
 640
 Gln Ser Arg Asp Tyr Ala Trp Tyr Asp Asn Ile Pro His Lys Glu Leu
 170 175 180

agt att gag aaa gct atc cag aac tgg att caa gta gaa ggg gaa aga
 688
 Ser Ile Glu Lys Ala Ile Gln Asn Trp Ile Gln Val Glu Gly Glu Arg
 185 190 195 200

ttc agg ttc cct ggt ggt ggc aca atg ttt cca cgt gga gct gat gct
 736
 Phe Arg Phe Pro Gly Gly Gly Thr Met Phe Pro Arg Gly Ala Asp Ala
 205 210 215

tac att gat gat att gct aga ctc att cct ctt act gat gga gcc att
 784
 Tyr Ile Asp Asp Ile Ala Arg Leu Ile Pro Leu Thr Asp Gly Ala Ile
 220 225 230

aga aca gct att gat aca gga tgt ggt gtg gcg agt ttt ggt gca tac
 832
 Arg Thr Ala Ile Asp Thr Gly Cys Gly Val Ala Ser Phe Gly Ala Tyr
 235 240 245

ttg ttg aag agg gat att gtg gct atg tca ttt gct cca agg gac act
 880
 Leu Leu Lys Arg Asp Ile Val Ala Met Ser Phe Ala Pro Arg Asp Thr
 250 255 260

cat gaa gct caa gtt caa ttt gcg ttg gaa cgt gga gtt cct gcg att
 928
 His Glu Ala Gln Val Gln Phe Ala Leu Glu Arg Gly Val Pro Ala Ile
 265 270 275 280

atc ggg att atg gga tca aga agg ctt cct tat cca gct aga gct ttt
 976
 Ile Gly Ile Met Gly Ser Arg Arg Leu Pro Tyr Pro Ala Arg Ala Phe
 285 290 295
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 1024
 Asp Leu Ala His Cys Ser Arg Cys Leu Ile Pro Trp Phe Gln Asn Asp
 300 305 310
 ggt ttg tac ttg acc gaa gtg gac cgg gtt tta aga ccg ggc ggt tat
 1072
 Gly Leu Tyr Leu Thr Glu Val Asp Arg Val Leu Arg Pro Gly Gly Tyr
 315 320 325
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 1120
 Trp Ile Leu Ser Gly Pro Pro Ile Asn Trp Lys Lys Tyr Trp Lys Gly
 330 335 340
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 1168
 Trp Glu Arg Ser Gln Glu Asp Leu Lys Gln Glu Gln Asp Ser Ile Glu
 345 350 355 360
 gat gca gca aga agt ctt tgt tgg aag aaa gtt aca gaa aag ggt gat
 1216
 Asp Ala Ala Arg Ser Leu Cys Trp Lys Lys Val Thr Glu Lys Gly Asp
 365 370 375
 tta tca att tgg caa aag cct atc aat cac gtt gag tgt aac aaa ctc
 1264
 Leu Ser Ile Trp Gln Lys Pro Ile Asn His Val Glu Cys Asn Lys Leu
 380 385 390
 aaa cga gtt cac aaa act cct cct cta tgc agt aaa tca gat tta ccc
 1312
 Lys Arg Val His Lys Thr Pro Pro Leu Cys Ser Lys Ser Asp Leu Pro
 395 400 405
 gat ttt gct tgg tac aaa gat ttg gaa tct tgt gta aca cca tta cca
 1360
 Asp Phe Ala Trp Tyr Lys Asp Leu Glu Ser Cys Val Thr Pro Leu Pro
 410 415 420
 gaa gca aac agt tca gac gaa ttc gca ggc ggt gca ttg gag gat tgg
 1408
 Glu Ala Asn Ser Ser Asp Glu Phe Ala Gly Gly Ala Leu Glu Asp Trp
 425 430 435 440
 cca aac cga gct ttt gcg gtg cca cct agg ata atc ggg gga acc att
 1456
 Pro Asn Arg Ala Phe Ala Val Pro Pro Arg Ile Ile Gly Gly Thr Ile
 445 450 455
 ccg gac att aat gct gag aaa ttc aga gaa gac aat gaa gtg tgg aag
 1504
 Pro Asp Ile Asn Ala Glu Lys Phe Arg Glu Asp Asn Glu Val Trp Lys
 460 465 470

gag aga ata tca tat tac aaa cag ata atg cca gag ctt tca aga gga
1552

Glu Arg Ile Ser Tyr Tyr Lys Gln Ile Met Pro Glu Leu Ser Arg Gly
475 480 485

aga ttt agg aac ata atg gac atg aat gca tac ttg gga gga ttt gct
1600

Arg Phe Arg Asn Ile Met Asp Met Asn Ala Tyr Leu Gly Gly Phe Ala
490 495 500

gcg gca atg atg aaa tat cca tct tgg gtt atg aat gtg gtt cct gtg
1648

Ala Ala Met Met Lys Tyr Pro Ser Trp Val Met Asn Val Val Pro Val
505 510 515 520

gat gct gag aag caa acg tta ggg gtt atc ttt gaa cga gga ttt ata
1696

Asp Ala Glu Lys Gln Thr Leu Gly Val Ile Phe Glu Arg Gly Phe Ile
525 530 535

ggg act tat caa gat tgg tgt gaa gga ttc tct acg tat ccg aga act
1744

Gly Thr Tyr Gln Asp Trp Cys Glu Gly Phe Ser Thr Tyr Pro Arg Thr
540 545 550

tat gat ttg att cat gct ggt gga ttg ttc agc att tat gag aac agg
1792

Tyr Asp Leu Ile His Ala Gly Gly Leu Phe Ser Ile Tyr Glu Asn Arg
555 560 565

tgt gat gtt aca tta ata cta ctt gag atg gat aga att ttg aga cca
1840

Cys Asp Val Thr Leu Ile Leu Leu Glu Met Asp Arg Ile Leu Arg Pro
570 575 580

gaa gga acc gtg gtg ttt aga gac act gtg gaa atg ttg acg aag ata
1888

Glu Gly Thr Val Val Phe Arg Asp Thr Val Glu Met Leu Thr Lys Ile
585 590 595 600

caa agc ata acc aat gga atg agg tgg aag agt cgg att ttg gat cat
1936

Gln Ser Ile Thr Asn Gly Met Arg Trp Lys Ser Arg Ile Leu Asp His
605 610 615

gag aga ggt cct ttt aat cct gag aag atc ctt ctc gct gta aaa tcc
1984

Glu Arg Gly Pro Phe Asn Pro Glu Lys Ile Leu Leu Ala Val Lys Ser
620 625 630

tat tgg acc ggt cct tct tct tag ctagtcttag ctttcttgga actctctact
2038

Tyr Trp Thr Gly Pro Ser Ser
635

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2098

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2153

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Val Leu Gly Ser Trp Gln Thr Asn Thr Val Pro Thr Ser Ser Ser Glu
35 40 45

Ala Tyr Ser Arg Met Gly Cys Asp Glu Thr Ser Thr Thr Thr Arg Ala
50 55 60

Gln Thr Thr Gln Thr Gln Thr Asn Pro Ser Ser Asp Asp Thr Ser Ser
65 70 75 80

Ser Leu Ser Ser Ser Glu Pro Val Glu Leu Asp Phe Glu Ser His His
85 90 95

Lys Leu Glu Leu Lys Ile Thr Asn Gln Thr Val Lys Tyr Phe Glu Pro
100 105 110

Cys Asp Met Ser Leu Ser Glu Tyr Thr Pro Cys Glu Asp Arg Glu Arg
115 120 125

Gly Arg Arg Phe Asp Arg Asn Met Met Lys Tyr Arg Glu Arg His Cys
130 135 140

Pro Ser Lys Asp Glu Leu Leu Tyr Cys Leu Ile Pro Pro Pro Pro Asn
145 150 155 160

Tyr Lys Ile Pro Phe Lys Trp Pro Gln Ser Arg Asp Tyr Ala Trp Tyr
165 170 175

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Gly Gly Val Gly Leu Asn Leu Thr Ala Ala Ser Ser Val Phe Leu
1190 1195 1200

Met Asp Pro Trp Trp Asn Pro Ala Val Glu Glu Gln Ala Ile Met
1205 1210 1215

Arg Ile His Arg Ile Gly Gln Lys Arg Thr Val Phe Val Arg Arg
1220 1225 1230

Phe Ile Val Lys Asp Thr Val Glu Glu Arg Met Gln Gln Val Gln
1235 1240 1245

Ala Arg Lys Gln Arg Met Ile Ala Gly Ala Leu Thr Asp Glu Glu
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 103
 Ser Ser Thr Ile Ala Arg Lys Thr Trp Glu Leu Glu Asn Ser Ile Leu
 5 10 15 20
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 151
 Thr Val Asp Ser Pro Asp Ser Thr Ser Asp Asn Ile Phe Tyr Tyr Asp
 25 30 35
 gat act tca cag act agg ttc cag caa gag aaa ccg tgg gag aat gat
 199
 Asp Thr Ser Gln Thr Arg Phe Gln Gln Glu Lys Pro Trp Glu Asn Asp
 40 45 50
 cct cac tac ttt aaa cga gtc aag atc tca gcg ctc gct ctt ctt aag
 247
 Pro His Tyr Phe Lys Arg Val Lys Ile Ser Ala Leu Ala Leu Leu Lys
 55 60 65
 atg gtg gtt cac gct cgc tct ggt ggt aca att gaa ata atg ggt ctt
 295
 Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu
 70 75 80
 atg caa ggt aag acc gat ggt gat act atc att gtt atg gat gct ttt
 343
 Met Gln Gly Lys Thr Asp Gly Asp Thr Ile Ile Val Met Asp Ala Phe
 85 90 95 100
 gct tta cca gtg gaa ggt act gag aca agg gtt aat gct cag gat gat
 391
 Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Asp Asp
 105 110 115
 gct tat gag tac atg gtt gag tat tca cag acc aac aag ctc gcg ggg
 439
 Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Asn Lys Leu Ala Gly
 120 125 130
 cgg ctg gag aat gtt gtt gga tgg tat cac tct cac cct gga tat gga
 487
 Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly
 135 140 145
 tgc tgg ctc tcc ggt att gat gtt tct acg cag acg ctt aac caa cag
 535
 Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Thr Leu Asn Gln Gln
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 583
 His Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val
 165 170 175 180
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 631
 Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Ser Lys Gly
 185 190 195

tat aag cct cca gat gaa cct gtt tct gag tat caa act att cct tta
679

Tyr Lys Pro Pro Asp Glu Pro Val Ser Glu Tyr Gln Thr Ile Pro Leu
200 205 210

aat aag att gag gac ttt ggt gtt cac tgc aaa cag tac tat tca tta
727

Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu
215 220 225

gat gtc act tat ttc aag tca tct ctt gat tct cac ctt ctg gat cta
775

Asp Val Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu
230 235 240

cta tgg aac aag tac tgg gtg aac act ctt tct tct tct cca ctg ctg
823

Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu
245 250 255 260

ggt aat gga gac tat gtt gct gga caa ata tca gac tta gct gag aag
871

Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys
265 270 275

ctt gag caa gcc gag agt cat ctg gtt cag tct cgc ttt gga gga gtt
919

Leu Glu Gln Ala Glu Ser His Leu Val Gln Ser Arg Phe Gly Gly Val
280 285 290

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967

Val Pro Ser Ser Leu His Lys Lys Lys Glu Asp Glu Ser Gln Leu Thr
295 300 305

aag ata act cgg gat agc gca aag ata act gtg gaa cag gtc cat gga
1015

Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln Val His Gly
310 315 320

cta atg tcg cag gtc ata aaa gat gaa tta ttc aac tca atg cgt cag
1063

Leu Met Ser Gln Val Ile Lys Asp Glu Leu Phe Asn Ser Met Arg Gln
325 330 335 340

tcc aac aac aaa tct ccc act gac tcg tcg gat cca gac cct atg att
1111

Ser Asn Asn Lys Ser Pro Thr Asp Ser Ser Asp Pro Asp Pro Met Ile
345 350 355

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1160

Thr Tyr

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1220

cgcgccgct aaaaaaaaaac aggaaattga aaaaaattca tccattccaa catctttatt
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1340

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1374

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35 40 45

Trp Glu Asn Asp Pro His Tyr Phe Lys Arg Val Lys Ile Ser Ala Leu
50 55 60

Ala Leu Leu Lys Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu
65 70 75 80

Ile Met Gly Leu Met Gln Gly Lys Thr Asp Gly Asp Thr Ile Ile Val
85 90 95

Met Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn
100 105 110

Ala Gln Asp Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Asn
115 120 125

Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His
130 135 140

Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Thr
145 150 155 160

Leu Asn Gln Gln His Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro
165 170 175

Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr
180 185 190

Tyr Ser Lys Gly Tyr Lys Pro Pro Asp Glu Pro Val Ser Glu Tyr Gln
195 200 205

Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln
 210 215 220

Tyr Tyr Ser Leu Asp Val Thr Tyr Phe Lys Ser Ser Leu Asp Ser His
 225 230 235 240

Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser
 245 250 255

Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp
 260 265 270

Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser His Leu Val Gln Ser Arg
 275 280 285

Phe Gly Gly Val Val Pro Ser Ser Leu His Lys Lys Lys Glu Asp Glu
 290 295 300

Ser Gln Leu Thr Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu
 305 310 315 320

Gln Val His Gly Leu Met Ser Gln Val Ile Lys Asp Glu Leu Phe Asn
 325 330 335

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 340 345 350

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 Glu Glu Arg Val Lys Asp Asn Glu Glu Glu Asp Glu Glu Glu Leu Glu
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 144
 Ala Val Ala Arg Ser Ser Gly Ser Asp Asp Asp Glu Val Ala Ala Ala
 35 40 45

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 192
 Asp Glu Ser Pro Val Ser Asp Gly Glu Ala Ala Pro Val Glu Asp Asp
 50 55 60

tac gag gac gaa gaa gat gag gaa aaa gct gaa atc agc aaa cgt gag
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 Tyr Glu Asp Glu Glu Asp Glu Glu Lys Ala Glu Ile Ser Lys Arg Glu
 65 70 75 80

aaa gcc aga ctt aaa gag atg cag aag ttg aag aag cag aag att caa
 288
 Lys Ala Arg Leu Lys Glu Met Gln Lys Leu Lys Lys Gln Lys Ile Gln
 85 90 95

gag atg ctg gag tcg cag aat gct tcc att gac gcg gat atg aac aat
 336
 Glu Met Leu Glu Ser Gln Asn Ala Ser Ile Asp Ala Asp Met Asn Asn
 100 105 110

aag gga aaa ggg aga ctg aag tat ctt ctg cag caa act gag tta ttt
 384
 Lys Gly Lys Gly Arg Leu Lys Tyr Leu Leu Gln Gln Thr Glu Leu Phe
 115 120 125

gcc cac ttt gct aaa agt gat gga tct tct tct cag aag aag gca aaa
 432
 Ala His Phe Ala Lys Ser Asp Gly Ser Ser Ser Gln Lys Lys Ala Lys
 130 135 140

gga agg gga cgt cat gct tcc aaa ata act gaa gag gag gaa gac gaa
 480
 Gly Arg Gly Arg His Ala Ser Lys Ile Thr Glu Glu Glu Glu Asp Glu
 145 150 155 160

gag tat cta aag gaa gaa gag gat ggc tta act gga tct gga aac aca
 528
 Glu Tyr Leu Lys Glu Glu Glu Asp Gly Leu Thr Gly Ser Gly Asn Thr
 165 170 175

cgg tta ctc aca cag ccc tct tgt att caa ggg aag atg aga gat tac
 576
 Arg Leu Leu Thr Gln Pro Ser Cys Ile Gln Gly Lys Met Arg Asp Tyr
 180 185 190

caa tta gct ggt ttg aac tgg ctc att cgt ctt tat gag aat ggc ata
 624
 Gln Leu Ala Gly Leu Asn Trp Leu Ile Arg Leu Tyr Glu Asn Gly Ile
 195 200 205

aat gga att ctt gct gat gaa atg ggt ctg ggg aag acg ctt caa acg
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 Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Leu Gln Thr
 210 215 220

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 720
 Ile Ser Leu Leu Ala Tyr Leu His Glu Tyr Arg Gly Ile Asn Gly Pro
 225 230 235 240

cat atg gtg gtt gct cca aaa tca aca ctt ggt aat tgg atg aac gaa
 768
 His Met Val Val Ala Pro Lys Ser Thr Leu Gly Asn Trp Met Asn Glu
 245 250 255

att cgc cgg ttt tgt cct gtc cta cgt gct gtg aag ttc ctt ggt aat
 816
 Ile Arg Arg Phe Cys Pro Val Leu Arg Ala Val Lys Phe Leu Gly Asn
 260 265 270

cct gag gag agg aga cat att cga gaa gac ctg cta gtt gct ggg aaa
 864
 Pro Glu Glu Arg Arg His Ile Arg Glu Asp Leu Leu Val Ala Gly Lys
 275 280 285

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 912
 Phe Asp Ile Cys Val Thr Ser Phe Glu Met Ala Ile Lys Glu Lys Thr
 290 295 300

gca ctt cgt cgg ttt agc tgg cgt tat att atc att gat gaa gcg cat
 960
 Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile Ile Ile Asp Glu Ala His
 305 310 315 320

cga atc aag aac gag aat tca ctc ctt tct aaa acc atg aga ctt ttt
 1008
 Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser Lys Thr Met Arg Leu Phe
 325 330 335

agc acc aat tat cgg ctt ctt atc acg ggg acc ccc ctt cag aat aat
 1056
 Ser Thr Asn Tyr Arg Leu Leu Ile Thr Gly Thr Pro Leu Gln Asn Asn
 340 345 350

ctc cat gaa ctg tgg gct ctt cta aat ttt ctt ctg cct gag att ttt
 1104
 Leu His Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro Glu Ile Phe
 355 360 365

agt tca gca gag act ttt gat gaa tgg ttt caa att tct ggt gag aat
 1152
 Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe Gln Ile Ser Gly Glu Asn
 370 375 380

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 1200
 Asp Gln Gln Glu Val Val Gln Gln Leu His Lys Val Leu Arg Pro Phe
 385 390 395 400

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 1248
 Leu Leu Arg Arg Leu Lys Ser Asp Val Glu Lys Gly Leu Pro Pro Lys
 405 410 415

aag gag acc ata ctt aaa gtt ggt atg tct cag atg caa aag caa tac
 1296
 Lys Glu Thr Ile Leu Lys Val Gly Met Ser Gln Met Gln Lys Gln Tyr
 420 425 430

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 1344
 Tyr Lys Ala Leu Leu Gln Lys Asp Leu Glu Ala Val Asn Ala Gly Gly
 435 440 445
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 1392
 Glu Arg Lys Arg Leu Leu Asn Ile Ala Met Gln Leu Arg Lys Cys Cys
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 aat cac ccc tat ctc ttc cag ggt gca gaa cct ggt ccc cca tat acc
 1440
 Asn His Pro Tyr Leu Phe Gln Gly Ala Glu Pro Gly Pro Pro Tyr Thr
 465 470 475 480
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 1488
 Thr Gly Asp His Leu Ile Thr Asn Ala Gly Lys Met Val Leu Leu Asp
 485 490 495
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 1536
 Lys Leu Leu Pro Lys Leu Lys Glu Arg Asp Ser Arg Val Leu Ile Phe
 500 505 510
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 1584
 Ser Gln Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr Leu Met Tyr
 515 520 525
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 1632
 Arg Gly Tyr Leu Tyr Cys Arg Ile Asp Gly Asn Thr Gly Gly Asp Glu
 530 535 540
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 1680
 Arg Asp Ala Ser Ile Glu Ala Tyr Asn Lys Pro Gly Ser Glu Lys Phe
 545 550 555 560
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 1728
 Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala
 565 570 575
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 1776
 Thr Ala Asp Val Val Ile Leu Tyr Asp Ser Asp Trp Asn Pro Gln Val
 580 585 590
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 1824
 Asp Leu Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln Lys Lys Glu
 595 600 605
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 1872
 Val Gln Val Phe Arg Phe Cys Thr Glu Ser Ala Ile Glu Glu Lys Val
 610 615 620

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 1920
 Ile Glu Arg Ala Tyr Lys Lys Leu Ala Leu Asp Ala Leu Val Ile Gln
 625 630 635 640

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 1968
 Gln Gly Arg Leu Ala Glu Gln Lys Ser Lys Ser Val Asn Lys Asp Glu
 645 650 655

ttg ctt caa atg gta aga tat ggt gct gag atg gtg ttc agt tct aaa
 2016
 Leu Leu Gln Met Val Arg Tyr Gly Ala Glu Met Val Phe Ser Ser Lys
 660 665 670

gat agc aca atc aca gac gag gat att gat aga atc att gcc aaa gga
 2064
 Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg Ile Ile Ala Lys Gly
 675 680 685

gaa gag gca aca gct gaa ctt gat gct aag atg aag aaa ttc aca gaa
 2112
 Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys Met Lys Lys Phe Thr Glu
 690 695 700

gat gct ata cag ttt aaa atg gat gac agt gct gac ttc tat gat ttt
 2160
 Asp Ala Ile Gln Phe Lys Met Asp Asp Ser Ala Asp Phe Tyr Asp Phe
 705 710 715 720

gat gat gac aat aag gat gaa aac aag ctc gat ttt aaa aag att gta
 2208
 Asp Asp Asp Asn Lys Asp Glu Asn Lys Leu Asp Phe Lys Lys Ile Val
 725 730 735

agc gac aat tgg aat gat ccc ccc aag cgg gag aga aag cgc aac tac
 2256
 Ser Asp Asn Trp Asn Asp Pro Pro Lys Arg Glu Arg Lys Arg Asn Tyr
 740 745 750

tct gaa tct gag tac ttt aag caa aca ttg cgg caa ggt gct cca gct
 2304
 Ser Glu Ser Glu Tyr Phe Lys Gln Thr Leu Arg Gln Gly Ala Pro Ala
 755 760 765

aaa cct aaa gag cct aga att ccg cgc atg ccc cag ttg cac gat ttc
 2352
 Lys Pro Lys Glu Pro Arg Ile Pro Arg Met Pro Gln Leu His Asp Phe
 770 775 780

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 2400
 Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu Leu Tyr Glu Lys Glu Val
 785 790 795 800

cgt tat ctc atg caa aca cat cag aaa aat cag ttg aaa gac aca att
 2448
 Arg Tyr Leu Met Gln Thr His Gln Lys Asn Gln Leu Lys Asp Thr Ile
 805 810 815

gat gtt gaa gaa cca gaa ggt ggg gat ccc tta act act gaa gaa gta
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 Asp Val Glu Glu Pro Glu Gly Gly Asp Pro Leu Thr Thr Glu Glu Val
 820 825 830

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 2544
 Glu Glu Lys Glu Gly Leu Leu Glu Glu Gly Phe Ser Thr Trp Ser Arg
 835 840 845

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 2592
 Arg Asp Phe Asn Thr Phe Leu Arg Ala Cys Glu Lys Tyr Gly Arg Asn
 850 855 860

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 2640
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 865 870 875 880

gtt gaa aga tat gcc aaa gta ttt aaa gag cgg tac aag gag ctg aac
 2688
 Val Glu Arg Tyr Ala Lys Val Phe Lys Glu Arg Tyr Lys Glu Leu Asn
 885 890 895

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 2736
 Asp Tyr Asp Arg Ile Ile Lys Asn Ile Glu Arg Gly Glu Ala Arg Ile
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 2784
 Ser Arg Lys Asp Glu Ile Met Lys Ala Ile Gly Lys Lys Leu Asp Arg
 915 920 925

tac aga aac cct tgg ctg gaa ctg aag att caa tat ggt cag aac aaa
 2832
 Tyr Arg Asn Pro Trp Leu Glu Leu Lys Ile Gln Tyr Gly Gln Asn Lys
 930 935 940

ggc aag ctg tac aat gaa gag tgt gac cgt ttc atg atc tgc atg att
 2880
 Gly Lys Leu Tyr Asn Glu Glu Cys Asp Arg Phe Met Ile Cys Met Ile
 945 950 955 960

cac aaa ctt ggt tat ggg aat tgg gat gag cta aag gca gca ttt agg
 2928
 His Lys Leu Gly Tyr Gly Asn Trp Asp Glu Leu Lys Ala Ala Phe Arg
 965 970 975

aca tcg tct gtg ttc agg ttt gac tgg ttt gtg aaa tcc cgc acg agt
 2976
 Thr Ser Ser Val Phe Arg Phe Asp Trp Phe Val Lys Ser Arg Thr Ser
 980 985 990

cag gaa ctt gca aga aga tgc gac act ctg att cga ctg atc gag aaa
 3024
 Gln Glu Leu Ala Arg Arg Cys Asp Thr Leu Ile Arg Leu Ile Glu Lys
 995 1000 1005

gag aac cag gag ttt gat gaa aga gag agg caa gcc cgc aaa gag
3069

Glu Asn Gln Glu Phe Asp Glu Arg Glu Arg Gln Ala Arg Lys Glu
1010 1015 1020

aag aag ctc gcg aag agt gca aca cca tca aag cga cct tta gga
3114

Lys Lys Leu Ala Lys Ser Ala Thr Pro Ser Lys Arg Pro Leu Gly
1025 1030 1035

aga caa gca agt gag agt cct tca tcg acg aag aag cgg aag cac
3159

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3174

Leu Ser Met Arg
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35 40 45

Asp Glu Ser Pro Val Ser Asp Gly Glu Ala Ala Pro Val Glu Asp Asp
50 55 60

Tyr Glu Asp Glu Glu Asp Glu Glu Lys Ala Glu Ile Ser Lys Arg Glu
65 70 75 80

Lys Ala Arg Leu Lys Glu Met Gln Lys Leu Lys Lys Gln Lys Ile Gln
85 90 95

Glu Met Leu Glu Ser Gln Asn Ala Ser Ile Asp Ala Asp Met Asn Asn
100 105 110

Lys Gly Lys Gly Arg Leu Lys Tyr Leu Leu Gln Gln Thr Glu Leu Phe
115 120 125

Ala His Phe Ala Lys Ser Asp Gly Ser Ser Ser Gln Lys Lys Ala Lys
130 135 140

Gly Arg Gly Arg His Ala Ser Lys Ile Thr Glu Glu Glu Glu Asp Glu

145 150 155 160
 Glu Tyr Leu Lys Glu Glu Glu Asp Gly Leu Thr Gly Ser Gly Asn Thr
 165 170 175
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 180 185 190
 Gln Leu Ala Gly Leu Asn Trp Leu Ile Arg Leu Tyr Glu Asn Gly Ile
 195 200 205
 Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Leu Gln Thr
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 Ile Ser Leu Leu Ala Tyr Leu His Glu Tyr Arg Gly Ile Asn Gly Pro
 225 230 235 240
 His Met Val Val Ala Pro Lys Ser Thr Leu Gly Asn Trp Met Asn Glu
 245 250 255
 Ile Arg Arg Phe Cys Pro Val Leu Arg Ala Val Lys Phe Leu Gly Asn
 260 265 270
 Pro Glu Glu Arg Arg His Ile Arg Glu Asp Leu Leu Val Ala Gly Lys
 275 280 285
 Phe Asp Ile Cys Val Thr Ser Phe Glu Met Ala Ile Lys Glu Lys Thr
 290 295 300
 Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile Ile Ile Asp Glu Ala His
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 325 330 335
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 340 345 350
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 370 375 380
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 385 390 395 400

Leu Leu Arg Arg Leu Lys Ser Asp Val Glu Lys Gly Leu Pro Pro Lys
 405 410 415

Lys Glu Thr Ile Leu Lys Val Gly Met Ser Gln Met Gln Lys Gln Tyr
 420 425 430

Tyr Lys Ala Leu Leu Gln Lys Asp Leu Glu Ala Val Asn Ala Gly Gly
 435 440 445

Glu Arg Lys Arg Leu Leu Asn Ile Ala Met Gln Leu Arg Lys Cys Cys
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Asn His Pro Tyr Leu Phe Gln Gly Ala Glu Pro Gly Pro Pro Tyr Thr
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Thr Gly Asp His Leu Ile Thr Asn Ala Gly Lys Met Val Leu Leu Asp
 485 490 495

Lys Leu Leu Pro Lys Leu Lys Glu Arg Asp Ser Arg Val Leu Ile Phe
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Ser Gln Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr Leu Met Tyr
 515 520 525

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 530 535 540

Arg Asp Ala Ser Ile Glu Ala Tyr Asn Lys Pro Gly Ser Glu Lys Phe
 545 550 555 560

Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala
 565 570 575

Thr Ala Asp Val Val Ile Leu Tyr Asp Ser Asp Trp Asn Pro Gln Val
 580 585 590

Asp Leu Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln Lys Lys Glu
 595 600 605

Val Gln Val Phe Arg Phe Cys Thr Glu Ser Ala Ile Glu Glu Lys Val
 610 615 620

Ile Glu Arg Ala Tyr Lys Lys Leu Ala Leu Asp Ala Leu Val Ile Gln
 625 630 635 640

Gln Gly Arg Leu Ala Glu Gln Lys Ser Lys Ser Val Asn Lys Asp Glu
 645 650 655
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 660 665 670
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 675 680 685
 Glu Glu Ala Thr Ala Glu Leu Asp Ala Lys Met Lys Lys Phe Thr Glu
 690 695 700
 Asp Ala Ile Gln Phe Lys Met Asp Asp Ser Ala Asp Phe Tyr Asp Phe
 705 710 715 720
 Asp Asp Asp Asn Lys Asp Glu Asn Lys Leu Asp Phe Lys Lys Ile Val
 725 730 735
 Ser Asp Asn Trp Asn Asp Pro Pro Lys Arg Glu Arg Lys Arg Asn Tyr
 740 745 750
 Ser Glu Ser Glu Tyr Phe Lys Gln Thr Leu Arg Gln Gly Ala Pro Ala
 755 760 765
 Lys Pro Lys Glu Pro Arg Ile Pro Arg Met Pro Gln Leu His Asp Phe
 770 775 780
 Gln Phe Phe Asn Ile Gln Arg Leu Thr Glu Leu Tyr Glu Lys Glu Val
 785 790 795 800
 Arg Tyr Leu Met Gln Thr His Gln Lys Asn Gln Leu Lys Asp Thr Ile
 805 810 815
 Asp Val Glu Glu Pro Glu Gly Gly Asp Pro Leu Thr Thr Glu Glu Val
 820 825 830
 Glu Glu Lys Glu Gly Leu Leu Glu Glu Gly Phe Ser Thr Trp Ser Arg
 835 840 845
 Arg Asp Phe Asn Thr Phe Leu Arg Ala Cys Glu Lys Tyr Gly Arg Asn
 850 855 860
 Asp Ile Lys Ser Ile Ala Ser Glu Met Glu Gly Lys Thr Glu Glu Glu
 865 870 875 880

Val Glu Arg Tyr Ala Lys Val Phe Lys Glu Arg Tyr Lys Glu Leu Asn
 885 890 895
 Asp Tyr Asp Arg Ile Ile Lys Asn Ile Glu Arg Gly Glu Ala Arg Ile
 900 905 910
 Ser Arg Lys Asp Glu Ile Met Lys Ala Ile Gly Lys Lys Leu Asp Arg
 915 920 925
 Tyr Arg Asn Pro Trp Leu Glu Leu Lys Ile Gln Tyr Gly Gln Asn Lys
 930 935 940
 Gly Lys Leu Tyr Asn Glu Glu Cys Asp Arg Phe Met Ile Cys Met Ile
 945 950 955 960
 His Lys Leu Gly Tyr Gly Asn Trp Asp Glu Leu Lys Ala Ala Phe Arg
 965 970 975
 Thr Ser Ser Val Phe Arg Phe Asp Trp Phe Val Lys Ser Arg Thr Ser
 980 985 990
 Gln Glu Leu Ala Arg Arg Cys Asp Thr Leu Ile Arg Leu Ile Glu Lys
 995 1000 1005
 Glu Asn Gln Glu Phe Asp Glu Arg Glu Arg Gln Ala Arg Lys Glu
 1010 1015 1020
 Lys Lys Leu Ala Lys Ser Ala Thr Pro Ser Lys Arg Pro Leu Gly
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 104
 Met Ala Thr Thr Thr Thr Thr Thr Thr Ala Arg Phe Ser Asp Ser Tyr
 5 10 15

gag ttc agc aac aca agc ggc aat agc ttc ttc gcc gcc gag tca tct
 152
 Glu Phe Ser Asn Thr Ser Gly Asn Ser Phe Phe Ala Ala Glu Ser Ser
 20 25 30

ctt gat tat ccg acg gaa ttt ctc acg cca ccg gag gta tca gct ctt
 200
 Leu Asp Tyr Pro Thr Glu Phe Leu Thr Pro Pro Glu Val Ser Ala Leu
 35 40 45

aaa ctt ctg tct aac tgc ctc gag tct gtt ttc gac tcg ccg gag acg
 248
 Lys Leu Leu Ser Asn Cys Leu Glu Ser Val Phe Asp Ser Pro Glu Thr
 50 55 60 65

ttc tac agc gat gct aag cta gtt ctc gcc ggc ggc cgg gaa gtt tct
 296
 Phe Tyr Ser Asp Ala Lys Leu Val Leu Ala Gly Gly Arg Glu Val Ser
 70 75 80

ttt cac cgt tgt att ctt tcc gcg aga att cct gtc ttc aaa agc gct
 344
 Phe His Arg Cys Ile Leu Ser Ala Arg Ile Pro Val Phe Lys Ser Ala
 85 90 95

tta gcc acc gtg aag gaa caa aaa tcc tcc acc acc gtg aag ctc cag
 392
 Leu Ala Thr Val Lys Glu Gln Lys Ser Ser Thr Thr Val Lys Leu Gln
 100 105 110

ctg aaa gag atc gcc aga gat tac gaa gtc ggc ttt gac tcg gtt gtg
 440
 Leu Lys Glu Ile Ala Arg Asp Tyr Glu Val Gly Phe Asp Ser Val Val
 115 120 125

gcg gtt ttg gcg tat gtt tac agc ggc aga gtg agg tcc ccg ccg aag
 488
 Ala Val Leu Ala Tyr Val Tyr Ser Gly Arg Val Arg Ser Pro Pro Lys
 130 135 140 145

gga gct tct gct tgc gta gac gac gat tgt tgc cac gtg gct tgc cgg
 536
 Gly Ala Ser Ala Cys Val Asp Asp Asp Cys Cys His Val Ala Cys Arg
 150 155 160

tca aag gtg gat ttc atg gtg gag gtt ctt tat ctg tct ttc gtt ttc
 584
 Ser Lys Val Asp Phe Met Val Glu Val Leu Tyr Leu Ser Phe Val Phe
 165 170 175

cag att caa gaa tta gtt act ctg tat gag agg cag ttc ttg gaa att
 632
 Gln Ile Gln Glu Leu Val Thr Leu Tyr Glu Arg Gln Phe Leu Glu Ile
 180 185 190

gta gac aaa gtt gta gtc gaa gac atc ttg gtt ata ttc aag ctt gat
 680
 Val Asp Lys Val Val Val Glu Asp Ile Leu Val Ile Phe Lys Leu Asp
 195 200 205

act cta tgt ggt aca aca tac aag aag ctt ttg gat aga tgc ata gaa
 728
 Thr Leu Cys Gly Thr Thr Tyr Lys Lys Leu Leu Asp Arg Cys Ile Glu
 210 215 220 225
 att atc gtg aag tct gat ata gaa cta gtt agt ctt gag aag tct tta
 776
 Ile Ile Val Lys Ser Asp Ile Glu Leu Val Ser Leu Glu Lys Ser Leu
 230 235 240
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 824
 Pro Gln His Ile Phe Lys Gln Ile Ile Asp Ile Arg Glu Ala Leu Cys
 245 250 255
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 872
 Leu Glu Pro Pro Lys Leu Glu Arg His Val Lys Asn Ile Tyr Lys Ala
 260 265 270
 cta gac tca gat gat gtt gag ctt gtc aag atg ctt ttg cta gaa gga
 920
 Leu Asp Ser Asp Asp Val Glu Leu Val Lys Met Leu Leu Leu Glu Gly
 275 280 285
 cac acc aat ctc gat gag gcg tat gct ctt cat ttt gct atc gct cac
 968
 His Thr Asn Leu Asp Glu Ala Tyr Ala Leu His Phe Ala Ile Ala His
 290 295 300 305
 tgc gct gtg aag acc gcg tat gat ctc ctc gag ctt gag ctt gcg gat
 1016
 Cys Ala Val Lys Thr Ala Tyr Asp Leu Leu Glu Leu Glu Leu Ala Asp
 310 315 320
 gtt aac ctt aga aat ccg agg gga tac act gtg ctt cat gtt gct gcg
 1064
 Val Asn Leu Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala
 325 330 335
 atg cgg aag gag ccg aag ttg ata ata tct ttg tta atg aaa ggg gca
 1112
 Met Arg Lys Glu Pro Lys Leu Ile Ile Ser Leu Leu Met Lys Gly Ala
 340 345 350
 aat att tta gac aca aca ttg gat ggt aga acc gct tta gtg att gta
 1160
 Asn Ile Leu Asp Thr Thr Leu Asp Gly Arg Thr Ala Leu Val Ile Val
 355 360 365
 aaa cga ctc act aaa gcg gat gac tac aaa act agt acg gag gac ggt
 1208
 Lys Arg Leu Thr Lys Ala Asp Asp Tyr Lys Thr Ser Thr Glu Asp Gly
 370 375 380 385
 acg cct tct ctg aaa ggc gga tta tgc ata gag gta ctt gag cat gaa
 1256
 Thr Pro Ser Leu Lys Gly Gly Leu Cys Ile Glu Val Leu Glu His Glu
 390 395 400

caa aaa cta gaa tat ttg tcg cct ata gag gct tca ctt tct ctt cca
 1304
 Gln Lys Leu Glu Tyr Leu Ser Pro Ile Glu Ala Ser Leu Ser Leu Pro
 405 410 415

gta act cca gag gag ttg agg atg agg ttg ctc tat tat gaa aac cga
 1352
 Val Thr Pro Glu Glu Leu Arg Met Arg Leu Leu Tyr Tyr Glu Asn Arg
 420 425 430

gtt gca ctt gct cga ctt ctc ttt cca gtg gaa act gaa act gta cag
 1400
 Val Ala Leu Ala Arg Leu Leu Phe Pro Val Glu Thr Glu Thr Val Gln
 435 440 445

ggt att gcc aaa ttg gag gaa aca tgc gag ttt aca gct tct agt ctc
 1448
 Gly Ile Ala Lys Leu Glu Glu Thr Cys Glu Phe Thr Ala Ser Ser Leu
 450 455 460 465

gag cct gat cat cac att ggt gaa aag cgg aca tca cta gac cta aat
 1496
 Glu Pro Asp His His Ile Gly Glu Lys Arg Thr Ser Leu Asp Leu Asn
 470 475 480

atg gcg ccg ttc caa atc cat gag aag cat ttg agt aga cta aga gca
 1544
 Met Ala Pro Phe Gln Ile His Glu Lys His Leu Ser Arg Leu Arg Ala
 485 490 495

ctt tgt aaa acc gtg gaa ctg ggg aaa cgc tac ttc aaa cga tgt tcg
 1592
 Leu Cys Lys Thr Val Glu Leu Gly Lys Arg Tyr Phe Lys Arg Cys Ser
 500 505 510

ctt gat cac ttt atg gat act gag gac ttg aat cat ctt gct agc gta
 1640
 Leu Asp His Phe Met Asp Thr Glu Asp Leu Asn His Leu Ala Ser Val
 515 520 525

gaa gaa gat act cct gag aaa cgg cta caa aag aag caa agg tac atg
 1688
 Glu Glu Asp Thr Pro Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met
 530 535 540 545

gaa cta caa gag act ctg atg aag acc ttt agt gag gac aag gag gaa
 1736
 Glu Leu Gln Glu Thr Leu Met Lys Thr Phe Ser Glu Asp Lys Glu Glu
 550 555 560

tgt gga aag tct tcc aca ccg aaa cca acc tct gcg gtg agg tct aat
 1784
 Cys Gly Lys Ser Ser Thr Pro Lys Pro Thr Ser Ala Val Arg Ser Asn
 565 570 575

aga aaa ctc tct cac cgg cgc cta aaa gtg gac aaa cgg gat ttt ttg
 1832
 Arg Lys Leu Ser His Arg Arg Leu Lys Val Asp Lys Arg Asp Phe Leu
 580 585 590

aaa cga cct tac ggg aac ggg gat taa ggaatgggaa atcatattcc
1879

Lys Arg Pro Tyr Gly Asn Gly Asp
595 600

atttcactcc cacaactaaa aatgatgtat gtcctatatc atgatgtttc gtgagtttca
1939

aataaattga aacgtacata tatcagtttt tcatctacgt gactgcgttg tatagttttc
1999

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2059

tttttagcca attatatata cggg
2083

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Tyr Glu Phe Ser Asn Thr Ser Gly Asn Ser Phe Phe Ala Ala Glu Ser
20 25 30

Ser Leu Asp Tyr Pro Thr Glu Phe Leu Thr Pro Pro Glu Val Ser Ala
35 40 45

Leu Lys Leu Leu Ser Asn Cys Leu Glu Ser Val Phe Asp Ser Pro Glu
50 55 60

Thr Phe Tyr Ser Asp Ala Lys Leu Val Leu Ala Gly Gly Arg Glu Val
65 70 75 80

Ser Phe His Arg Cys Ile Leu Ser Ala Arg Ile Pro Val Phe Lys Ser
85 90 95

Ala Leu Ala Thr Val Lys Glu Gln Lys Ser Ser Thr Thr Val Lys Leu
100 105 110

Gln Leu Lys Glu Ile Ala Arg Asp Tyr Glu Val Gly Phe Asp Ser Val
115 120 125

Val Ala Val Leu Ala Tyr Val Tyr Ser Gly Arg Val Arg Ser Pro Pro
130 135 140

Lys Gly Ala Ser Ala Cys Val Asp Asp Asp Cys Cys His Val Ala Cys
145 150 155 160

Arg Ser Lys Val Asp Phe Met Val Glu Val Leu Tyr Leu Ser Phe Val
 165 170 175

Phe Gln Ile Gln Glu Leu Val Thr Leu Tyr Glu Arg Gln Phe Leu Glu
 180 185 190

Ile Val Asp Lys Val Val Val Glu Asp Ile Leu Val Ile Phe Lys Leu
 195 200 205

Asp Thr Leu Cys Gly Thr Thr Tyr Lys Lys Leu Leu Asp Arg Cys Ile
 210 215 220

Glu Ile Ile Val Lys Ser Asp Ile Glu Leu Val Ser Leu Glu Lys Ser
 225 230 235 240

Leu Pro Gln His Ile Phe Lys Gln Ile Ile Asp Ile Arg Glu Ala Leu
 245 250 255

Cys Leu Glu Pro Pro Lys Leu Glu Arg His Val Lys Asn Ile Tyr Lys
 260 265 270

Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Met Leu Leu Leu Glu
 275 280 285

Gly His Thr Asn Leu Asp Glu Ala Tyr Ala Leu His Phe Ala Ile Ala
 290 295 300

His Cys Ala Val Lys Thr Ala Tyr Asp Leu Leu Glu Leu Glu Leu Ala
 305 310 315 320

Asp Val Asn Leu Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala
 325 330 335

Ala Met Arg Lys Glu Pro Lys Leu Ile Ile Ser Leu Leu Met Lys Gly
 340 345 350

Ala Asn Ile Leu Asp Thr Thr Leu Asp Gly Arg Thr Ala Leu Val Ile
 355 360 365

Val Lys Arg Leu Thr Lys Ala Asp Asp Tyr Lys Thr Ser Thr Glu Asp
 370 375 380

Gly Thr Pro Ser Leu Lys Gly Gly Leu Cys Ile Glu Val Leu Glu His
 385 390 395 400

Glu Gln Lys Leu Glu Tyr Leu Ser Pro Ile Glu Ala Ser Leu Ser Leu

405 410 415
 Pro Val Thr Pro Glu Glu Leu Arg Met Arg Leu Leu Tyr Tyr Glu Asn
 420 425 430
 Arg Val Ala Leu Ala Arg Leu Leu Phe Pro Val Glu Thr Glu Thr Val
 435 440 445
 Gln Gly Ile Ala Lys Leu Glu Glu Thr Cys Glu Phe Thr Ala Ser Ser
 450 455 460
 Leu Glu Pro Asp His His Ile Gly Glu Lys Arg Thr Ser Leu Asp Leu
 465 470 475 480
 Asn Met Ala Pro Phe Gln Ile His Glu Lys His Leu Ser Arg Leu Arg
 485 490 495
 Ala Leu Cys Lys Thr Val Glu Leu Gly Lys Arg Tyr Phe Lys Arg Cys
 500 505 510
 Ser Leu Asp His Phe Met Asp Thr Glu Asp Leu Asn His Leu Ala Ser
 515 520 525
 Val Glu Glu Asp Thr Pro Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr
 530 535 540
 Met Glu Leu Gln Glu Thr Leu Met Lys Thr Phe Ser Glu Asp Lys Glu
 545 550 555 560
 Glu Cys Gly Lys Ser Ser Thr Pro Lys Pro Thr Ser Ala Val Arg Ser
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 104
 His Trp Arg Pro Ala Glu Asp Glu Lys Leu Arg Glu Leu Val Glu Gln
 10 15 20

ttt ggt cct cat aat tgg aac gcc ata gct cag aag ctc tct ggt cga
 152
 Phe Gly Pro His Asn Trp Asn Ala Ile Ala Gln Lys Leu Ser Gly Arg
 25 30 35

tct ggt aag agt tgt aga ttg aga tgg ttt aat caa ttg gat cct agg
 200
 Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe Asn Gln Leu Asp Pro Arg
 40 45 50

att aac cga aac cct ttc acg gag gaa gaa gaa gaa agg ctt tta gcg
 248
 Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu Glu Glu Arg Leu Leu Ala
 55 60 65 70

cct cat cgg atc cat ggg aac aga tgg tct gtg atc gct aga ttt ttt
 296
 Pro His Arg Ile His Gly Asn Arg Trp Ser Val Ile Ala Arg Phe Phe
 75 80 85

ccc ggt cga act gat aac gct gtt aaa aac cat tgg cac gtc atc atg
 344
 Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Trp His Val Ile Met
 90 95 100

gct cgt cgt ggc cga gaa cgg tcc aag ctc cgt cca cga ggc ctt ggc
 392
 Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg Pro Arg Gly Leu Gly
 105 110 115

cat gat ggc acg gtg gct gcg act ggg atg att ggt aat tat aaa gac
 440
 His Asp Gly Thr Val Ala Ala Thr Gly Met Ile Gly Asn Tyr Lys Asp
 120 125 130

tgc gat aag gag aga aga ttg gca acc aca acc gct atc aat ttt cct
 488
 Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr Ala Ile Asn Phe Pro
 135 140 145 150

tat caa ttc tct cat att aat cat ttt caa gtc ctc aaa gag tcc ttg
 536
 Tyr Gln Phe Ser His Ile Asn His Phe Gln Val Leu Lys Glu Ser Leu
 155 160 165

acc gga aag atc ggg ttc aga aat agt act act cca ata caa gaa gga
 584
 Thr Gly Lys Ile Gly Phe Arg Asn Ser Thr Thr Pro Ile Gln Glu Gly
 170 175 180

gca ata gac caa act aaa cga ccg atg gag ttc tac aat ttt ctc caa
 632
 Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe Tyr Asn Phe Leu Gln
 185 190 195

gta aac acg gat tcg aag ata cac gaa ttg ata gat aat tca aga aaa
680

Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile Asp Asn Ser Arg Lys
200 205 210

gac gaa gaa gaa gat gtc gat caa aac aac cga att cgt aac gag aat
728

Asp Glu Glu Glu Asp Val Asp Gln Asn Asn Arg Ile Arg Asn Glu Asn
215 220 225 230

tgt gtt cca ttt ttc gac ttt ttg tct gtt gga aac tct gcc tct cag
776

Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn Ser Ala Ser Gln
235 240 245

ggt tta tgt taa tttgtccgta ccacatgtac tataagggtg accatatgtt
828

Gly Leu Cys

aactaaagat aatgtagaaa gtactaatca attagagctc ctgtttgagc caaatgtgaa
888

aattagttaa gacatcccaa acattttctt gtataacaca tataagggtg tacttttato
948

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1008

aaaaaaaaaa aa
1020

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384

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20 25 30

Gln Lys Leu Ser Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe
35 40 45

Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu
50 55 60

Glu Glu Arg Leu Leu Ala Pro His Arg Ile His Gly Asn Arg Trp Ser
65 70 75 80

Val Ile Ala Arg Phe Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn
85 90 95

His Trp His Val Ile Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu

100 105 110
 Arg Pro Arg Gly Leu Gly His Asp Gly Thr Val Ala Ala Thr Gly Met
 115 120 125
 Ile Gly Asn Tyr Lys Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr
 130 135 140
 Thr Ala Ile Asn Phe Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln
 145 150 155 160
 Val Leu Lys Glu Ser Leu Thr Gly Lys Ile Gly Phe Arg Asn Ser Thr
 165 170 175
 Thr Pro Ile Gln Glu Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu
 180 185 190
 Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu
 195 200 205
 Ile Asp Asn Ser Arg Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn
 210 215 220
 Arg Ile Arg Asn Glu Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val
 225 230 235 240
 Gly Asn Ser Ala Ser Gln Gly Leu Cys
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 106
 Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Thr Glu
 1 5 10 15
 gaa gat agt ctc ttg aga cag tgc att aat aag tat gga gaa ggc aaa
 154
 Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys
 20 25 30
 tgg cac caa gtt cct gta aga gct ggg cta aac cgg tgc agg aaa agt
 202
 Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
 35 40 45

tgt aga tta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga
 250
 Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
 50 55 60
 aaa ctt agc tct gat gaa gtc gat ctt ctt ctt cgc ctt cat agg ctt
 298
 Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu
 65 70 75 80
 cta ggg aat agg tgg tct tta att gct gga aga tta cct ggt cgg acc
 346
 Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
 85 90 95
 gca aat gac gtc aag aat tac tgg aac act cat ctg agt aag aaa cat
 394
 Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
 100 105 110
 gaa ccg tgt tgt aag ata aag atg aaa aag aga gac att acg ccc att
 442
 Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile
 115 120 125
 cct aca aca ccg gca cta aaa aac aat gtt tat aag cct cga cct cga
 490
 Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg
 130 135 140
 tcc ttc aca gtt aac aac gac tgc aac cat ctc aat gcc cca cca aaa
 538
 Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys
 145 150 155 160
 gtt gac gtt aat cct cca tgc ctt gga ctt aac atc aat aat gtt tgt
 586
 Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys
 165 170 175
 gac aat agt atc ata tac aac aaa gat aag aag aaa gac caa cta gtg
 634
 Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val
 180 185 190
 aat aat ttg att gat gga gat aat atg tgg tta gag aaa ttc cta agg
 682
 Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Arg
 195 200 205
 aaa gcc aag agg tag atattttggt tcctgaagcg acgacaacag aaaaggggga
 737
 Lys Ala Lys Arg
 210
 caccttggt tttgacgttg atcaactttg gagtcttttc gatggagaga ctgtgaaatt
 797
 tgattagtgt ttcgaacatt tgtttgcgtt tgtgtatagg tttgctttca ccttttaatt
 857

tgtgtgtttt gataaataag ctaatagttt ttagcatttt aatgaaatat ttcaagtttc
917

cggtgttac
925

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Glu Asp Ser Leu Leu Arg Gln Cys Ile Asn Lys Tyr Gly Glu Gly Lys
20 25 30

Trp His Gln Val Pro Val Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50 55 60

Lys Leu Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Arg Leu
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Glu Pro Cys Cys Lys Ile Lys Met Lys Lys Arg Asp Ile Thr Pro Ile
115 120 125

Pro Thr Thr Pro Ala Leu Lys Asn Asn Val Tyr Lys Pro Arg Pro Arg
130 135 140

Ser Phe Thr Val Asn Asn Asp Cys Asn His Leu Asn Ala Pro Pro Lys
145 150 155 160

Val Asp Val Asn Pro Pro Cys Leu Gly Leu Asn Ile Asn Asn Val Cys
165 170 175

Asp Asn Ser Ile Ile Tyr Asn Lys Asp Lys Lys Lys Asp Gln Leu Val
180 185 190

Asn Asn Leu Ile Asp Gly Asp Asn Met Trp Leu Glu Lys Phe Leu Arg
195 200 205

Lys Ala Lys Arg
210

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gag caa gct ttg ttg tct atg gaa gct tta cct tta ggt ttc aga ttc
97
Glu Gln Ala Leu Leu Ser Met Glu Ala Leu Pro Leu Gly Phe Arg Phe
15 20 25 30
aga cca acg gat gaa gaa ctc atc aat cat tac cta agg tta aaa atc
145
Arg Pro Thr Asp Glu Glu Leu Ile Asn His Tyr Leu Arg Leu Lys Ile
35 40 45
aac ggc cgt gat tta gag gtt aga gtc atc cct gag atc gat gtt tgc
193
Asn Gly Arg Asp Leu Glu Val Arg Val Ile Pro Glu Ile Asp Val Cys
50 55 60
aag tgg gaa cca tgg gac tta cct ggg cta tcg gtg ata aag aca gat
241
Lys Trp Glu Pro Trp Asp Leu Pro Gly Leu Ser Val Ile Lys Thr Asp
65 70 75
gat caa gaa tgg ttc ttt ttt tgt cct cgt gat cga aag tat ccg agt
289
Asp Gln Glu Trp Phe Phe Phe Cys Pro Arg Asp Arg Lys Tyr Pro Ser
80 85 90
ggt cat cgt tct aat aga gct act gat att ggt tac tgg aaa gct act
337
Gly His Arg Ser Asn Arg Ala Thr Asp Ile Gly Tyr Trp Lys Ala Thr
95 100 105 110
ggg aaa gat cga act att aag tct aag aag atg att att ggt atg aag
385
Gly Lys Asp Arg Thr Ile Lys Ser Lys Lys Met Ile Ile Gly Met Lys
115 120 125
aag act ctt gtt ttc tat cgt gga aga gct cct aga gga gag cgt act
433
Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Arg Gly Glu Arg Thr
130 135 140
aat tgg att atg cat gag tat cgt gct aca gac aag gaa cta gat ggt
481
Asn Trp Ile Met His Glu Tyr Arg Ala Thr Asp Lys Glu Leu Asp Gly
145 150 155
act gga cct ggt cag aat ccg tat gtt ttg tgt cgc ttg ttc cac aag
529

Thr Gly Pro Gly Gln Asn Pro Tyr Val Leu Cys Arg Leu Phe His Lys
 160 165 170
 cct agt gat agt tgt gat cct gca cac tgt gag gaa ata gag aaa gtt
 577
 Pro Ser Asp Ser Cys Asp Pro Ala His Cys Glu Glu Ile Glu Lys Val
 175 180 185 190
 aat ttt act cca acc acc acc act aga tgc tct cct gat gac aca tct
 625
 Asn Phe Thr Pro Thr Thr Thr Thr Arg Cys Ser Pro Asp Asp Thr Ser
 195 200 205
 tct gaa atg gtc caa gaa aca gct aca tct ggt gta cat gct cta gat
 673
 Ser Glu Met Val Gln Glu Thr Ala Thr Ser Gly Val His Ala Leu Asp
 210 215 220
 aga tca gat gac act gag agg tgt tta agt gac aag ggc aat aat gat
 721
 Arg Ser Asp Asp Thr Glu Arg Cys Leu Ser Asp Lys Gly Asn Asn Asp
 225 230 235
 gtg aaa cct gat gtt tca gtg ata aac aat act tct gtc aat cac gct
 769
 Val Lys Pro Asp Val Ser Val Ile Asn Asn Thr Ser Val Asn His Ala
 240 245 250
 gaa act tct cgt gcc aaa gac cgt aat ttg ggc aag acg tta gta gag
 817
 Glu Thr Ser Arg Ala Lys Asp Arg Asn Leu Gly Lys Thr Leu Val Glu
 255 260 265 270
 gaa aat cca ctt cta agg gac gtt cca act ctt cat gga ccc atc ttg
 865
 Glu Asn Pro Leu Leu Arg Asp Val Pro Thr Leu His Gly Pro Ile Leu
 275 280 285
 agt gag aaa tca tat tat cca gga cag tca agc atc ggt ttt gct aca
 913
 Ser Glu Lys Ser Tyr Tyr Pro Gly Gln Ser Ser Ile Gly Phe Ala Thr
 290 295 300
 tct cac atg gat tct atg tat tct agt gat ttt gga aac tgt gat tat
 961
 Ser His Met Asp Ser Met Tyr Ser Ser Asp Phe Gly Asn Cys Asp Tyr
 305 310 315
 ggg cta cat ttt caa gat ggt gcc tct gaa caa gat gca tct tta aca
 1009
 Gly Leu His Phe Gln Asp Gly Ala Ser Glu Gln Asp Ala Ser Leu Thr
 320 325 330
 gat gtc ttg gat gaa gta ttc cat aac cat aat gaa tcc tct aat gac
 1057
 Asp Val Leu Asp Glu Val Phe His Asn His Asn Glu Ser Ser Asn Asp
 335 340 345 350
 agg aaa gac ttt gta ctt ccg aat atg atg cat tgg cct ggt aat aca
 1105
 Arg Lys Asp Phe Val Leu Pro Asn Met Met His Trp Pro Gly Asn Thr

355	360	365
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1153		
Arg Leu Leu Ser Thr Glu Tyr Pro Phe Leu Lys Asp Ser Val Ala Phe		
370	375	380
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1201		
Val Asp Gly Ser Ala Glu Val Ser Gly Ser Gln Gln Phe Val Pro Asp		
385	390	395
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1249		
Ile Leu Ala Ser Arg Trp Val Ser Glu Gln Asn Val Asp Ser Lys Glu		
400	405	410
gca gta gag att cta tct tca acc ggg tcc tct cgg acc ttg acg cca		
1297		
Ala Val Glu Ile Leu Ser Ser Thr Gly Ser Ser Arg Thr Leu Thr Pro		
415	420	425
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1345		
Leu His Asn Asn Val Phe Gly Gln Tyr Ala Ser Ser Ser Tyr Ala Ala		
435	440	445
atc gat cca ttt aac tat aat gtc aat cag cct gaa cag tca tcc ttt		
1393		
Ile Asp Pro Phe Asn Tyr Asn Val Asn Gln Pro Glu Gln Ser Ser Phe		
450	455	460
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1441		
Glu Gln Ser His Val Asp Arg Asn Ile Ser Pro Ser Asn Ile Phe Glu		
465	470	475
ttc aag gct agg tct cga gag aat cag aga gat ctg gac tct gtt gtg		
1489		
Phe Lys Ala Arg Ser Arg Glu Asn Gln Arg Asp Leu Asp Ser Val Val		
480	485	490
gac caa ggc act gct cct aga aga att cgg ctg cag atc gaa cag cca		
1537		
Asp Gln Gly Thr Ala Pro Arg Arg Ile Arg Leu Gln Ile Glu Gln Pro		
495	500	505
ttg acg cca gtt acc aac aag aaa gag aga gat gcg gac aac tat gaa		
1585		
Leu Thr Pro Val Thr Asn Lys Lys Glu Arg Asp Ala Asp Asn Tyr Glu		
515	520	525
gaa gaa gat gaa gta caa tct gcc atg tcc aag gtc gta gag gaa gaa		
1633		
Glu Glu Asp Glu Val Gln Ser Ala Met Ser Lys Val Val Glu Glu Glu		
530	535	540
ccg gct aat tta agt gct cag ggg act gct cag agg aga atc cgc ctg		
1681		
Pro Ala Asn Leu Ser Ala Gln Gly Thr Ala Gln Arg Arg Ile Arg Leu		
545	550	555

cag acg aga ttg agg aag cct ctc ata acc cta aac aat aca aaa aga
1729

Gln Thr Arg Leu Arg Lys Pro Leu Ile Thr Leu Asn Asn Thr Lys Arg
560 565 570

aac tca aat ggc aga gaa gga gaa gca agc cat agg aag tgt gaa atg
1777

Asn Ser Asn Gly Arg Glu Gly Glu Ala Ser His Arg Lys Cys Glu Met
575 580 585 590

cag gaa aaa gaa gat ata tca tca tca tca tca tgg cag aaa cag aag
1825

Gln Glu Lys Glu Asp Ile Ser Ser Ser Ser Ser Trp Gln Lys Gln Lys
595 600 605

aag agc ttg gtg cag ttt agt agt gtg gtg ata ata gtg gcg gtg ata
1873

Lys Ser Leu Val Gln Phe Ser Ser Val Val Ile Ile Val Ala Val Ile
610 615 620

gtt gtt tta gta gaa ata tgg aaa gag tca aga gat gcg aaa tgt agc
1921

Val Val Leu Val Glu Ile Trp Lys Glu Ser Arg Asp Ala Lys Cys Ser
625 630 635

ttc ttg ttt cat caa tta gat tcc ttc aaa ggc atg ttt act tga
1966

Phe Leu Phe His Gln Leu Asp Ser Phe Lys Gly Met Phe Thr
640 645 650

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1989

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20 25 30

Thr Asp Glu Glu Leu Ile Asn His Tyr Leu Arg Leu Lys Ile Asn Gly
35 40 45

Arg Asp Leu Glu Val Arg Val Ile Pro Glu Ile Asp Val Cys Lys Trp
50 55 60

Glu Pro Trp Asp Leu Pro Gly Leu Ser Val Ile Lys Thr Asp Asp Gln
65 70 75 80

Glu Trp Phe Phe Phe Cys Pro Arg Asp Arg Lys Tyr Pro Ser Gly His
85 90 95

Arg Ser Asn Arg Ala Thr Asp Ile Gly Tyr Trp Lys Ala Thr Gly Lys
 100 105 110

Asp Arg Thr Ile Lys Ser Lys Lys Met Ile Ile Gly Met Lys Lys Thr
 115 120 125

Leu Val Phe Tyr Arg Gly Arg Ala Pro Arg Gly Glu Arg Thr Asn Trp
 130 135 140

Ile Met His Glu Tyr Arg Ala Thr Asp Lys Glu Leu Asp Gly Thr Gly
 145 150 155 160

Pro Gly Gln Asn Pro Tyr Val Leu Cys Arg Leu Phe His Lys Pro Ser
 165 170 175

Asp Ser Cys Asp Pro Ala His Cys Glu Glu Ile Glu Lys Val Asn Phe
 180 185 190

Thr Pro Thr Thr Thr Arg Cys Ser Pro Asp Asp Thr Ser Ser Glu
 195 200 205

Met Val Gln Glu Thr Ala Thr Ser Gly Val His Ala Leu Asp Arg Ser
 210 215 220

Asp Asp Thr Glu Arg Cys Leu Ser Asp Lys Gly Asn Asn Asp Val Lys
 225 230 235 240

Pro Asp Val Ser Val Ile Asn Asn Thr Ser Val Asn His Ala Glu Thr
 245 250 255

Ser Arg Ala Lys Asp Arg Asn Leu Gly Lys Thr Leu Val Glu Glu Asn
 260 265 270

Pro Leu Leu Arg Asp Val Pro Thr Leu His Gly Pro Ile Leu Ser Glu
 275 280 285

Lys Ser Tyr Tyr Pro Gly Gln Ser Ser Ile Gly Phe Ala Thr Ser His
 290 295 300

Met Asp Ser Met Tyr Ser Ser Asp Phe Gly Asn Cys Asp Tyr Gly Leu
 305 310 315 320

His Phe Gln Asp Gly Ala Ser Glu Gln Asp Ala Ser Leu Thr Asp Val
 325 330 335

Leu Asp Glu Val Phe His Asn His Asn Glu Ser Ser Asn Asp Arg Lys
 340 345 350

Asp Phe Val Leu Pro Asn Met Met His Trp Pro Gly Asn Thr Arg Leu
 355 360 365

Leu Ser Thr Glu Tyr Pro Phe Leu Lys Asp Ser Val Ala Phe Val Asp
 370 375 380

Gly Ser Ala Glu Val Ser Gly Ser Gln Gln Phe Val Pro Asp Ile Leu
 385 390 395 400

Ala Ser Arg Trp Val Ser Glu Gln Asn Val Asp Ser Lys Glu Ala Val
 405 410 415

Glu Ile Leu Ser Ser Thr Gly Ser Ser Arg Thr Leu Thr Pro Leu His
 420 425 430

Asn Asn Val Phe Gly Gln Tyr Ala Ser Ser Ser Tyr Ala Ala Ile Asp
 435 440 445

Pro Phe Asn Tyr Asn Val Asn Gln Pro Glu Gln Ser Ser Phe Glu Gln
 450 455 460

Ser His Val Asp Arg Asn Ile Ser Pro Ser Asn Ile Phe Glu Phe Lys
 465 470 475 480

Ala Arg Ser Arg Glu Asn Gln Arg Asp Leu Asp Ser Val Val Asp Gln
 485 490 495

Gly Thr Ala Pro Arg Arg Ile Arg Leu Gln Ile Glu Gln Pro Leu Thr
 500 505 510

Pro Val Thr Asn Lys Lys Glu Arg Asp Ala Asp Asn Tyr Glu Glu Glu
 515 520 525

Asp Glu Val Gln Ser Ala Met Ser Lys Val Val Glu Glu Glu Pro Ala
 530 535 540

Asn Leu Ser Ala Gln Gly Thr Ala Gln Arg Arg Ile Arg Leu Gln Thr
 545 550 555 560

Arg Leu Arg Lys Pro Leu Ile Thr Leu Asn Asn Thr Lys Arg Asn Ser
 565 570 575

Asn Gly Arg Glu Gly Glu Ala Ser His Arg Lys Cys Glu Met Gln Glu

726

115	120	125
cgc ttt gag aac tca gaa ctt	cgg aat ctg aac aac cac ctt	agg tct
432		
Arg Phe Glu Asn Ser Glu Leu Arg Asn Leu Asn Asn His Leu Arg Ser		
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480		
Glu Asn Gln Arg Leu Arg Glu Ala Ile His Gln Ala Leu Cys Pro Lys		
145	150	155
160		
tgt gga ggc caa act gca att ggc gaa atg acc ttc gaa gag cac cat		
528		
Cys Gly Gly Gln Thr Ala Ile Gly Glu Met Thr Phe Glu Glu His His		
165	170	175
ctt cgc atc ctc aac gct cgt ttg act gaa gag atc aag caa ctt tcc		
576		
Leu Arg Ile Leu Asn Ala Arg Leu Thr Glu Glu Ile Lys Gln Leu Ser		
180	185	190
gtg aca gcg gaa aag ata tca agg ctt acg ggg ata cca gta agg agc		
624		
Val Thr Ala Glu Lys Ile Ser Arg Leu Thr Gly Ile Pro Val Arg Ser		
195	200	205
cat ccc cgt gtg tct cct cct aat cct cct cca aat ttc gag ttc ggg		
672		
His Pro Arg Val Ser Pro Pro Asn Pro Pro Pro Asn Phe Glu Phe Gly		
210	215	220
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720		
Met Gly Ser Lys Gly Asn Val Gly Asn His Ser Arg Glu Thr Thr Gly		
225	230	235
240		
cct gca gat gct aat acc aag ccg atc atc atg gag ttg gca ttt gga		
768		
Pro Ala Asp Ala Asn Thr Lys Pro Ile Ile Met Glu Leu Ala Phe Gly		
245	250	255
gcc atg gag gag ctc ttg gtg atg gct caa gtg gct gaa cca ctg tgg		
816		
Ala Met Glu Glu Leu Leu Val Met Ala Gln Val Ala Glu Pro Leu Trp		
260	265	270
atg gga gga ttt aat ggc act agc tta gct ttg aac ttg gat gaa tac		
864		
Met Gly Gly Phe Asn Gly Thr Ser Leu Ala Leu Asn Leu Asp Glu Tyr		
275	280	285
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912		
Glu Lys Thr Phe Arg Thr Gly Leu Gly Pro Arg Leu Gly Gly Phe Arg		
290	295	300
acc gag gca tcc agg gaa act gca ctc gtg gca atg tgt cct act ggc		
960		
Thr Glu Ala Ser Arg Glu Thr Ala Leu Val Ala Met Cys Pro Thr Gly		
305	310	315
320		

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 Ile Val Glu Met Leu Met Gln Glu Asn Leu Trp Ser Thr Met Phe Ala
 325 330 335

gga att gtt ggt aga gcc agg act cat gaa cag ata atg gct gat gct
 1056
 Gly Ile Val Gly Arg Ala Arg Thr His Glu Gln Ile Met Ala Asp Ala
 340 345 350

gct gga aac ttc aat gga aat ctc caa ata atg agt gct gag tac caa
 1104
 Ala Gly Asn Phe Asn Gly Asn Leu Gln Ile Met Ser Ala Glu Tyr Gln
 355 360 365

gtg ctt tcc ccg cta gtc aca acc cgc gaa agc tac ttc gtc cgc tac
 1152
 Val Leu Ser Pro Leu Val Thr Thr Arg Glu Ser Tyr Phe Val Arg Tyr
 370 375 380

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 1200
 Cys Lys Gln Gln Gly Glu Gly Leu Trp Ala Val Val Asp Ile Ser Ile
 385 390 395 400

gac cat ctc ctc cca aac atc aac cta aaa tgt cgc cgc cga ccc tct
 1248
 Asp His Leu Leu Pro Asn Ile Asn Leu Lys Cys Arg Arg Arg Pro Ser
 405 410 415

gga tgt ctg att caa gaa atg cat agt ggt tac tcc aag gtt aca tgg
 1296
 Gly Cys Leu Ile Gln Glu Met His Ser Gly Tyr Ser Lys Val Thr Trp
 420 425 430

gtg gaa cat gtg gaa gta gat gat gca gga agt tac agc atc ttt gag
 1344
 Val Glu His Val Glu Val Asp Asp Ala Gly Ser Tyr Ser Ile Phe Glu
 435 440 445

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 1392
 Lys Leu Ile Cys Thr Gly Gln Ala Phe Ala Ala Asn Arg Trp Val Gly
 450 455 460

aca ttg gta cgc cag tgt gag cgg ata tct agc atc ttg tcg aca gat
 1440
 Thr Leu Val Arg Gln Cys Glu Arg Ile Ser Ser Ile Leu Ser Thr Asp
 465 470 475 480

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 Phe Gln Ser Val Asp Ser Gly Asp His Ile Thr Leu Thr Asn His Gly
 485 490 495

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 1536
 Lys Met Ser Met Leu Lys Ile Ala Glu Arg Ile Ala Arg Thr Phe Phe
 500 505 510

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 1584
 Ala Gly Met Thr Asn Ala Thr Gly Ser Thr Ile Phe Ser Gly Val Glu
 515 520 525

gga gaa gat atc aga gtg atg aca atg aag agc gtg aat gat cca gga
 1632
 Gly Glu Asp Ile Arg Val Met Thr Met Lys Ser Val Asn Asp Pro Gly
 530 535 540

aag cct ccc ggt gtc att att tgt gca gcc act tcc ttt tgg ctt cct
 1680
 Lys Pro Pro Gly Val Ile Ile Cys Ala Ala Thr Ser Phe Trp Leu Pro
 545 550 555 560

gct cct cct aac act gtc ttt gac ttc ctc aga gag gct act cac cga
 1728
 Ala Pro Pro Asn Thr Val Phe Asp Phe Leu Arg Glu Ala Thr His Arg
 565 570 575

cac aat tgg gat gtt ctc tgc aac gga gag atg atg cac aag ata gca
 1776
 His Asn Trp Asp Val Leu Cys Asn Gly Glu Met Met His Lys Ile Ala
 580 585 590

gag att acg aat ggg ata gac aaa agg aac tgt gca agt tta ctc cgg
 1824
 Glu Ile Thr Asn Gly Ile Asp Lys Arg Asn Cys Ala Ser Leu Leu Arg
 595 600 605

cat gga cac act agc aag agc aag atg atg ata gtt caa gag act tct
 1872
 His Gly His Thr Ser Lys Ser Lys Met Met Ile Val Gln Glu Thr Ser
 610 615 620

act gac cca aca gct tca ttt gtg ctt tat gcg cct gtt gat atg aca
 1920
 Thr Asp Pro Thr Ala Ser Phe Val Leu Tyr Ala Pro Val Asp Met Thr
 625 630 635 640

tca atg gat att act ctc cat gga ggt ggt gat cct gac ttt gtg gtg
 1968
 Ser Met Asp Ile Thr Leu His Gly Gly Gly Asp Pro Asp Phe Val Val
 645 650 655

atc ctg cct tct ggt ttt gct att ttt cca gat ggt acg ggt aag cct
 2016
 Ile Leu Pro Ser Gly Phe Ala Ile Phe Pro Asp Gly Thr Gly Lys Pro
 660 665 670

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 2064
 Gly Gly Lys Glu Gly Gly Ser Leu Leu Thr Ile Ser Phe Gln Met Leu
 675 680 685

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 2112
 Val Glu Ser Gly Pro Glu Ala Arg Leu Ser Val Ser Ser Val Ala Thr
 690 695 700

act gag aat ctg att cgt aca acc gtg cgg agg atc aaa gat ttg ttt
2160

Thr Glu Asn Leu Ile Arg Thr Thr Val Arg Arg Ile Lys Asp Leu Phe
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2178

Pro Cys Gln Thr Ala
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Asn Thr Asn Ala Gly Asn Asp Ser Gly Asp Gln Asp Phe Asp Ser Gly
35 40 45

Asn Thr Ser Ser Gly Asn His Gly Glu Gly Leu Gly Asn Asn Gln Ala
50 55 60

Pro Arg His Lys Lys Lys Lys Tyr Asn Arg His Thr Gln Leu Gln Ile
65 70 75 80

Ser Glu Met Glu Ala Phe Phe Arg Glu Cys Pro His Pro Asp Asp Lys
85 90 95

Gln Arg Tyr Asp Leu Ser Ala Gln Leu Gly Leu Asp Pro Val Gln Ile
100 105 110

Lys Phe Trp Phe Gln Asn Lys Arg Thr Gln Asn Lys Asn Gln Gln Glu
115 120 125

Arg Phe Glu Asn Ser Glu Leu Arg Asn Leu Asn Asn His Leu Arg Ser
130 135 140

Glu Asn Gln Arg Leu Arg Glu Ala Ile His Gln Ala Leu Cys Pro Lys
145 150 155 160

Cys Gly Gly Gln Thr Ala Ile Gly Glu Met Thr Phe Glu Glu His His
165 170 175

Leu Arg Ile Leu Asn Ala Arg Leu Thr Glu Glu Ile Lys Gln Leu Ser
180 185 190

Val Thr Ala Glu Lys Ile Ser Arg Leu Thr Gly Ile Pro Val Arg Ser
 195 200 205
 His Pro Arg Val Ser Pro Pro Asn Pro Pro Pro Asn Phe Glu Phe Gly
 210 215 220
 Met Gly Ser Lys Gly Asn Val Gly Asn His Ser Arg Glu Thr Thr Gly
 225 230 235 240
 Pro Ala Asp Ala Asn Thr Lys Pro Ile Ile Met Glu Leu Ala Phe Gly
 245 250 255
 Ala Met Glu Glu Leu Leu Val Met Ala Gln Val Ala Glu Pro Leu Trp
 260 265 270
 Met Gly Gly Phe Asn Gly Thr Ser Leu Ala Leu Asn Leu Asp Glu Tyr
 275 280 285
 Glu Lys Thr Phe Arg Thr Gly Leu Gly Pro Arg Leu Gly Gly Phe Arg
 290 295 300
 Thr Glu Ala Ser Arg Glu Thr Ala Leu Val Ala Met Cys Pro Thr Gly
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 Ile Val Glu Met Leu Met Gln Glu Asn Leu Trp Ser Thr Met Phe Ala
 325 330 335
 Gly Ile Val Gly Arg Ala Arg Thr His Glu Gln Ile Met Ala Asp Ala
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 Ala Gly Asn Phe Asn Gly Asn Leu Gln Ile Met Ser Ala Glu Tyr Gln
 355 360 365
 Val Leu Ser Pro Leu Val Thr Thr Arg Glu Ser Tyr Phe Val Arg Tyr
 370 375 380
 Cys Lys Gln Gln Gly Glu Gly Leu Trp Ala Val Val Asp Ile Ser Ile
 385 390 395 400
 Asp His Leu Leu Pro Asn Ile Asn Leu Lys Cys Arg Arg Arg Pro Ser
 405 410 415
 Gly Cys Leu Ile Gln Glu Met His Ser Gly Tyr Ser Lys Val Thr Trp
 420 425 430

Val Glu His Val Glu Val Asp Asp Ala Gly Ser Tyr Ser Ile Phe Glu
435 440 445

Lys Leu Ile Cys Thr Gly Gln Ala Phe Ala Ala Asn Arg Trp Val Gly
450 455 460

Thr Leu Val Arg Gln Cys Glu Arg Ile Ser Ser Ile Leu Ser Thr Asp
465 470 475 480

Phe Gln Ser Val Asp Ser Gly Asp His Ile Thr Leu Thr Asn His Gly
485 490 495

Lys Met Ser Met Leu Lys Ile Ala Glu Arg Ile Ala Arg Thr Phe Phe
500 505 510

Ala Gly Met Thr Asn Ala Thr Gly Ser Thr Ile Phe Ser Gly Val Glu
515 520 525

Gly Glu Asp Ile Arg Val Met Thr Met Lys Ser Val Asn Asp Pro Gly
530 535 540

Lys Pro Pro Gly Val Ile Ile Cys Ala Ala Thr Ser Phe Trp Leu Pro
545 550 555 560

Ala Pro Pro Asn Thr Val Phe Asp Phe Leu Arg Glu Ala Thr His Arg
565 570 575

His Asn Trp Asp Val Leu Cys Asn Gly Glu Met Met His Lys Ile Ala
580 585 590

Glu Ile Thr Asn Gly Ile Asp Lys Arg Asn Cys Ala Ser Leu Leu Arg
595 600 605

His Gly His Thr Ser Lys Ser Lys Met Met Ile Val Gln Glu Thr Ser
610 615 620

Thr Asp Pro Thr Ala Ser Phe Val Leu Tyr Ala Pro Val Asp Met Thr
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Ser Met Asp Ile Thr Leu His Gly Gly Gly Asp Pro Asp Phe Val Val
645 650 655

Ile Leu Pro Ser Gly Phe Ala Ile Phe Pro Asp Gly Thr Gly Lys Pro
660 665 670

Gly Gly Lys Glu Gly Gly Ser Leu Leu Thr Ile Ser Phe Gln Met Leu

675

680

685

Val Glu Ser Gly Pro Glu Ala Arg Leu Ser Val Ser Ser Val Ala Thr
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 96
 Gln Ile Leu Gln Leu Trp Leu Lys Leu Ile Ala Val Gly Trp Asn Leu
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 144
 Gly Ser Asn Asp Asp Glu Leu Tyr Thr Glu Leu Trp Lys Ala Cys Ala
 35 40 45
 ggg cca ctt gtg gaa gtt cct cgt tat ggt gaa aga gtt ttc tac ttc
 192
 Gly Pro Leu Val Glu Val Pro Arg Tyr Gly Glu Arg Val Phe Tyr Phe
 50 55 60
 cct caa ggt cac atg gaa caa ttg gtt gct tcg act aat caa gga gtt
 240
 Pro Gln Gly His Met Glu Gln Leu Val Ala Ser Thr Asn Gln Gly Val
 65 70 75 80
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 Val Asp Gln Glu Ile Pro Val Phe Asn Leu Pro Pro Lys Ile Leu Cys
 85 90 95
 cgt gtt ctt agt gtt acg tta aaa gca gaa cat gag acc gat gag gtt
 336
 Arg Val Leu Ser Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val
 100 105 110
 tac gct cag atc aca tta caa cca gaa gaa gat caa agt gaa cca aca
 384
 Tyr Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr
 115 120 125
 agt ctt gac cca cct tta gta gaa cca gct aaa cca acg gtt gat tct
 432

Ser Leu Asp Pro Pro Leu Val Glu Pro Ala Lys Pro Thr Val Asp Ser
 130 135 140
 ttt gtg aag att cta aca gct tca gat aca agc aca cat ggt gga ttc
 480
 Phe Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe
 145 150 155 160
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 528
 Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met
 165 170 175
 aca caa cct aca ccg act caa gaa ctt gta gct aga gat ctt cac ggc
 576
 Thr Gln Pro Thr Pro Thr Gln Glu Leu Val Ala Arg Asp Leu His Gly
 180 185 190
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 624
 Tyr Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His
 195 200 205
 tta ctt aca acc ggt tgg agt aca ttt gta acc tcg aaa aga ctt gta
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 Ala Gly Asp Ala Phe Val Phe Leu Arg Gly Glu Thr Gly Asp Leu Arg
 225 230 235 240
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 Val Gly Val Arg Arg Leu Ala Lys Gln Gln Ser Thr Met Pro Ala Ser
 245 250 255
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 Val Ile Ser Ser Gln Ser Met Arg Leu Gly Val Leu Ala Thr Ala Ser
 260 265 270
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 864
 His Ala Val Thr Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg
 275 280 285
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 912
 Ile Ser Gln Phe Ile Ile Ser Val Asn Lys Tyr Met Met Ala Met Lys
 290 295 300
 aac ggg ttt tct ctc ggt atg cgg tat agg atg aga ttc gaa gga gaa
 960
 Asn Gly Phe Ser Leu Gly Met Arg Tyr Arg Met Arg Phe Glu Gly Glu
 305 310 315 320
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325	330	335
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Leu Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Ile Gln 340 345 350		
tgg gac gag cca tct tct ata cag aga cca aac aag gtc tca ccg tgg 1104		
Trp Asp Glu Pro Ser Ser Ile Gln Arg Pro Asn Lys Val Ser Pro Trp 355 360 365		
gag atc gag cct ttc tca cca tcc gcg ctt aca cca acc cct act caa 1152		
Glu Ile Glu Pro Phe Ser Pro Ser Ala Leu Thr Pro Thr Pro Thr Gln 370 375 380		
caa caa tca aag tcc aaa cgg tcc aga cca atc tca gaa atc aca ggg 1200		
Gln Gln Ser Lys Ser Lys Arg Ser Arg Pro Ile Ser Glu Ile Thr Gly 385 390 395 400		
agt cct gta gct tct agt ttc ttg agt agt ttc tcg cag agc cac gag 1248		
Ser Pro Val Ala Ser Ser Phe Leu Ser Ser Phe Ser Gln Ser His Glu 405 410 415		
tct aat cca tcg gtc aaa ctg ttg ttt caa gat cca gca acc gag aga 1296		
Ser Asn Pro Ser Val Lys Leu Leu Phe Gln Asp Pro Ala Thr Glu Arg 420 425 430		
aac tca aac aaa tca gtg ttt tca agt gga tta caa tgc aag ata acc 1344		
Asn Ser Asn Lys Ser Val Phe Ser Ser Gly Leu Gln Cys Lys Ile Thr 435 440 445		
gag gct ccg gtc aca agt agt tgt agg tta ttc gga ttc gat ctc acg 1392		
Glu Ala Pro Val Thr Ser Ser Cys Arg Leu Phe Gly Phe Asp Leu Thr 450 455 460		
agc aag cct gct tct gct aca att cct cat gac aag cag cta ata agt 1440		
Ser Lys Pro Ala Ser Ala Thr Ile Pro His Asp Lys Gln Leu Ile Ser 465 470 475 480		
gtg gat tca aat ata tct gat tct acc acc aag tgt caa gat cct aac 1488		
Val Asp Ser Asn Ile Ser Asp Ser Thr Thr Lys Cys Gln Asp Pro Asn 485 490 495		
tct tca aac tca cca aaa gag cag aaa caa caa aca tcc aca aga agc 1536		
Ser Ser Asn Ser Pro Lys Glu Gln Lys Gln Gln Thr Ser Thr Arg Ser 500 505 510		
cga atc aag gtg caa atg caa gga aca gcg gtt gga cgc gcg gtt gat 1584		
Arg Ile Lys Val Gln Met Gln Gly Thr Ala Val Gly Arg Ala Val Asp 515 520 525		

tta aca ttg ttg aga tca tac gat gaa cta ata aaa gag cta gag aaa
1632

Leu Thr Leu Leu Arg Ser Tyr Asp Glu Leu Ile Lys Glu Leu Glu Lys
530 535 540

atg ttt gag att gaa gga gaa ctt agt cct aaa gac aaa tgg gct atc
1680

Met Phe Glu Ile Glu Gly Glu Leu Ser Pro Lys Asp Lys Trp Ala Ile
545 550 555 560

gtg ttt aca gac gat gaa gga gat agg atg ctt gta gga gat gat cca
1728

Val Phe Thr Asp Asp Glu Gly Asp Arg Met Leu Val Gly Asp Asp Pro
565 570 575

tgg aat gag ttc tgt aaa atg gca aag aag tta ttc ata tat ccg agt
1776

Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Leu Phe Ile Tyr Pro Ser
580 585 590

gat gag gtc aag aaa atg agg tcg aag tcg ttg ttg ggt gat aaa ggt
1824

Asp Glu Val Lys Lys Met Arg Ser Lys Ser Leu Leu Gly Asp Lys Gly
595 600 605

acg atc gta aat ctt gaa tca gat cag agg aca gtt cac gtt taa
1869

Thr Ile Val Asn Leu Glu Ser Asp Gln Arg Thr Val His Val
610 615 620

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20 25 30

Gly Ser Asn Asp Asp Glu Leu Tyr Thr Glu Leu Trp Lys Ala Cys Ala
35 40 45

Gly Pro Leu Val Glu Val Pro Arg Tyr Gly Glu Arg Val Phe Tyr Phe
50 55 60

Pro Gln Gly His Met Glu Gln Leu Val Ala Ser Thr Asn Gln Gly Val
65 70 75 80

Val Asp Gln Glu Ile Pro Val Phe Asn Leu Pro Pro Lys Ile Leu Cys
85 90 95

Arg Val Leu Ser Val Thr Leu Lys Ala Glu His Glu Thr Asp Glu Val
100 105 110

Tyr Ala Gln Ile Thr Leu Gln Pro Glu Glu Asp Gln Ser Glu Pro Thr
 115 120 125

Ser Leu Asp Pro Pro Leu Val Glu Pro Ala Lys Pro Thr Val Asp Ser
 130 135 140

Phe Val Lys Ile Leu Thr Ala Ser Asp Thr Ser Thr His Gly Gly Phe
 145 150 155 160

Ser Val Leu Arg Lys His Ala Thr Glu Cys Leu Pro Ser Leu Asp Met
 165 170 175

Thr Gln Pro Thr Pro Thr Gln Glu Leu Val Ala Arg Asp Leu His Gly
 180 185 190

Tyr Glu Trp Arg Phe Lys His Ile Phe Arg Gly Gln Pro Arg Arg His
 195 200 205

Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Thr Ser Lys Arg Leu Val
 210 215 220

Ala Gly Asp Ala Phe Val Phe Leu Arg Gly Glu Thr Gly Asp Leu Arg
 225 230 235 240

Val Gly Val Arg Arg Leu Ala Lys Gln Gln Ser Thr Met Pro Ala Ser
 245 250 255

Val Ile Ser Ser Gln Ser Met Arg Leu Gly Val Leu Ala Thr Ala Ser
 260 265 270

His Ala Val Thr Thr Thr Thr Ile Phe Val Val Phe Tyr Lys Pro Arg
 275 280 285

Ile Ser Gln Phe Ile Ile Ser Val Asn Lys Tyr Met Met Ala Met Lys
 290 295 300

Asn Gly Phe Ser Leu Gly Met Arg Tyr Arg Met Arg Phe Glu Gly Glu
 305 310 315 320

Glu Ser Pro Glu Arg Ile Phe Thr Gly Thr Ile Ile Gly Ser Gly Asp
 325 330 335

Leu Ser Ser Gln Trp Pro Ala Ser Lys Trp Arg Ser Leu Gln Ile Gln
 340 345 350

Trp Asp Glu Pro Ser Ser Ile Gln Arg Pro Asn Lys Val Ser Pro Trp
 355 360 365

Glu Ile Glu Pro Phe Ser Pro Ser Ala Leu Thr Pro Thr Pro Thr Gln
 370 375 380

Gln Gln Ser Lys Ser Lys Arg Ser Arg Pro Ile Ser Glu Ile Thr Gly
 385 390 395 400

Ser Pro Val Ala Ser Ser Phe Leu Ser Ser Phe Ser Gln Ser His Glu
 405 410 415

Ser Asn Pro Ser Val Lys Leu Leu Phe Gln Asp Pro Ala Thr Glu Arg
 420 425 430

Asn Ser Asn Lys Ser Val Phe Ser Ser Gly Leu Gln Cys Lys Ile Thr
 435 440 445

Glu Ala Pro Val Thr Ser Ser Cys Arg Leu Phe Gly Phe Asp Leu Thr
 450 455 460

Ser Lys Pro Ala Ser Ala Thr Ile Pro His Asp Lys Gln Leu Ile Ser
 465 470 475 480

Val Asp Ser Asn Ile Ser Asp Ser Thr Thr Lys Cys Gln Asp Pro Asn
 485 490 495

Ser Ser Asn Ser Pro Lys Glu Gln Lys Gln Gln Thr Ser Thr Arg Ser
 500 505 510

Arg Ile Lys Val Gln Met Gln Gly Thr Ala Val Gly Arg Ala Val Asp
 515 520 525

Leu Thr Leu Leu Arg Ser Tyr Asp Glu Leu Ile Lys Glu Leu Glu Lys
 530 535 540

Met Phe Glu Ile Glu Gly Glu Leu Ser Pro Lys Asp Lys Trp Ala Ile
 545 550 555 560

Val Phe Thr Asp Asp Glu Gly Asp Arg Met Leu Val Gly Asp Asp Pro
 565 570 575

Trp Asn Glu Phe Cys Lys Met Ala Lys Lys Leu Phe Ile Tyr Pro Ser
 580 585 590

Asp Glu Val Lys Lys Met Arg Ser Lys Ser Leu Leu Gly Asp Lys Gly
 595 600 605

Thr Ile Val Asn Leu Glu Ser Asp Gln Arg Thr Val His Val
 610 615 620

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 96
 Pro Lys Ser Thr Ser Asp Asn Asp Leu Gly Ile Thr Gly Ser Arg Glu
 20 25 30
 gat gac ttt gag acc aag tca ggt acc gaa gtc act act gag aat cct
 144
 Asp Asp Phe Glu Thr Lys Ser Gly Thr Glu Val Thr Thr Glu Asn Pro
 35 40 45
 tct ggt gaa gag ctt caa gat cct agc caa cgt ccc aac aaa aag aag
 192
 Ser Gly Glu Glu Leu Gln Asp Pro Ser Gln Arg Pro Asn Lys Lys Lys
 50 55 60
 cgt tac cat cgc cac acg caa cgc caa att caa gag ctc gaa tca ttc
 240
 Arg Tyr His Arg His Thr Gln Arg Gln Ile Gln Glu Leu Glu Ser Phe
 65 70 75 80
 ttt aag gaa tgt cct cat cca gat gat aag caa cga aaa gag ttg agc
 288
 Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Glu Leu Ser
 85 90 95
 cgt gat ctc aat tta gag cct ctt caa gtt aag ttt tgg ttc caa aac
 336
 Arg Asp Leu Asn Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn
 100 105 110
 aaa cgc aca cag atg aag gca caa agt gag agg cat gag aac cag att
 384
 Lys Arg Thr Gln Met Lys Ala Gln Ser Glu Arg His Glu Asn Gln Ile
 115 120 125
 cta aag tca gac aat gac aag ctc aga gca gag aac aat aga tac aaa
 432
 Leu Lys Ser Asp Asn Asp Lys Leu Arg Ala Glu Asn Asn Arg Tyr Lys
 130 135 140
 gaa gct cta agc aat gct aca tgc cct aac tgt ggc ggt cca gct gct
 480
 Glu Ala Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly Gly Pro Ala Ala
 145 150 155 160

att gga gaa atg tct ttt gac gaa caa cat ctc agg atc gaa aat gct
 528
 Ile Gly Glu Met Ser Phe Asp Glu Gln His Leu Arg Ile Glu Asn Ala
 165 170 175

cgg ctc cgc gaa gag att gat agg atc tct gct att gct gcg aaa tac
 576
 Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Ala Lys Tyr
 180 185 190

gtt ggg aag ccg tta gga tcg tct ttc gct cca cta gcg atc cac gcg
 624
 Val Gly Lys Pro Leu Gly Ser Ser Phe Ala Pro Leu Ala Ile His Ala
 195 200 205

cct tct cgt tcg ctt gat ctt gaa gtt gga aac ttt ggg aac cag aca
 672
 Pro Ser Arg Ser Leu Asp Leu Glu Val Gly Asn Phe Gly Asn Gln Thr
 210 215 220

ggc ttt gta gga gaa atg tat gga aca ggg gac att ttg agg tca gtt
 720
 Gly Phe Val Gly Glu Met Tyr Gly Thr Gly Asp Ile Leu Arg Ser Val
 225 230 235 240

tcg att cct tct gag act gat aag cct ata atc gtg gag cta gcg gtt
 768
 Ser Ile Pro Ser Glu Thr Asp Lys Pro Ile Ile Val Glu Leu Ala Val
 245 250 255

gca gct atg gag gaa ctc gtg aga atg gct caa act gga gat cct tta
 816
 Ala Ala Met Glu Glu Leu Val Arg Met Ala Gln Thr Gly Asp Pro Leu
 260 265 270

tgg ctt tca acc gat aat tca gtc gag att ctc aac gaa gaa gag tat
 864
 Trp Leu Ser Thr Asp Asn Ser Val Glu Ile Leu Asn Glu Glu Glu Tyr
 275 280 285

ttc aga acg ttt ccg aga gga att gga cca aag cca tta gga tta aga
 912
 Phe Arg Thr Phe Pro Arg Gly Ile Gly Pro Lys Pro Leu Gly Leu Arg
 290 295 300

tca gag gcg tca aga caa tct gca gtt gtt ata atg aat cac atc aat
 960
 Ser Glu Ala Ser Arg Gln Ser Ala Val Val Ile Met Asn His Ile Asn
 305 310 315 320

ctc gtt gag att ctc atg gat gtg aat caa tgg tct tgt gtt ttc tct
 1008
 Leu Val Glu Ile Leu Met Asp Val Asn Gln Trp Ser Cys Val Phe Ser
 325 330 335

ggg att gtg tca aga gcc ttg aca ctt gaa gtt ctt tca act gga gtt
 1056
 Gly Ile Val Ser Arg Ala Leu Thr Leu Glu Val Leu Ser Thr Gly Val
 340 345 350

gct ggg aac tac aac ggt gct tta caa gtg atg aca gct gag ttt caa
 1104
 Ala Gly Asn Tyr Asn Gly Ala Leu Gln Val Met Thr Ala Glu Phe Gln
 355 360 365

gtt cca tca ccc cta gtc cca acg cgt gag aac tac ttt gtg aga tac
 1152
 Val Pro Ser Pro Leu Val Pro Thr Arg Glu Asn Tyr Phe Val Arg Tyr
 370 375 380

tgc aaa caa cac agt gac ggc tct tgg gct gtg gtt gat gtc tct ttg
 1200
 Cys Lys Gln His Ser Asp Gly Ser Trp Ala Val Val Asp Val Ser Leu
 385 390 395 400

gac agc ctt aga cca agt act cca atc tta aga act aga aga agg cct
 1248
 Asp Ser Leu Arg Pro Ser Thr Pro Ile Leu Arg Thr Arg Arg Arg Pro
 405 410 415

tca ggt tgt ctg att caa gaa ttg cct aat ggt tat tct aag gtt aca
 1296
 Ser Gly Cys Leu Ile Gln Glu Leu Pro Asn Gly Tyr Ser Lys Val Thr
 420 425 430

tgg ata gag cat atg gag gta gat gat aga tca gtt cac aac atg tat
 1344
 Trp Ile Glu His Met Glu Val Asp Asp Arg Ser Val His Asn Met Tyr
 435 440 445

aaa ccg ttg gtt cag tcc ggt tta gct ttc ggt gcg aaa cgt tgg gtg
 1392
 Lys Pro Leu Val Gln Ser Gly Leu Ala Phe Gly Ala Lys Arg Trp Val
 450 455 460

gct aca ctc gaa cga caa tgc gag cgg ctt gct agc tcc atg gcc agc
 1440
 Ala Thr Leu Glu Arg Gln Cys Glu Arg Leu Ala Ser Ser Met Ala Ser
 465 470 475 480

aac att cct ggt gat ctt tcc gtg ata acg agt cct gaa gga agg aag
 1488
 Asn Ile Pro Gly Asp Leu Ser Val Ile Thr Ser Pro Glu Gly Arg Lys
 485 490 495

agt atg ttg aag cta gct gag aga atg gtt atg agt ttc tgc agt ggt
 1536
 Ser Met Leu Lys Leu Ala Glu Arg Met Val Met Ser Phe Cys Ser Gly
 500 505 510

gtt ggc gcg tcg act gca cac gct tgg aca aca atg tcg aca aca gga
 1584
 Val Gly Ala Ser Thr Ala His Ala Trp Thr Thr Met Ser Thr Thr Gly
 515 520 525

tcc gat gat gtt cgg gtc atg acc cgc aag agt atg gat gat cca gga
 1632
 Ser Asp Asp Val Arg Val Met Thr Arg Lys Ser Met Asp Asp Pro Gly
 530 535 540

aga cct ccg ggt att gtt ctt agt gca gct act tca ttc tgg atc cca
 1680
 Arg Pro Pro Gly Ile Val Leu Ser Ala Ala Thr Ser Phe Trp Ile Pro
 545 550 555 560

gtt gct ccc aaa cgt gtt ttt gat ttc ctc cgt gac gaa aat tca aga
 1728
 Val Ala Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu Asn Ser Arg
 565 570 575

aaa gag tgg gat att ctg tca aat gga ggt atg gtt cag gaa atg gct
 1776
 Lys Glu Trp Asp Ile Leu Ser Asn Gly Gly Met Val Gln Glu Met Ala
 580 585 590

cat ata gcc aat ggt cat gaa cct gga aac tgt gtc tcc ttg ctc cga
 1824
 His Ile Ala Asn Gly His Glu Pro Gly Asn Cys Val Ser Leu Leu Arg
 595 600 605

gtc aat agt gga aac tcg agc cag agc aac atg ttg att cta caa gag
 1872
 Val Asn Ser Gly Asn Ser Ser Gln Ser Asn Met Leu Ile Leu Gln Glu
 610 615 620

agc tgt aca gat gca tca gga tcg tat gtg att tac gcg cca gtg gat
 1920
 Ser Cys Thr Asp Ala Ser Gly Ser Tyr Val Ile Tyr Ala Pro Val Asp
 625 630 635 640

ata gtg gcg atg aat gtg gtt cta agc ggt gga gat cct gat tac gtg
 1968
 Ile Val Ala Met Asn Val Val Leu Ser Gly Gly Asp Pro Asp Tyr Val
 645 650 655

gcg ttg ttg ccg tct ggt ttt gct att tta ccg gat ggt tcg gtt gga
 2016
 Ala Leu Leu Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly Ser Val Gly
 660 665 670

gga gga gat ggg aat cag cat cag gaa atg gtt tct act act tct tct
 2064
 Gly Gly Asp Gly Asn Gln His Gln Glu Met Val Ser Thr Thr Ser Ser
 675 680 685

ggg agt tgt ggt ggt tcg ctt tta acc gtt gcg ttt cag att ctt gtt
 2112
 Gly Ser Cys Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val
 690 695 700

gac tct gtt cct aca gct aaa ctc tca ctt ggc tcg gtg gct acg gtt
 2160
 Asp Ser Val Pro Thr Ala Lys Leu Ser Leu Gly Ser Val Ala Thr Val
 705 710 715 720

aat agt ctg atc aaa tgt acg gtg gag agg att aaa gct gct gtt tct
 2208
 Asn Ser Leu Ile Lys Cys Thr Val Glu Arg Ile Lys Ala Ala Val Ser
 725 730 735

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 2232
 Cys Asp Val Gly Gly Gly Ala
 740

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Met Tyr His Pro Asn Met Phe Glu Ser His His Met Phe Asp Met Thr
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 20 25 30

Asp Asp Phe Glu Thr Lys Ser Gly Thr Glu Val Thr Thr Glu Asn Pro
 35 40 45

Ser Gly Glu Glu Leu Gln Asp Pro Ser Gln Arg Pro Asn Lys Lys Lys
 50 55 60

Arg Tyr His Arg His Thr Gln Arg Gln Ile Gln Glu Leu Glu Ser Phe
 65 70 75 80

Phe Lys Glu Cys Pro His Pro Asp Asp Lys Gln Arg Lys Glu Leu Ser
 85 90 95

Arg Asp Leu Asn Leu Glu Pro Leu Gln Val Lys Phe Trp Phe Gln Asn
 100 105 110

Lys Arg Thr Gln Met Lys Ala Gln Ser Glu Arg His Glu Asn Gln Ile
 115 120 125

Leu Lys Ser Asp Asn Asp Lys Leu Arg Ala Glu Asn Asn Arg Tyr Lys
 130 135 140

Glu Ala Leu Ser Asn Ala Thr Cys Pro Asn Cys Gly Gly Pro Ala Ala
 145 150 155 160

Ile Gly Glu Met Ser Phe Asp Glu Gln His Leu Arg Ile Glu Asn Ala
 165 170 175

Arg Leu Arg Glu Glu Ile Asp Arg Ile Ser Ala Ile Ala Lys Tyr
 180 185 190

Val Gly Lys Pro Leu Gly Ser Ser Phe Ala Pro Leu Ala Ile His Ala
 195 200 205

Pro Ser Arg Ser Leu Asp Leu Glu Val Gly Asn Phe Gly Asn Gln Thr
 210 215 220

 Gly Phe Val Gly Glu Met Tyr Gly Thr Gly Asp Ile Leu Arg Ser Val
 225 230 235 240

 Ser Ile Pro Ser Glu Thr Asp Lys Pro Ile Ile Val Glu Leu Ala Val
 245 250 255

 Ala Ala Met Glu Glu Leu Val Arg Met Ala Gln Thr Gly Asp Pro Leu
 260 265 270

 Trp Leu Ser Thr Asp Asn Ser Val Glu Ile Leu Asn Glu Glu Glu Tyr
 275 280 285

 Phe Arg Thr Phe Pro Arg Gly Ile Gly Pro Lys Pro Leu Gly Leu Arg
 290 295 300

 Ser Glu Ala Ser Arg Gln Ser Ala Val Val Ile Met Asn His Ile Asn
 305 310 315 320

 Leu Val Glu Ile Leu Met Asp Val Asn Gln Trp Ser Cys Val Phe Ser
 325 330 335

 Gly Ile Val Ser Arg Ala Leu Thr Leu Glu Val Leu Ser Thr Gly Val
 340 345 350

 Ala Gly Asn Tyr Asn Gly Ala Leu Gln Val Met Thr Ala Glu Phe Gln
 355 360 365

 Val Pro Ser Pro Leu Val Pro Thr Arg Glu Asn Tyr Phe Val Arg Tyr
 370 375 380

 Cys Lys Gln His Ser Asp Gly Ser Trp Ala Val Val Asp Val Ser Leu
 385 390 395 400

 Asp Ser Leu Arg Pro Ser Thr Pro Ile Leu Arg Thr Arg Arg Arg Pro
 405 410 415

 Ser Gly Cys Leu Ile Gln Glu Leu Pro Asn Gly Tyr Ser Lys Val Thr
 420 425 430

 Trp Ile Glu His Met Glu Val Asp Asp Arg Ser Val His Asn Met Tyr
 435 440 445

 Lys Pro Leu Val Gln Ser Gly Leu Ala Phe Gly Ala Lys Arg Trp Val

450 455 460
 Ala Thr Leu Glu Arg Gln Cys Glu Arg Leu Ala Ser Ser Met Ala Ser
 465 470 475 480
 Asn Ile Pro Gly Asp Leu Ser Val Ile Thr Ser Pro Glu Gly Arg Lys
 485 490 495
 Ser Met Leu Lys Leu Ala Glu Arg Met Val Met Ser Phe Cys Ser Gly
 500 505 510
 Val Gly Ala Ser Thr Ala His Ala Trp Thr Thr Met Ser Thr Thr Gly
 515 520 525
 Ser Asp Asp Val Arg Val Met Thr Arg Lys Ser Met Asp Asp Pro Gly
 530 535 540
 Arg Pro Pro Gly Ile Val Leu Ser Ala Ala Thr Ser Phe Trp Ile Pro
 545 550 555 560
 Val Ala Pro Lys Arg Val Phe Asp Phe Leu Arg Asp Glu Asn Ser Arg
 565 570 575
 Lys Glu Trp Asp Ile Leu Ser Asn Gly Gly Met Val Gln Glu Met Ala
 580 585 590
 His Ile Ala Asn Gly His Glu Pro Gly Asn Cys Val Ser Leu Leu Arg
 595 600 605
 Val Asn Ser Gly Asn Ser Ser Gln Ser Asn Met Leu Ile Leu Gln Glu
 610 615 620
 Ser Cys Thr Asp Ala Ser Gly Ser Tyr Val Ile Tyr Ala Pro Val Asp
 625 630 635 640
 Ile Val Ala Met Asn Val Val Leu Ser Gly Gly Asp Pro Asp Tyr Val
 645 650 655
 Ala Leu Leu Pro Ser Gly Phe Ala Ile Leu Pro Asp Gly Ser Val Gly
 660 665 670
 Gly Gly Asp Gly Asn Gln His Gln Glu Met Val Ser Thr Thr Ser Ser
 675 680 685
 Gly Ser Cys Gly Gly Ser Leu Leu Thr Val Ala Phe Gln Ile Leu Val
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 114

Met Met Met Asp Glu Phe Met
 1 5

gat ctt aga cca gtg aag tac aca gag cac aag aot gtt atc aga aag
 162

Asp Leu Arg Pro Val Lys Tyr Thr Glu His Lys Thr Val Ile Arg Lys
 10 15 20

tac act aaa aag tcg tct atg gag agg aag acc agt gtt cgt gac tcg
 210

Tyr Thr Lys Lys Ser Ser Met Glu Arg Lys Thr Ser Val Arg Asp Ser
 25 30 35

gcc agg ttg gtt cgg gtc tca atg acg gat cgt gac gcc act gat tca
 258

Ala Arg Leu Val Arg Val Ser Met Thr Asp Arg Asp Ala Thr Asp Ser
 40 45 50 55

tca agc gac gag gaa gag ttt ctg ttc cct cga aga cgt gtc aag aga
 306

Ser Ser Asp Glu Glu Glu Phe Leu Phe Pro Arg Arg Arg Val Lys Arg
 60 65 70

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 354

Leu Ile Asn Glu Ile Arg Val Glu Pro Ser Ser Ser Ser Thr Gly Asp
 75 80 85

gtc tct gct tct ccg acg aag gac cgg aaa aga atc aac gtt gat tct
 402

Val Ser Ala Ser Pro Thr Lys Asp Arg Lys Arg Ile Asn Val Asp Ser
 90 95 100

acg gtt caa aag ccc tct gtt tcc ggc caa aac cag aag aag tac cgc
 450

Thr Val Gln Lys Pro Ser Val Ser Gly Gln Asn Gln Lys Lys Tyr Arg
 105 110 115

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 498
 Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
 120 125 130 135
 cct gag caa cgc cgg aga atc tgg ctc ggt act ttt gca acg gcg gag
 546
 Pro Glu Gln Arg Arg Arg Ile Trp Leu Gly Thr Phe Ala Thr Ala Glu
 140 145 150
 gaa gct gcc atc gtc tac gac aac gca gca atc aaa ctt cgt ggc cct
 594
 Glu Ala Ala Ile Val Tyr Asp Asn Ala Ala Ile Lys Leu Arg Gly Pro
 155 160 165
 gat gct ctt acc aac ttc acc gta caa cca gaa cca gaa ccg gta caa
 642
 Asp Ala Leu Thr Asn Phe Thr Val Gln Pro Glu Pro Glu Pro Val Gln
 170 175 180
 gaa caa gaa caa gaa ccg gag agc aac atg tcg gtt tcg ata tca gaa
 690
 Glu Gln Glu Gln Glu Pro Glu Ser Asn Met Ser Val Ser Ile Ser Glu
 185 190 195
 tca atg gac gat tct caa cat cta tca tct ccg aca tcg gtt ctc aac
 738
 Ser Met Asp Asp Ser Gln His Leu Ser Ser Pro Thr Ser Val Leu Asn
 200 205 210 215
 tac caa aca tat gtc tcg gag gaa cca atc gat agt ctt atc aaa ccg
 786
 Tyr Gln Thr Tyr Val Ser Glu Glu Pro Ile Asp Ser Leu Ile Lys Pro
 220 225 230
 gtt aaa caa gag ttt ctt gaa cca gaa caa gag cca ata agc tgg cat
 834
 Val Lys Gln Glu Phe Leu Glu Pro Glu Gln Glu Pro Ile Ser Trp His
 235 240 245
 ctt gga gaa ggt aat act aat act aat gat gat tca ttt cca ttg gac
 882
 Leu Gly Glu Gly Asn Thr Asn Thr Asn Asp Asp Ser Phe Pro Leu Asp
 250 255 260
 att aca ttt ctc gac aac tat ttc aat gaa tca tta cca gac atc tcc
 930
 Ile Thr Phe Leu Asp Asn Tyr Phe Asn Glu Ser Leu Pro Asp Ile Ser
 265 270 275
 atc ttc gat caa cct atg tct cct att caa cca aca gag aat gat ttc
 978
 Ile Phe Asp Gln Pro Met Ser Pro Ile Gln Pro Thr Glu Asn Asp Phe
 280 285 290 295
 ttc aac gac ctt atg tta ttc gat agc aac gca gaa gaa tac tac tcc
 1026
 Phe Asn Asp Leu Met Leu Phe Asp Ser Asn Ala Glu Glu Tyr Tyr Ser
 300 305 310

tcc gag atc aaa gag att ggt tca tcg ttc aac gat ctt gat gat tct
1074

Ser Glu Ile Lys Glu Ile Gly Ser Ser Phe Asn Asp Leu Asp Asp Ser
315 320 325

ttg ata tcc gat ctc tta ctt gtg tga ttttttgcc attaaccaaa
1121

Leu Ile Ser Asp Leu Leu Leu Val
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1136

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Lys Thr Ser Val Arg Asp Ser Ala Arg Leu Val Arg Val Ser Met Thr
35 40 45

Asp Arg Asp Ala Thr Asp Ser Ser Ser Asp Glu Glu Glu Phe Leu Phe
50 55 60

Pro Arg Arg Arg Val Lys Arg Leu Ile Asn Glu Ile Arg Val Glu Pro
65 70 75 80

Ser Ser Ser Ser Thr Gly Asp Val Ser Ala Ser Pro Thr Lys Asp Arg
85 90 95

Lys Arg Ile Asn Val Asp Ser Thr Val Gln Lys Pro Ser Val Ser Gly
100 105 110

Gln Asn Gln Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys
115 120 125

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Gly Thr Phe Ala Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn Ala
145 150 155 160

Ala Ile Lys Leu Arg Gly Pro Asp Ala Leu Thr Asn Phe Thr Val Gln
165 170 175

Pro Glu Pro Glu Pro Val Gln Glu Gln Glu Gln Glu Pro Glu Ser Asn
 180 185 190

Met Ser Val Ser Ile Ser Glu Ser Met Asp Asp Ser Gln His Leu Ser
 195 200 205

Ser Pro Thr Ser Val Leu Asn Tyr Gln Thr Tyr Val Ser Glu Glu Pro
 210 215 220

Ile Asp Ser Leu Ile Lys Pro Val Lys Gln Glu Phe Leu Glu Pro Glu
 225 230 235 240

Gln Glu Pro Ile Ser Trp His Leu Gly Glu Gly Asn Thr Asn Thr Asn
 245 250 255

Asp Asp Ser Phe Pro Leu Asp Ile Thr Phe Leu Asp Asn Tyr Phe Asn
 260 265 270

Glu Ser Leu Pro Asp Ile Ser Ile Phe Asp Gln Pro Met Ser Pro Ile
 275 280 285

Gln Pro Thr Glu Asn Asp Phe Phe Asn Asp Leu Met Leu Phe Asp Ser
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Arg Cys Lys Glu Arg Arg Asn Val Ile Lys Glu Ala Val Ser Ala Ser
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 206

Lys Ala Phe Ala Ala Gly His Phe Ala Tyr Ala Ile Ala Leu Lys Asn
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 50 55 60

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 302
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 398
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 100 105 110

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 115 120 125

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 686
 Pro Ala Asn Ser Met Ala Trp Asp Tyr Phe Phe Met Val Glu Asn Met
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 734
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 260 265 270

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 275 280 285

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 Lys Thr Ser Ala Ala Ala Ser Ser Ser Val Asn Leu Met Lys Ile Leu
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 Val Ser Lys Met Leu Glu Ala Thr Arg Leu His Tyr His Ser Asn Phe
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 Ala Asp Asn Arg Gly Tyr Val Asp His Ser Ala Arg Val Met Arg Val
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 Ile Thr Trp Asn Lys Ser Leu Arg Gly Ile Ser Asn Gly Glu Gly Gly
 385 390 395

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 Lys Asp Asp Gln Glu Ser Asp Glu His Glu Thr His Ala Thr Val Leu
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 Glu Lys Val Ser Ser Pro Pro Arg Pro Gln Arg Pro Pro Ile Gln Ala
 595 600 605
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 1934
 Leu Leu His Ser Trp His Asp Arg Leu Glu Lys Leu Pro Asp Glu Val
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gcc aaa tca gct atc tcc tct ttc gcg gca gtc atc aaa acc atc ttg
1982

Ala Lys Ser Ala Ile Ser Ser Phe Ala Ala Val Ile Lys Thr Ile Leu
625 630 635

ctg cac cag gaa gag gag atg aaa ctg aaa gag aaa tgc gaa gaa aca
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Leu His Gln Glu Glu Glu Met Lys Leu Lys Glu Lys Cys Glu Glu Thr
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2078

Arg Arg Glu Phe Ile Arg Lys Lys Gln Gly Phe Glu Asp Trp Tyr Gln
660 665 670

aaa cat ttg caa aag aga ggg cca aca gag gaa gct gaa ggc ggg gac
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Lys His Leu Gln Lys Arg Gly Pro Thr Glu Glu Ala Glu Gly Gly Asp
675 680 685

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2174

Asp Ala Thr Thr Ser Ser Arg Asp His Val Thr Glu Arg Arg Ile Ala
690 695 700

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2222

Val Glu Thr Leu Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala His Gln
705 710 715

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2270

Arg His Cys Val Gln Val Arg Glu Lys Ser Leu Asn Ser Leu Lys Ile
720 725 730 735

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2318

Arg Leu Pro Glu Ile Phe Arg Ala Leu Ser Asp Tyr Ala His Ala Cys
740 745 750

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2366

Ala Asp Ser Tyr Glu Lys Leu Arg Ile Ile Ser Gln Ser Gln Lys Ser
755 760 765

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Gly Ala Ala Leu Ser Asp Tyr Gly His Gly Glu Ser Asp Gln Lys Ala	50	55	60
Leu Asp Asp Val Leu Leu Asp Gln Gln His Tyr Glu Lys Gln Ser Arg	65	70	75
Asn Asn Val Asp Pro Ala Ser Pro Gln Pro Pro Pro Pro Pro Ile	85	90	95
Glu Asn Leu Pro Pro Pro Pro Pro Pro Leu Pro Lys Phe Ser Pro Ser	100	105	110
Pro Ile Lys Arg Ala Ile Ser Leu Pro Ser Met Ala Val Arg Gly Arg	115	120	125
Lys Val Gln Thr Leu Asp Gly Met Ala Ile Glu Glu Glu Glu Asp	130	135	140
Glu Glu Glu Glu Glu Glu Val Lys Gly Ser Gly Arg Asp Thr Ala Gln	145	150	155
Glu Glu Glu Glu Pro Arg Thr Pro Glu Asn Val Gly Lys Ser Asn Gly	165	170	175
Arg Lys Arg Leu Glu Lys Thr Thr Pro Glu Ile Val Ser Ala Ser Pro	180	185	190
Ala Asn Ser Met Ala Trp Asp Tyr Phe Phe Met Val Glu Asn Met Pro	195	200	205
Gly Pro Asn Leu Asp Asp Arg Glu Val Arg Asn Gly Tyr Glu Asn Gln	210	215	220
Ser Ser His Phe Gln Phe Asn Glu Glu Asp Asp Glu Glu Glu Glu Glu	225	230	235
Glu Glu Arg Ser Gly Ile Tyr Arg Lys Lys Ser Gly Ser Gly Lys Val	245	250	255

Val Glu Glu Met Glu Pro Lys Thr Pro Glu Lys Val Glu Glu Glu Glu
 260 265 270

Glu Glu Asp Glu Glu Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu
 275 280 285

Glu Val Val Val Glu Val Lys Lys Lys Lys Gly Lys Ala Lys Ile
 290 295 300

Glu His Ser Ser Thr Ala Pro Pro Glu Phe Arg Arg Ala Val Ala Lys
 305 310 315 320

Thr Ser Ala Ala Ala Ser Ser Ser Val Asn Leu Met Lys Ile Leu Asp
 325 330 335

Glu Ile Asp Asp Arg Phe Leu Lys Ala Ser Glu Cys Ala Gln Glu Val
 340 345 350

Ser Lys Met Leu Glu Ala Thr Arg Leu His Tyr His Ser Asn Phe Ala
 355 360 365

Asp Asn Arg Gly Tyr Val Asp His Ser Ala Arg Val Met Arg Val Ile
 370 375 380

Thr Trp Asn Lys Ser Leu Arg Gly Ile Ser Asn Gly Glu Gly Gly Lys
 385 390 395 400

Asp Asp Gln Glu Ser Asp Glu His Glu Thr His Ala Thr Val Leu Asp
 405 410 415

Lys Leu Leu Ala Trp Glu Lys Lys Leu Tyr Asp Glu Val Lys Gln Gly
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Glu Leu Met Lys Ile Glu Tyr Gln Lys Lys Val Ser Leu Leu Asn Arg
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His Lys Lys Arg Gly Ala Ser Ala Glu Thr Val Glu Lys Thr Lys Ala
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Ala Val Ser His Leu His Thr Arg Tyr Ile Val Asp Met Gln Ser Met
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 485 490 495

Pro Arg Leu Val Ala Leu Val Glu Gly Met Ala Lys Met Trp Thr Asn
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Met Cys Ile His His Asp Thr Gln Leu Gly Ile Val Gly Glu Leu Lys
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Ala Leu Glu Ile Ser Thr Ser Leu Lys Glu Thr Thr Lys Gln His His
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Phe Asp Thr Leu Val Thr His Gln Lys Gln Tyr Ile Asn Ser Leu Asn
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Asn Trp Leu Lys Leu Asn Leu Ile Pro Ile Glu Ser Ser Leu Lys Glu
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Lys Val Ser Ser Pro Pro Arg Pro Gln Arg Pro Pro Ile Gln Ala Leu
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Leu His Ser Trp His Asp Arg Leu Glu Lys Leu Pro Asp Glu Val Ala
 610 615 620

Lys Ser Ala Ile Ser Ser Phe Ala Ala Val Ile Lys Thr Ile Leu Leu
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His Gln Glu Glu Glu Met Lys Leu Lys Glu Lys Cys Glu Glu Thr Arg
 645 650 655

Arg Glu Phe Ile Arg Lys Lys Gln Gly Phe Glu Asp Trp Tyr Gln Lys
 660 665 670

His Leu Gln Lys Arg Gly Pro Thr Glu Glu Ala Glu Gly Gly Asp Asp
 675 680 685

Ala Thr Thr Ser Ser Arg Asp His Val Thr Glu Arg Arg Ile Ala Val
 690 695 700

Glu Thr Leu Lys Lys Arg Leu Glu Glu Glu Glu Glu Ala His Gln Arg
 705 710 715 720

His Cys Val Gln Val Arg Glu Lys Ser Leu Asn Ser Leu Lys Ile Arg
 725 730 735

Leu Pro Glu Ile Phe Arg Ala Leu Ser Asp Tyr Ala His Ala Cys Ala
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Val Asn Gln Phe Ser Gly Phe Gln Thr Gly Phe Thr Pro Trp Glu Trp
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gat tgc tct gat ctg ttt ttc gtg gac caa atg tct ctt gaa ccg gcc
 203

Asp Cys Ser Asp Leu Phe Phe Val Asp Gln Met Ser Leu Glu Pro Ala
 35 40 45

atc cct agt cct tgt tat ggt gaa tcc gac act ggt tcc gtc aaa att
 251

Ile Pro Ser Pro Cys Tyr Gly Glu Ser Asp Thr Gly Ser Val Lys Ile
 50 55 60

aat tcc ggt tct cat gac atg aaa acc ggt tct gac gaa tct tgt gcc
 299

Asn Ser Gly Ser His Asp Met Lys Thr Gly Ser Asp Glu Ser Cys Ala
 65 70 75

ggt ttc gtc aaa att aat cct cgt tgt gac gac gcc gac ata tca aac
 347

Gly Phe Val Lys Ile Asn Pro Arg Cys Asp Asp Ala Asp Ile Ser Asn
 80 85 90 95

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 395

Asp Leu Pro Cys Ser Gln Ala Asp Glu Pro Asp Ser Asp Asp Thr Lys
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 443

Gln Leu Thr Ala Ile Thr Asn Phe Gly Ser Gly Glu Asn Asn His Asn
 115 120 125

cgg aaa aaa atg atc caa ccg gag atg acc gac gag cgg aag agg aag
 491

Arg Lys Lys Met Ile Gln Pro Glu Met Thr Asp Glu Arg Lys Arg Lys
 130 135 140

agg atg gag tca aac cgg gaa tca gcg aaa cgg tca aga atg cgt aaa
 539

Arg Met Glu Ser Asn Arg Glu Ser Ala Lys Arg Ser Arg Met Arg Lys
 145 150 155

caa agt cac att gat aac tta cga gag caa gta aac cgg ttg gat tta
 587

Gln Ser His Ile Asp Asn Leu Arg Glu Gln Val Asn Arg Leu Asp Leu
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Glu Asn Arg Glu Leu Gly Asn Arg Leu Arg Leu Val Leu His Gln Leu
 180 185 190

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 683

Gln Arg Val Asn Ser Asp Asn Asn Arg Leu Val Thr Glu Gln Glu Ile
 195 200 205

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 210 215 220

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Thr Glu Gln Asn His Pro His Leu Gln
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Cys Ser Asp Leu Phe Phe Val Asp Gln Met Ser Leu Glu Pro Ala Ile
 35 40 45

Pro Ser Pro Cys Tyr Gly Glu Ser Asp Thr Gly Ser Val Lys Ile Asn
 50 55 60

Ser Gly Ser His Asp Met Lys Thr Gly Ser Asp Glu Ser Cys Ala Gly
 65 70 75 80

Phe Val Lys Ile Asn Pro Arg Cys Asp Asp Ala Asp Ile Ser Asn Asp
 85 90 95

Leu Pro Cys Ser Gln Ala Asp Glu Pro Asp Ser Asp Asp Thr Lys Gln
 100 105 110

Leu Thr Ala Ile Thr Asn Phe Gly Ser Gly Glu Asn Asn His Asn Arg
 115 120 125

Lys Lys Met Ile Gln Pro Glu Met Thr Asp Glu Arg Lys Arg Lys Arg
 130 135 140

Met Glu Ser Asn Arg Glu Ser Ala Lys Arg Ser Arg Met Arg Lys Gln
 145 150 155 160

Ser His Ile Asp Asn Leu Arg Glu Gln Val Asn Arg Leu Asp Leu Glu
 165 170 175

Asn Arg Glu Leu Gly Asn Arg Leu Arg Leu Val Leu His Gln Leu Gln
 180 185 190

Arg Val Asn Ser Asp Asn Asn Arg Leu Val Thr Glu Gln Glu Ile Leu
 195 200 205

Arg Leu Arg Leu Ser Glu Met Arg Arg Ile Leu Ile Ile Arg Gln Leu
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696
Gln Leu Lys Ser Phe Trp Ser Lys Gly Met Glu Gly Asp Leu Asn Val
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Asp Pro Asp Val Ser Met Ile Ala Ala Glu Ala Pro Asn Leu Leu Ser
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 130 135 140
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 144
 Pro Ser Tyr Ser Leu Pro Leu Pro Tyr Ser Pro Gln Met Arg Asn Tyr
 35 40 45

tgg att gcg cag atg gga aac gca act gat gtt aag cat cat gcg ttt
 192
 Trp Ile Ala Gln Met Gly Asn Ala Thr Asp Val Lys His His Ala Phe
 50 55 60

cca cta acc agg ata aag aaa atc atg aag tcc aac ccg gaa gtg aac
 240
 Pro Leu Thr Arg Ile Lys Lys Ile Met Lys Ser Asn Pro Glu Val Asn
 65 70 75 80

atg gtc act gca gag gct ccg gtc ctt ata tcg aag gcc tgt gag atg
 288
 Met Val Thr Ala Glu Ala Pro Val Leu Ile Ser Lys Ala Cys Glu Met
 85 90 95

ctc att ctt gat ctc aca atg cga tcg tgg ctt cat acc gtg gag ggc
 336
 Leu Ile Leu Asp Leu Thr Met Arg Ser Trp Leu His Thr Val Glu Gly
 100 105 110

ggt cgc caa act ctc aag aga tcc gat acg ctc acg aga tcc gat atc
 384
 Gly Arg Gln Thr Leu Lys Arg Ser Asp Thr Leu Thr Arg Ser Asp Ile
 115 120 125

tcc gcc gca acg act cgt agt ttc aaa ttt acc ttc ctt ggc gac gtt
 432
 Ser Ala Ala Thr Thr Arg Ser Phe Lys Phe Thr Phe Leu Gly Asp Val
 130 135 140

gtc cca aga gac cct tcc gtc gtt acc gat gat ccc gtg cta cat ccg
 480
 Val Pro Arg Asp Pro Ser Val Val Thr Asp Asp Pro Val Leu His Pro
 145 150 155 160

gac ggt gaa gta ctt cct ccg gga acg gtg ata gga tat ccg gtg ttt
 528
 Asp Gly Glu Val Leu Pro Pro Gly Thr Val Ile Gly Tyr Pro Val Phe
 165 170 175

gat tgt aat ggt gtg tac gcg tca ccg cca cag atg cag gag tgg ccg
 576
 Asp Cys Asn Gly Val Tyr Ala Ser Pro Pro Gln Met Gln Glu Trp Pro
 180 185 190

gcg gtg cct ggt gac gga gag gag gca gct ggg gaa att gga gga agc
 624
 Ala Val Pro Gly Asp Gly Glu Glu Ala Ala Gly Glu Ile Gly Gly Ser
 195 200 205

agc ggc ggt aat tga
 639
 Ser Gly Gly Asn
 210

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Met Glu Glu Asn Asn Gly Asn Asn Asn His Tyr Leu Pro Gln Pro Ser
1 5 10 15

Ser Ser Gln Leu Pro Pro Pro Pro Leu Tyr Tyr Gln Ser Met Pro Leu
20 25 30

Pro Ser Tyr Ser Leu Pro Leu Pro Tyr Ser Pro Gln Met Arg Asn Tyr
35 40 45

Trp Ile Ala Gln Met Gly Asn Ala Thr Asp Val Lys His His Ala Phe
50 55 60

Pro Leu Thr Arg Ile Lys Lys Ile Met Lys Ser Asn Pro Glu Val Asn
65 70 75 80

Met Val Thr Ala Glu Ala Pro Val Leu Ile Ser Lys Ala Cys Glu Met
85 90 95

Leu Ile Leu Asp Leu Thr Met Arg Ser Trp Leu His Thr Val Glu Gly
100 105 110

Gly Arg Gln Thr Leu Lys Arg Ser Asp Thr Leu Thr Arg Ser Asp Ile
115 120 125

Ser Ala Ala Thr Thr Arg Ser Phe Lys Phe Thr Phe Leu Gly Asp Val
130 135 140

Val Pro Arg Asp Pro Ser Val Val Thr Asp Asp Pro Val Leu His Pro
145 150 155 160

Asp Gly Glu Val Leu Pro Pro Gly Thr Val Ile Gly Tyr Pro Val Phe
165 170 175

Asp Cys Asn Gly Val Tyr Ala Ser Pro Pro Gln Met Gln Glu Trp Pro
180 185 190

Ala Val Pro Gly Asp Gly Glu Glu Ala Ala Gly Glu Ile Gly Gly Ser
195 200 205

Ser Gly Gly Asn
210

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 1 5 10 15
 aat ctt aac aac gag tca aaa gaa aca tct gag aac agt gat gac caa
 96
 Asn Leu Asn Asn Glu Ser Lys Glu Thr Ser Glu Asn Ser Asp Asp Gln
 20 25 30
 cac agc gag atc aca aca att aca tcg gaa gaa gag aaa aca act gaa
 144
 His Ser Glu Ile Thr Thr Ile Thr Ser Glu Glu Glu Lys Thr Thr Glu
 35 40 45
 ctg aag aaa cca gac aag att ctt cca tgt ccg aga tgc aac agc gca
 192
 Leu Lys Lys Pro Asp Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Ala
 50 55 60
 gac acc aaa ttc tgt tac tac aac aac tac aac gtt aac cag cca cgt
 240
 Asp Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg
 65 70 75 80
 cac ttc tgt aga aaa tgc cag agg tat tgg acc gct ggt gga tcc atg
 288
 His Phe Cys Arg Lys Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met
 85 90 95
 agg atc gtc ccg gtt ggc tca ggc cgt cgc aag aac aag gga tgg gtt
 336
 Arg Ile Val Pro Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Val
 100 105 110
 tct tca gac cag tac ctg cac atc act tcc gag gat act gac aat tac
 384
 Ser Ser Asp Gln Tyr Leu His Ile Thr Ser Glu Asp Thr Asp Asn Tyr
 115 120 125
 aat agc tcc tca aca aag att cta agc ttc gag tct tcg gac tct ttg
 432
 Asn Ser Ser Ser Thr Lys Ile Leu Ser Phe Glu Ser Ser Asp Ser Leu
 130 135 140
 gta act gag agg cct aag cat caa tca aac gaa gtg aag ata aac gct
 480
 Val Thr Glu Arg Pro Lys His Gln Ser Asn Glu Val Lys Ile Asn Ala
 145 150 155 160
 gaa cct gtt tca caa gaa ccc aac aac ttc caa ggg tta ctt cct ccc
 528
 Glu Pro Val Ser Gln Glu Pro Asn Asn Phe Gln Gly Leu Leu Pro Pro
 165 170 175
 caa gca tcc cct gtt tcg cct cct tgg cct tac caa tac cct cca aac
 576
 Gln Ala Ser Pro Val Ser Pro Pro Trp Pro Tyr Gln Tyr Pro Pro Asn
 180 185 190

cct agt ttc tac cac atg ccc gtc tac tgg ggc tgc gcg ata ccg gtt
624

Pro Ser Phe Tyr His Met Pro Val Tyr Trp Gly Cys Ala Ile Pro Val
195 200 205

tgg tct acc ctc gac act tct aca tgt ctt ggg aaa agg aca aga gac
672

Trp Ser Thr Leu Asp Thr Ser Thr Cys Leu Gly Lys Arg Thr Arg Asp
210 215 220

gaa act tct cat gaa act gtt aaa gag agt aaa aat gct ttt gag aga
720

Glu Thr Ser His Glu Thr Val Lys Glu Ser Lys Asn Ala Phe Glu Arg
225 230 235 240

aca agc ttg ctt ttg gaa tct cag agc atc aaa aat gaa aca agt atg
768

Thr Ser Leu Leu Leu Glu Ser Gln Ser Ile Lys Asn Glu Thr Ser Met
245 250 255

gct aca aat aac cat gtg tgg tat cca gta ccg atg acc cgc gag aag
816

Ala Thr Asn Asn His Val Trp Tyr Pro Val Pro Met Thr Arg Glu Lys
260 265 270

aca caa gaa ttc agc ttt ttc agt aat gga gct gaa aca aag agc agc
864

Thr Gln Glu Phe Ser Phe Phe Ser Asn Gly Ala Glu Thr Lys Ser Ser
275 280 285

aac aac aga ttc gtc cct gaa acg tat ctt aac ctg caa gca aac cct
912

Asn Asn Arg Phe Val Pro Glu Thr Tyr Leu Asn Leu Gln Ala Asn Pro
290 295 300

gca gcc atg gca aga tct atg aac ttc aga gag agc ata taa
954

Ala Ala Met Ala Arg Ser Met Asn Phe Arg Glu Ser Ile
305 310 315

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406

Met Asn Asn Gln Ser Val Thr Asp Asn Thr Ser Leu Lys Leu Ser Ser
1 5 10 15

Asn Leu Asn Asn Glu Ser Lys Glu Thr Ser Glu Asn Ser Asp Asp Gln
20 25 30

His Ser Glu Ile Thr Thr Ile Thr Ser Glu Glu Glu Lys Thr Thr Glu
35 40 45

Leu Lys Lys Pro Asp Lys Ile Leu Pro Cys Pro Arg Cys Asn Ser Ala
50 55 60

Asp Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Val Asn Gln Pro Arg
65 70 75 80

His Phe Cys Arg Lys Cys Gln Arg Tyr Trp Thr Ala Gly Gly Ser Met
85 90 95

Arg Ile Val Pro Val Gly Ser Gly Arg Arg Lys Asn Lys Gly Trp Val
100 105 110

Ser Ser Asp Gln Tyr Leu His Ile Thr Ser Glu Asp Thr Asp Asn Tyr
115 120 125

Asn Ser Ser Ser Thr Lys Ile Leu Ser Phe Glu Ser Ser Asp Ser Leu
130 135 140

Val Thr Glu Arg Pro Lys His Gln Ser Asn Glu Val Lys Ile Asn Ala
145 150 155 160

Glu Pro Val Ser Gln Glu Pro Asn Asn Phe Gln Gly Leu Leu Pro Pro
165 170 175

Gln Ala Ser Pro Val Ser Pro Pro Trp Pro Tyr Gln Tyr Pro Pro Asn
180 185 190

Pro Ser Phe Tyr His Met Pro Val Tyr Trp Gly Cys Ala Ile Pro Val
195 200 205

Trp Ser Thr Leu Asp Thr Ser Thr Cys Leu Gly Lys Arg Thr Arg Asp
210 215 220

Glu Thr Ser His Glu Thr Val Lys Glu Ser Lys Asn Ala Phe Glu Arg
225 230 235 240

Thr Ser Leu Leu Leu Glu Ser Gln Ser Ile Lys Asn Glu Thr Ser Met
245 250 255

Ala Thr Asn Asn His Val Trp Tyr Pro Val Pro Met Thr Arg Glu Lys
260 265 270

Thr Gln Glu Phe Ser Phe Phe Ser Asn Gly Ala Glu Thr Lys Ser Ser
275 280 285

Asn Asn Arg Phe Val Pro Glu Thr Tyr Leu Asn Leu Gln Ala Asn Pro
290 295 300

Ala Ala Met Ala Arg Ser Met Asn Phe Arg Glu Ser Ile

305

310

315

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 49

Met Glu Gly Val Asp Asn Thr Asn Pro Met Leu Thr Leu Glu Glu
 1 5 10 15

ggc gaa aac aac aat cct ttt tct tcc tta gat gac aaa aca tta atg
 97

Gly Glu Asn Asn Asn Pro Phe Ser Ser Leu Asp Asp Lys Thr Leu Met
 20 25 30

atg atg gct cct tcg tta atc ttt tcg ggc gat gta ggt cca tct tct
 145

Met Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser Ser
 35 40 45

tct tct tgt act cca gca ggt tat cat cta tct gct cag ctg gag aac
 193

Ser Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu Asn
 50 55 60

ttt cga gga ggt gga gga gag atg gga gga tta gtg agt aat aat agc
 241

Phe Arg Gly Gly Gly Gly Glu Met Gly Gly Leu Val Ser Asn Asn Ser
 65 70 75

aat aat agt gat cat aat aag aat tgc aac aaa gga aaa ggg aag aga
 289

Asn Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys Arg
 80 85 90 95

act ttg gca atg cag agg ata gct ttt cat aca agg agt gat gat gat
 337

Thr Leu Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp
 100 105 110

gtt ctt gat gat ggt tat cgt tgg cga aag tac ggt cag aaa tct gtc
 385

Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val
 115 120 125

aag aac aat gct cat ccc agg agc tat tat aga tgt aca tac cac aca
 433

Lys Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr
 130 135 140

tgc aac gtg aag aaa caa gtg caa aga ctg gca aaa gat cca aac gtt
 481

Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val
 145 150 155

gtc gta aca acc tac gaa ggt gtt cat aat cat cct tgt gag aag ctc
 529

Val Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu
 160 165 170 175

atg gag act ctt agc cct ctc ctt agg caa ctt cag ttc ctc tca aga
577

Met Glu Thr Leu Ser Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Arg
180 185 190

gtt tct gat ctg taa ttattgaatg ttaattagtgtgtgtaataca ttaattatgc
632

Val Ser Asp Leu
195

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658

<210> 408 <211> 195 <212> PRT <213> Arabidopsis thaliana <400>
408

Met Glu Gly Val Asp Asn Thr Asn Pro Met Leu Thr Leu Glu Glu Gly
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Glu Asn Asn Asn Pro Phe Ser Ser Leu Asp Asp Lys Thr Leu Met Met
20 25 30

Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser Ser Ser
35 40 45

Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu Asn Phe
50 55 60

Arg Gly Gly Gly Gly Glu Met Gly Gly Leu Val Ser Asn Asn Ser Asn
65 70 75 80

Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys Arg Thr
85 90 95

Leu Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp Val
100 105 110

Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys
115 120 125

Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr Cys
130 135 140

Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val Val
145 150 155 160

Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu Met
165 170 175

Glu Thr Leu Ser Pro Leu Leu Arg Gln Leu Gln Phe Leu Ser Arg Val
 180 185 190

Ser Asp Leu
 195

<210> 409 <211> 1172 <212> DNA <213> Arabidopsis thaliana <220>
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 60

aaaagaaaac actaaacca gatcgaaaac c atg tct att aac aac aac aac
 112

Met Ser Ile Asn Asn Asn Asn
 1 5

aac aac aac aac aat aac aac gat ggt ctt atg atc tca tca aac gga
 160

Asn Asn Asn Asn Asn Asn Asn Asp Gly Leu Met Ile Ser Ser Asn Gly
 10 15 20

gct tta atc gaa caa caa cca tca gtc gtt gtg aag aaa cca ccg gcg
 208

Ala Leu Ile Glu Gln Gln Pro Ser Val Val Val Lys Lys Pro Pro Ala
 25 30 35

aaa gat cga cat agc aaa gtc gat gga aga ggg aga aga atc cgt atg
 256

Lys Asp Arg His Ser Lys Val Asp Gly Arg Gly Arg Arg Ile Arg Met
 40 45 50 55

ccg att ata tgt gct gct cgt gtt ttt cag cta acg aga gag ctt ggt
 304

Pro Ile Ile Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu Leu Gly
 60 65 70

cat aag tca gat ggc caa aca att gaa tgg tta ctt cgt caa gca gag
 352

His Lys Ser Asp Gly Gln Thr Ile Glu Trp Leu Leu Arg Gln Ala Glu
 75 80 85

cct tct att ata gct gca aca gga act ggt aca act cca gcg agt ttc
 400

Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Thr Pro Ala Ser Phe
 90 95 100

tca act gct tct gtc tct atc cgt gga gcc acc aat tct act tct tta
 448

Ser Thr Ala Ser Val Ser Ile Arg Gly Ala Thr Asn Ser Thr Ser Leu
 105 110 115

gat cat aaa ccc act tct tta ctt ggt ggt acg tca ccg ttt ata ctt
 496

Asp His Lys Pro Thr Ser Leu Leu Gly Gly Thr Ser Pro Phe Ile Leu
 120 125 130 135

ggg aaa cgt gtt aga gct gat gag gat agt aat aat agt cat aat cat
544

Gly Lys Arg Val Arg Ala Asp Glu Asp Ser Asn Asn Ser His Asn His
140 145 150

agt tct gtt ggt aaa gat gag acc ttt acg aca aca cca gct ggg ttt
592

Ser Ser Val Gly Lys Asp Glu Thr Phe Thr Thr Thr Pro Ala Gly Phe
155 160 165

tgg gct gtt ccg gcg agg ccg gat ttt gga caa gtt tgg agt ttt gct
640

Trp Ala Val Pro Ala Arg Pro Asp Phe Gly Gln Val Trp Ser Phe Ala
170 175 180

gga gct cca caa gag atg ttt tta caa caa caa cat cat cat cag caa
688

Gly Ala Pro Gln Glu Met Phe Leu Gln Gln Gln His His His Gln Gln
185 190 195

cca ttg ttt gtt cat cag caa cag caa caa caa gct gca atg ggt gaa
736

Pro Leu Phe Val His Gln Gln Gln Gln Gln Gln Ala Ala Met Gly Glu
200 205 210 215

gct tct gct gct aga gtt ggg aat tat ctt ccg ggt cat ctt aat ttg
784

Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His Leu Asn Leu
220 225 230

ctt gct tct tta tcc ggt gga tct ccc ggg tcg gat cga aga gag gaa
832

Leu Ala Ser Leu Ser Gly Gly Ser Pro Gly Ser Asp Arg Arg Glu Glu
235 240 245

gat cca cgt taa tgggttaagc ccttttaggt ttgagggcaa aatttggtat
884

Asp Pro Arg
250

atatatttat tatcttctct tctctattgt tgcattggt tctctatgtg tgtgttttag
944

tggtgtaga gattgattg gtttcagaat ctctgcaagt gatttgagag ttttcgtag
1004

ctttaagtaa gttaaagacg gttgtttttg attagggtta aattagggtt taagaatctg
1064

ttgttttttt ggaggagat cgatttctta tcggatccaa gattactttt aggaaaaaag
1124

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1172

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Leu Met Ile Ser Ser Asn Gly Ala Leu Ile Glu Gln Gln Pro Ser Val
 20 25 30

Val Val Lys Lys Pro Pro Ala Lys Asp Arg His Ser Lys Val Asp Gly
 35 40 45

Arg Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe
 50 55 60

Gln Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu
 65 70 75 80

Trp Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr
 85 90 95

Gly Thr Thr Pro Ala Ser Phe Ser Thr Ala Ser Val Ser Ile Arg Gly
 100 105 110

Ala Thr Asn Ser Thr Ser Leu Asp His Lys Pro Thr Ser Leu Leu Gly
 115 120 125

Gly Thr Ser Pro Phe Ile Leu Gly Lys Arg Val Arg Ala Asp Glu Asp
 130 135 140

Ser Asn Asn Ser His Asn His Ser Ser Val Gly Lys Asp Glu Thr Phe
 145 150 155 160

Thr Thr Thr Pro Ala Gly Phe Trp Ala Val Pro Ala Arg Pro Asp Phe
 165 170 175

Gly Gln Val Trp Ser Phe Ala Gly Ala Pro Gln Glu Met Phe Leu Gln
 180 185 190

Gln Gln His His His Gln Gln Pro Leu Phe Val His Gln Gln Gln Gln
 195 200 205

Gln Gln Ala Ala Met Gly Glu Ala Ser Ala Ala Arg Val Gly Asn Tyr
 210 215 220

Leu Pro Gly His Leu Asn Leu Leu Ala Ser Leu Ser Gly Gly Ser Pro
 225 230 235 240

Gly Ser Asp Arg Arg Glu Glu Asp Pro Arg
 245 250

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 1 5 10 15
 agc tgt ctg atg ttg tta tca gga att gga gaa cac gac gga aga aag
 96
 Ser Cys Leu Met Leu Leu Ser Gly Ile Gly Glu His Asp Gly Arg Lys
 20 25 30
 aaa cgt gtt ttc cga tgc aag act tgt gag aga gac ttc gat tcg ttc
 144
 Lys Arg Val Phe Arg Cys Lys Thr Cys Glu Arg Asp Phe Asp Ser Phe
 35 40 45
 caa gct tta gga ggc cac cgt gca agc cac tcg aaa cta acc aac agt
 192
 Gln Ala Leu Gly Gly His Arg Ala Ser His Ser Lys Leu Thr Asn Ser
 50 55 60
 gac gat aaa tca ctt cct gga tca cca aag aag aag cct aaa act acg
 240
 Asp Asp Lys Ser Leu Pro Gly Ser Pro Lys Lys Lys Pro Lys Thr Thr
 65 70 75 80
 act acg acg acg gct cat act tgt ccg att tgt ggc ttg gag ttt ccg
 288
 Thr Thr Thr Thr Ala His Thr Cys Pro Ile Cys Gly Leu Glu Phe Pro
 85 90 95
 atg gga caa gct ctt ggt ggt cac atg agg aaa cat agg aac gag aaa
 336
 Met Gly Gln Ala Leu Gly Gly His Met Arg Lys His Arg Asn Glu Lys
 100 105 110
 gaa cga gaa aag gct tct aac gta ttg gtt acg cat tct ttc atg ccg
 384
 Glu Arg Glu Lys Ala Ser Asn Val Leu Val Thr His Ser Phe Met Pro
 115 120 125
 gag acg aca acg gtg acg act ttg aag aaa tcg agt agt ggg aag aga
 432
 Glu Thr Thr Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg
 130 135 140
 gtg gcg tgt ttg gat ttc gac tta act tcg gtg gag agc ttt gtc aac
 480
 Val Ala Cys Leu Asp Phe Asp Leu Thr Ser Val Glu Ser Phe Val Asn
 145 150 155 160
 acg gaa ttg gag ttg gga aga acg atg tac tga
 513
 Thr Glu Leu Glu Leu Gly Arg Thr Met Tyr
 165 170

<210> 412 <211> 170 <212> PRT <213> Arabidopsis thaliana <400>
412

Met Val Ala Glu Ser Asp Asn Arg Asp Leu Thr Val Asp Thr Ala Ala
1 5 10 15

Ser Cys Leu Met Leu Leu Ser Gly Ile Gly Glu His Asp Gly Arg Lys
20 25 30

Lys Arg Val Phe Arg Cys Lys Thr Cys Glu Arg Asp Phe Asp Ser Phe
35 40 45

Gln Ala Leu Gly Gly His Arg Ala Ser His Ser Lys Leu Thr Asn Ser
50 55 60

Asp Asp Lys Ser Leu Pro Gly Ser Pro Lys Lys Lys Pro Lys Thr Thr
65 70 75 80

Thr Thr Thr Thr Ala His Thr Cys Pro Ile Cys Gly Leu Glu Phe Pro
85 90 95

Met Gly Gln Ala Leu Gly Gly His Met Arg Lys His Arg Asn Glu Lys
100 105 110

Glu Arg Glu Lys Ala Ser Asn Val Leu Val Thr His Ser Phe Met Pro
115 120 125

Glu Thr Thr Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg
130 135 140

Val Ala Cys Leu Asp Phe Asp Leu Thr Ser Val Glu Ser Phe Val Asn
145 150 155 160

Thr Glu Leu Glu Leu Gly Arg Thr Met Tyr
165 170

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56

Met Glu Asp His Gln
1 5

aac cat cca cag tac ggt ata gaa caa cca tct tct caa ttc tcc tct
104

Asn His Pro Gln Tyr Gly Ile Glu Gln Pro Ser Ser Gln Phe Ser Ser
10 15 20

gat ctc ttc ggc ttc aac ctc gtt tca gcg ccg gac cag cac cat cgt
 152
 Asp Leu Phe Gly Phe Asn Leu Val Ser Ala Pro Asp Gln His His Arg
 25 30 35
 ctt cat ttc acc gac cat gag ata agt tta ttg cca cgt gga ata caa
 200
 Leu His Phe Thr Asp His Glu Ile Ser Leu Leu Pro Arg Gly Ile Gln
 40 45 50
 ggg ctt acg gtg gct gga aac aac agt aac act att aca acg atc cag
 248
 Gly Leu Thr Val Ala Gly Asn Asn Ser Asn Thr Ile Thr Thr Ile Gln
 55 60 65
 agt ggt ggc tgt gtt ggt ggg ttt agt ggc ttt acg gac ggc gga gga
 296
 Ser Gly Gly Cys Val Gly Gly Phe Ser Gly Phe Thr Asp Gly Gly Gly
 70 75 80 85
 aca ggg agg tgg ccg agg caa gag acg ttg atg ttg ttg gag gtc aga
 344
 Thr Gly Arg Trp Pro Arg Gln Glu Thr Leu Met Leu Leu Glu Val Arg
 90 95 100
 tct cgt ctt gat cac aag ttc aaa gaa gct aat caa aag ggt cct ctc
 392
 Ser Arg Leu Asp His Lys Phe Lys Glu Ala Asn Gln Lys Gly Pro Leu
 105 110 115
 tgg gat gaa gtt tct agg att atg tcg gag gaa cat gga tac act agg
 440
 Trp Asp Glu Val Ser Arg Ile Met Ser Glu Glu His Gly Tyr Thr Arg
 120 125 130
 agt ggc aag aag tgt aga gag aag ttc gag aat ctc tac aag tac tat
 488
 Ser Gly Lys Lys Cys Arg Glu Lys Phe Glu Asn Leu Tyr Lys Tyr Tyr
 135 140 145
 aaa aaa aca aaa gaa ggc aaa tcc ggt cgg cga caa gat ggt aaa aac
 536
 Lys Lys Thr Lys Glu Gly Lys Ser Gly Arg Arg Gln Asp Gly Lys Asn
 150 155 160 165
 tat aga ttt ttc cgg cag ctt gaa gcg ata tac ggc gaa tcc aaa gac
 584
 Tyr Arg Phe Phe Arg Gln Leu Glu Ala Ile Tyr Gly Glu Ser Lys Asp
 170 175 180
 tcg gtt tct tgc tat aac aac acg cag ttc ata atg acc aat gct ctt
 632
 Ser Val Ser Cys Tyr Asn Asn Thr Gln Phe Ile Met Thr Asn Ala Leu
 185 190 195
 cat agt aat ttc cgc gct tct aac att cat aac atc gtc cct cat cat
 680
 His Ser Asn Phe Arg Ala Ser Asn Ile His Asn Ile Val Pro His His
 200 205 210

cag aat ccc ttg atg acc aat acc aat act caa agt caa agc ctt agc
 728
 Gln Asn Pro Leu Met Thr Asn Thr Asn Thr Gln Ser Gln Ser Leu Ser
 215 220 225
 att tct aac aat ttc aac tcc tcc tcc gat ttg gat cta act tct tcc
 776
 Ile Ser Asn Asn Phe Asn Ser Ser Ser Asp Leu Asp Leu Thr Ser Ser
 230 235 240 245
 tct gaa gga aac gaa act act aaa aga gag ggg atg cat tgg aag gaa
 824
 Ser Glu Gly Asn Glu Thr Thr Lys Arg Glu Gly Met His Trp Lys Glu
 250 255 260
 aag atc aag gaa ttc att ggt gtt cat atg gag agg ttg ata gag aag
 872
 Lys Ile Lys Glu Phe Ile Gly Val His Met Glu Arg Leu Ile Glu Lys
 265 270 275
 caa gat ttt tgg ctt gag aag ttg atg aag att gtg gaa gac aaa gaa
 920
 Gln Asp Phe Trp Leu Glu Lys Leu Met Lys Ile Val Glu Asp Lys Glu
 280 285 290
 cat caa agg atg ctg aga gaa gag gaa tgg aga agg att gaa gcg gaa
 968
 His Gln Arg Met Leu Arg Glu Glu Glu Trp Arg Arg Ile Glu Ala Glu
 295 300 305
 agg atc gat aag gaa cgt tct ttt tgg aca aaa gag agg gag agg att
 1016
 Arg Ile Asp Lys Glu Arg Ser Phe Trp Thr Lys Glu Arg Glu Arg Ile
 310 315 320 325
 gaa gct cgg gat gtt gcg gtg att aat gcc ttg cag tac ttg acg gga
 1064
 Glu Ala Arg Asp Val Ala Val Ile Asn Ala Leu Gln Tyr Leu Thr Gly
 330 335 340
 agg gca ttg ata agg ccg gat tct tct tct cct aca gag agg att aat
 1112
 Arg Ala Leu Ile Arg Pro Asp Ser Ser Ser Pro Thr Glu Arg Ile Asn
 345 350 355
 ggg aat gga agc gat aaa atg atg gct gat aat gaa ttt gct gat gaa
 1160
 Gly Asn Gly Ser Asp Lys Met Met Ala Asp Asn Glu Phe Ala Asp Glu
 360 365 370
 gga aat aag ggc aag atg gat aaa aaa caa atg aat aag aaa agg aag
 1208
 Gly Asn Lys Gly Lys Met Asp Lys Lys Gln Met Asn Lys Lys Arg Lys
 375 380 385
 gag aaa tgg tca agc cac gga ggg aat cat cca aga acc aaa gag aat
 1256
 Glu Lys Trp Ser Ser His Gly Gly Asn His Pro Arg Thr Lys Glu Asn
 390 395 400 405

atg atg ata tac aac aat caa gaa act aag att aat gat ttt tgt cga
1304

Met Met Ile Tyr Asn Asn Gln Glu Thr Lys Ile Asn Asp Phe Cys Arg
410 415 420

gat gat gac caa tgc cat cat gaa ggt tac tca cct tca aac tcc aag
1352

Asp Asp Asp Gln Cys His His Glu Gly Tyr Ser Pro Ser Asn Ser Lys
425 430 435

aac gca gga act ccg agc tgc agc aat gcc atg gca gct agt aca aag
1400

Asn Ala Gly Thr Pro Ser Cys Ser Asn Ala Met Ala Ala Ser Thr Lys
440 445 450

tgc ttt cca ttg ctt gaa gga gaa gga gat cag aac ttg tgg gag ggt
1448

Cys Phe Pro Leu Leu Glu Gly Glu Gly Asp Gln Asn Leu Trp Glu Gly
455 460 465

tat ggt ttg aag caa agg aaa gaa aat aat cat cag taa gctacatttt
1497

Tyr Gly Leu Lys Gln Arg Lys Glu Asn Asn His Gln
470 475 480

tcattctcaa aatgaagaat aagagaactt agaaacgat
1536

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414

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Ser Gln Phe Ser Ser Asp Leu Phe Gly Phe Asn Leu Val Ser Ala Pro
20 25 30

Asp Gln His His Arg Leu His Phe Thr Asp His Glu Ile Ser Leu Leu
35 40 45

Pro Arg Gly Ile Gln Gly Leu Thr Val Ala Gly Asn Asn Ser Asn Thr
50 55 60

Ile Thr Thr Ile Gln Ser Gly Gly Cys Val Gly Gly Phe Ser Gly Phe
65 70 75 80

Thr Asp Gly Gly Gly Thr Gly Arg Trp Pro Arg Gln Glu Thr Leu Met
85 90 95

Leu Leu Glu Val Arg Ser Arg Leu Asp His Lys Phe Lys Glu Ala Asn
100 105 110

Gln Lys Gly Pro Leu Trp Asp Glu Val Ser Arg Ile Met Ser Glu Glu

115	120	125																	
His Gly Tyr Thr Arg Ser Gly Lys Lys Cys Arg Glu Lys Phe Glu Asn																			
130	135	140																	
Leu Tyr Lys Tyr Tyr Lys Lys Thr Lys Glu Gly Lys Ser Gly Arg Arg																			
145	150	155																	
Gln Asp Gly Lys Asn Tyr Arg Phe Phe Arg Gln Leu Glu Ala Ile Tyr																			
165	170	175																	
Gly Glu Ser Lys Asp Ser Val Ser Cys Tyr Asn Asn Thr Gln Phe Ile																			
180	185	190																	
Met Thr Asn Ala Leu His Ser Asn Phe Arg Ala Ser Asn Ile His Asn																			
195	200	205																	
Ile Val Pro His His Gln Asn Pro Leu Met Thr Asn Thr Asn Thr Gln																			
210	215	220																	
Ser Gln Ser Leu Ser Ile Ser Asn Asn Phe Asn Ser Ser Ser Asp Leu																			
225	230	235																	
Asp Leu Thr Ser Ser Ser Glu Gly Asn Glu Thr Thr Lys Arg Glu Gly																			
245	250	255																	
Met His Trp Lys Glu Lys Ile Lys Glu Phe Ile Gly Val His Met Glu																			
260	265	270																	
Arg Leu Ile Glu Lys Gln Asp Phe Trp Leu Glu Lys Leu Met Lys Ile																			
275	280	285																	
Val Glu Asp Lys Glu His Gln Arg Met Leu Arg Glu Glu Glu Trp Arg																			
290	295	300																	
Arg Ile Glu Ala Glu Arg Ile Asp Lys Glu Arg Ser Phe Trp Thr Lys																			
305	310	315																	
Glu Arg Glu Arg Ile Glu Ala Arg Asp Val Ala Val Ile Asn Ala Leu																			
325	330	335																	
Gln Tyr Leu Thr Gly Arg Ala Leu Ile Arg Pro Asp Ser Ser Ser Pro																			
340	345	350																	
Thr Glu Arg Ile Asn Gly Asn Gly Ser Asp Lys Met Met Ala Asp Asn																			
355	360	365																	

Glu Phe Ala Asp Glu Gly Asn Lys Gly Lys Met Asp Lys Lys Gln Met
 370 375 380

Asn Lys Lys Arg Lys Glu Lys Trp Ser Ser His Gly Gly Asn His Pro
 385 390 395 400

Arg Thr Lys Glu Asn Met Met Ile Tyr Asn Asn Gln Glu Thr Lys Ile
 405 410 415

Asn Asp Phe Cys Arg Asp Asp Asp Gln Cys His His Glu Gly Tyr Ser
 420 425 430

Pro Ser Asn Ser Lys Asn Ala Gly Thr Pro Ser Cys Ser Asn Ala Met
 435 440 445

Ala Ala Ser Thr Lys Cys Phe Pro Leu Leu Glu Gly Glu Gly Asp Gln
 450 455 460

Asn Leu Trp Glu Gly Tyr Gly Leu Lys Gln Arg Lys Glu Asn Asn His
 465 470 475 480

Gln

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 Met Gly Arg Val Lys Leu Lys Ile Lys Arg Leu Glu Ser Thr Ser Asn
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 agg caa gtt aca tac acg aag aga aaa aat ggg att ttg aag aaa gcc
 96
 Arg Gln Val Thr Tyr Thr Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala
 20 25 30
 aaa gag tta tcg att ttg tgt gat att gat att gtc ctt ctt atg ttt
 144
 Lys Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe
 35 40 45
 tcc cct acc gga aga gct act gct ttc cat gga gaa cac agg tat aat
 192
 Ser Pro Thr Gly Arg Ala Thr Ala Phe His Gly Glu His Arg Tyr Asn
 50 55 60
 tat caa aat cat tct tat gca ttg aag aaa act ttt aag aaa ctg gat
 240
 Tyr Gln Asn His Ser Tyr Ala Leu Lys Lys Thr Phe Lys Lys Leu Asp

65	70	75	80
cat gat gta aat ata cat gac ttt tta gga gca agg aat caa act att			
288			
His Asp Val Asn Ile His Asp Phe Leu Gly Ala Arg Asn Gln Thr Ile			
	85	90	95
gag gta tgg atc gac cat ctt cgg ttc atg aat ttt ctt gga tac ttt			
336			
Glu Val Trp Ile Asp His Leu Arg Phe Met Asn Phe Leu Gly Tyr Phe			
	100	105	110
tta atc tct ttg agt caa att gct aaa gtc tgt gtt aac att acc aca			
384			
Leu Ile Ser Leu Ser Gln Ile Ala Lys Val Cys Val Asn Ile Thr Thr			
	115	120	125
cga cag ggt cta agt aac caa gta gcc att tac caa gct cag cta atg			
432			
Arg Gln Gly Leu Ser Asn Gln Val Ala Ile Tyr Gln Ala Gln Leu Met			
	130	135	140
gag tgt cat agg agg ttg agt tgt tgg acg aac atc gat aga ata gaa			
480			
Glu Cys His Arg Arg Leu Ser Cys Trp Thr Asn Ile Asp Arg Ile Glu			
	145	150	155
aac act gag cac ctc gat tta ttg gaa gaa tca ttg agg aaa tcc att			
528			
Asn Thr Glu His Leu Asp Leu Leu Glu Glu Ser Leu Arg Lys Ser Ile			
	165	170	175
gaa aga atc cag att cac aag gaa cat tac aga aag aac caa ctc ttg			
576			
Glu Arg Ile Gln Ile His Lys Glu His Tyr Arg Lys Asn Gln Leu Leu			
	180	185	190
cca ata gaa tgt gca aca aca cag ttt cac agc ggg ata cag ttg cct			
624			
Pro Ile Glu Cys Ala Thr Thr Gln Phe His Ser Gly Ile Gln Leu Pro			
	195	200	205
atg gcg atg gga ggt aat agt agt atg caa gaa gct cac tcc atg tct			
672			
Met Ala Met Gly Gly Asn Ser Ser Met Gln Glu Ala His Ser Met Ser			
	210	215	220
tgg ctt cct gat aat gat cac cag caa aca atc tta cct ggt gat tcc			
720			
Trp Leu Pro Asp Asn Asp His Gln Gln Thr Ile Leu Pro Gly Asp Ser			
	225	230	235
agt ttt ctt ccc cat aga gag atg gat ggt tcg att ccc gtt tac tca			
768			
Ser Phe Leu Pro His Arg Glu Met Asp Gly Ser Ile Pro Val Tyr Ser			
	245	250	255
agc tgc ttc ttt gag tct acg aaa cca gaa gat cag ata tgc agc aac			
816			
Ser Cys Phe Phe Glu Ser Thr Lys Pro Glu Asp Gln Ile Cys Ser Asn			
	260	265	270

ccg gga caa cag ttt gag cag tta gaa caa caa gga aac ggt tgt ttg
 864
 Pro Gly Gln Gln Phe Glu Gln Leu Glu Gln Gln Gly Asn Gly Cys Leu
 275 280 285
 ggg tta caa caa ctt gga gag gaa tat tca tat cct aca ccg ttt ggt
 912
 Gly Leu Gln Gln Leu Gly Glu Glu Tyr Ser Tyr Pro Thr Pro Phe Gly
 290 295 300
 act act ttg gga atg gaa gaa gat caa gag aaa aag ata aaa tct gaa
 960
 Thr Thr Leu Gly Met Glu Glu Asp Gln Glu Lys Lys Ile Lys Ser Glu
 305 310 315 320
 atg gaa ttg aac aac ttg caa caa cag caa cag caa caa caa caa
 1008
 Met Glu Leu Asn Asn Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln
 325 330 335
 caa caa caa gat cct tca atg tat gat ccc atg gct aat aat aat ggt
 1056
 Gln Gln Gln Asp Pro Ser Met Tyr Asp Pro Met Ala Asn Asn Asn Gly
 340 345 350
 ggc tgc ttt cag att cct cat gat cag tcc atg ttt gtc aat gat cat
 1104
 Gly Cys Phe Gln Ile Pro His Asp Gln Ser Met Phe Val Asn Asp His
 355 360 365
 cat cat cat cat cac cac cat cat caa aat tgg gtt cca gat tca atg
 1152
 His His His His His His His His Gln Asn Trp Val Pro Asp Ser Met
 370 375 380
 ttt ggt cag act tct tac aac cag gtt tgt gtg ttc aca cct cca ttg
 1200
 Phe Gly Gln Thr Ser Tyr Asn Gln Val Cys Val Phe Thr Pro Pro Leu
 385 390 395 400
 gaa cta tct agg tag
 1215
 Glu Leu Ser Arg

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Arg Gln Val Thr Tyr Thr Lys Arg Lys Asn Gly Ile Leu Lys Lys Ala
 20 25 30

Lys Glu Leu Ser Ile Leu Cys Asp Ile Asp Ile Val Leu Leu Met Phe
 35 40 45

Ser Pro Thr Gly Arg Ala Thr Ala Phe His Gly Glu His Arg Tyr Asn
 50 55 60

Tyr Gln Asn His Ser Tyr Ala Leu Lys Lys Thr Phe Lys Lys Leu Asp
 65 70 75 80

His Asp Val Asn Ile His Asp Phe Leu Gly Ala Arg Asn Gln Thr Ile
 85 90 95

Glu Val Trp Ile Asp His Leu Arg Phe Met Asn Phe Leu Gly Tyr Phe
 100 105 110

Leu Ile Ser Leu Ser Gln Ile Ala Lys Val Cys Val Asn Ile Thr Thr
 115 120 125

Arg Gln Gly Leu Ser Asn Gln Val Ala Ile Tyr Gln Ala Gln Leu Met
 130 135 140

Glu Cys His Arg Arg Leu Ser Cys Trp Thr Asn Ile Asp Arg Ile Glu
 145 150 155 160

Asn Thr Glu His Leu Asp Leu Leu Glu Glu Ser Leu Arg Lys Ser Ile
 165 170 175

Glu Arg Ile Gln Ile His Lys Glu His Tyr Arg Lys Asn Gln Leu Leu
 180 185 190

Pro Ile Glu Cys Ala Thr Thr Gln Phe His Ser Gly Ile Gln Leu Pro
 195 200 205

Met Ala Met Gly Gly Asn Ser Ser Met Gln Glu Ala His Ser Met Ser
 210 215 220

Trp Leu Pro Asp Asn Asp His Gln Gln Thr Ile Leu Pro Gly Asp Ser
 225 230 235 240

Ser Phe Leu Pro His Arg Glu Met Asp Gly Ser Ile Pro Val Tyr Ser
 245 250 255

Ser Cys Phe Phe Glu Ser Thr Lys Pro Glu Asp Gln Ile Cys Ser Asn
 260 265 270

Pro Gly Gln Gln Phe Glu Gln Leu Glu Gln Gln Gly Asn Gly Cys Leu
 275 280 285

Gly Leu Gln Gln Leu Gly Glu Glu Tyr Ser Tyr Pro Thr Pro Phe Gly
 290 295 300
 Thr Thr Leu Gly Met Glu Glu Asp Gln Glu Lys Lys Ile Lys Ser Glu
 305 310 315 320
 Met Glu Leu Asn Asn Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln
 325 330 335
 Gln Gln Gln Asp Pro Ser Met Tyr Asp Pro Met Ala Asn Asn Asn Gly
 340 345 350
 Gly Cys Phe Gln Ile Pro His Asp Gln Ser Met Phe Val Asn Asp His
 355 360 365
 His His His His His His His His Gln Asn Trp Val Pro Asp Ser Met
 370 375 380
 Phe Gly Gln Thr Ser Tyr Asn Gln Val Cys Val Phe Thr Pro Pro Leu
 385 390 395 400
 Glu Leu Ser Arg

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 55 Met Glu Arg Arg Thr
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 aga cga gtg aag ttc aca gag aat cgt acg gtc aca aac gta gca gct
 103
 Arg Arg Val Lys Phe Thr Glu Asn Arg Thr Val Thr Asn Val Ala Ala
 10 15 20
 aca cca tct aac ggg tct ccg aga ctg gtc cgt atc act gtt act gat
 151
 Thr Pro Ser Asn Gly Ser Pro Arg Leu Val Arg Ile Thr Val Thr Asp
 25 30 35
 cct ttc gct act gac tcg tct agc gac gac gac gac aac aac aac gtc
 199
 Pro Phe Ala Thr Asp Ser Ser Ser Asp Asp Asp Asp Asn Asn Asn Val
 40 45 50
 acg gtg gtt cca aga gtg aaa cga tac gtg aag gag att aga ttc tgc
 247
 Thr Val Val Pro Arg Val Lys Arg Tyr Val Lys Glu Ile Arg Phe Cys
 55 60 65

caa ggt gaa tct tct tcc tcc acc gcg gcg agg aaa ggt aag cac aag
 295
 Gln Gly Glu Ser Ser Ser Ser Thr Ala Ala Arg Lys Gly Lys His Lys
 70 75 80 85
 gag gag gaa agc gta gtg gtt gaa gat gac gtg tcg acg tcg gtg aag
 343
 Glu Glu Glu Ser Val Val Val Glu Asp Asp Val Ser Thr Ser Val Lys
 90 95 100
 cct aaa aag tac aga ggc gtg aga cag aga cct tgg gga aaa ttc gcg
 391
 Pro Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Phe Ala
 105 110 115
 gcg gag att aga gat ccg tcg agc cgt act ccg att tgg ctt ggg act
 439
 Ala Glu Ile Arg Asp Pro Ser Ser Arg Thr Arg Ile Trp Leu Gly Thr
 120 125 130
 ttt gtc acg gcg gag gaa gct gct ata gcg tac gat aga gcc gcg att
 487
 Phe Val Thr Ala Glu Glu Ala Ala Ile Ala Tyr Asp Arg Ala Ala Ile
 135 140 145
 cat ctc aaa gga cct aaa gcg ctc acg aat ttc cta act ccg ccg acg
 535
 His Leu Lys Gly Pro Lys Ala Leu Thr Asn Phe Leu Thr Pro Pro Thr
 150 155 160 165
 cca acg ccg gtt atc gat ctc caa acg gtt tcc gcc tgc gat tac ggt
 583
 Pro Thr Pro Val Ile Asp Leu Gln Thr Val Ser Ala Cys Asp Tyr Gly
 170 175 180
 aga gat tct ccg cag agc ctt cat tca ccg acc tct gtt cta aga ttc
 631
 Arg Asp Ser Arg Gln Ser Leu His Ser Pro Thr Ser Val Leu Arg Phe
 185 190 195
 aac gtc aac gag gaa aca gag cat gag att gaa gcg atc gag cta tct
 679
 Asn Val Asn Glu Glu Thr Glu His Glu Ile Glu Ala Ile Glu Leu Ser
 200 205 210
 ccg gag aga aag tcg acg gtt ata aaa gaa gaa gaa gaa tcg tcg gcg
 727
 Pro Glu Arg Lys Ser Thr Val Ile Lys Glu Glu Glu Glu Ser Ser Ala
 215 220 225
 ggt ttg gtg ttc ccg gat ccg tat ctg tta ccg gat tta tct ctc gcc
 775
 Gly Leu Val Phe Pro Asp Pro Tyr Leu Leu Pro Asp Leu Ser Leu Ala
 230 235 240 245
 ggc gaa tgt ttt tgg gat acc gaa att gcc cct gac ctt ttg ttt ctc
 823
 Gly Glu Cys Phe Trp Asp Thr Glu Ile Ala Pro Asp Leu Leu Phe Leu
 250 255 260

gat gaa gaa acc aaa atc caa tca acg ttg tta cca aac aca gag gtt
871

Asp Glu Glu Thr Lys Ile Gln Ser Thr Leu Leu Pro Asn Thr Glu Val
265 270 275

tcg aaa caa gga gaa aac gaa act gaa gat ttc gag ttt ggt ttg att
919

Ser Lys Gln Gly Glu Asn Glu Thr Glu Asp Phe Glu Phe Gly Leu Ile
280 285 290

gat gat ttc gag tct tct cca tgg gat gtg gat cat ttc ttc gac cat
967

Asp Asp Phe Glu Ser Ser Pro Trp Asp Val Asp His Phe Phe Asp His
295 300 305

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1019

His His His Ser Phe Asp
310 315

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Thr Asn Val Ala Ala Thr Pro Ser Asn Gly Ser Pro Arg Leu Val Arg
20 25 30

Ile Thr Val Thr Asp Pro Phe Ala Thr Asp Ser Ser Ser Asp Asp Asp
35 40 45

Asp Asn Asn Asn Val Thr Val Val Pro Arg Val Lys Arg Tyr Val Lys
50 55 60

Glu Ile Arg Phe Cys Gln Gly Glu Ser Ser Ser Ser Thr Ala Ala Arg
65 70 75 80

Lys Gly Lys His Lys Glu Glu Glu Ser Val Val Val Glu Asp Asp Val
85 90 95

Ser Thr Ser Val Lys Pro Lys Lys Tyr Arg Gly Val Arg Gln Arg Pro
100 105 110

Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Ser Ser Arg Thr Arg
115 120 125

Ile Trp Leu Gly Thr Phe Val Thr Ala Glu Glu Ala Ala Ile Ala Tyr
130 135 140

Asp Arg Ala Ala Ile His Leu Lys Gly Pro Lys Ala Leu Thr Asn Phe

145 150 155 160
 Leu Thr Pro Pro Thr Pro Thr Pro Val Ile Asp Leu Gln Thr Val Ser
 165 170 175
 Ala Cys Asp Tyr Gly Arg Asp Ser Arg Gln Ser Leu His Ser Pro Thr
 180 185 190
 Ser Val Leu Arg Phe Asn Val Asn Glu Glu Thr Glu His Glu Ile Glu
 195 200 205
 Ala Ile Glu Leu Ser Pro Glu Arg Lys Ser Thr Val Ile Lys Glu Glu
 210 215 220
 Glu Glu Ser Ser Ala Gly Leu Val Phe Pro Asp Pro Tyr Leu Leu Pro
 225 230 235 240
 Asp Leu Ser Leu Ala Gly Glu Cys Phe Trp Asp Thr Glu Ile Ala Pro
 245 250 255
 Asp Leu Leu Phe Leu Asp Glu Glu Thr Lys Ile Gln Ser Thr Leu Leu
 260 265 270
 Pro Asn Thr Glu Val Ser Lys Gln Gly Glu Asn Glu Thr Glu Asp Phe
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 120
 atctctcaac attctctttc tctctgtaaa atg gag aaa cca gtg ttt gca cca
 174
 Met Glu Lys Pro Val Phe Ala Pro
 1 5
 tgg cgt tcc gac caa gtt ttc cgg cca ccg gag aca cca tta gag ccg
 222
 Trp Arg Ser Asp Gln Val Phe Arg Pro Pro Glu Thr Pro Leu Glu Pro

10	15	20
atg gag ttt ctc tct cgc tcc tgg agc gta tca gct cac gaa gtc tcc		
270		
Met Glu Phe Leu Ser Arg Ser Trp Ser Val Ser Ala His Glu Val Ser		
25	30	35 40
aaa gct ctc act cct tct cag caa ctc ctc tca aaa gcc tca atc gaa		
318		
Lys Ala Leu Thr Pro Ser Gln Gln Leu Leu Ser Lys Ala Ser Ile Glu		
	45	50 55
aac acc acc gtc att ctc gaa gaa ccc atc gcc gcc ggc gag acc gaa		
366		
Asn Thr Thr Val Ile Leu Glu Glu Pro Ile Ala Ala Gly Glu Thr Glu		
	60	65 70
acg gag gac aac agc ttc gtc tcc gga aac cct ttc tcc ttc gct tgc		
414		
Thr Glu Asp Asn Ser Phe Val Ser Gly Asn Pro Phe Ser Phe Ala Cys		
	75	80 85
tca gaa act tct cag atg gtc atg gat cgt atc tta tct cag tct cag		
462		
Ser Glu Thr Ser Gln Met Val Met Asp Arg Ile Leu Ser Gln Ser Gln		
	90	95 100
gaa gtg tcg cca cga aca tct ggt cgg ctt tct cat agc agc ggt cct		
510		
Glu Val Ser Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Gly Pro		
105	110	115 120
ctc aat ggt tct tta acc gac agt cct ccg att tcg ccg cat caa gtc		
558		
Leu Asn Gly Ser Leu Thr Asp Ser Pro Pro Ile Ser Pro His Gln Val		
	125	130 135
gac gac att aag caa ttt tgc cga tca aac aac aat ttc aac tct caa		
606		
Asp Asp Ile Lys Gln Phe Cys Arg Ser Asn Asn Asn Phe Asn Ser Gln		
	140	145 150
tac cgt tca acg gga aca act ccg gga cct atc act gca aca act aca		
654		
Tyr Arg Ser Thr Gly Thr Thr Pro Gly Pro Ile Thr Ala Thr Thr Thr		
	155	160 165
cag tcc aag aca gtt gga cgg tgg ttg aaa gac agg agg gag aaa aag		
702		
Gln Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg Glu Lys Lys		
	170	175 180
aag gaa gag atg aga gca cac aat gct cag ata cat gct gct gta tca		
750		
Lys Glu Glu Met Arg Ala His Asn Ala Gln Ile His Ala Ala Val Ser		
185	190	195 200
gta gct ggt gtg gca gcc gcg gtg gct gct atc gcg gct gca act gct		
798		
Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala Ala Thr Ala		
	205	210 215

gct tcg tcg agt gct gga aaa gat gag aat atg gct aag acg gat atg
 846
 Ala Ser Ser Ser Ala Gly Lys Asp Glu Asn Met Ala Lys Thr Asp Met
 220 225 230

gct gtg gct tct gct gca aca ctt gtg gct gct caa tgt gtg gaa gct
 894
 Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Gln Cys Val Glu Ala
 235 240 245

gct gaa gtt atg gga gct gag agg gat cat tta gct tcc gtt gtt agt
 942
 Ala Glu Val Met Gly Ala Glu Arg Asp His Leu Ala Ser Val Val Ser
 250 255 260

tct gct gtt aat gtt cga tct gcg gga gat atc atg aca tta acc gct
 990
 Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr Leu Thr Ala
 265 270 275 280

gga gca gcc aca gcg tta aga gga gtg gct aca ttg aag gct aga gct
 1038
 Gly Ala Ala Thr Ala Leu Arg Gly Val Ala Thr Leu Lys Ala Arg Ala
 285 290 295

atg aag gag gtg tgg cac att gca tca gtt att coa atg gat aaa gga
 1086
 Met Lys Glu Val Trp His Ile Ala Ser Val Ile Pro Met Asp Lys Gly
 300 305 310

atc aat ctc gga ggt tgc agc aat gtt aat ggt aac ggg agc tat gtc
 1134
 Ile Asn Leu Gly Gly Cys Ser Asn Val Asn Gly Asn Gly Ser Tyr Val
 315 320 325

agc tca agc agc agt cat agt ggc gaa ttt cta gtt gag gat aat ttc
 1182
 Ser Ser Ser Ser Ser His Ser Gly Glu Phe Leu Val Glu Asp Asn Phe
 330 335 340

ttg gga cat tgc aat aga gaa tgg ctt gct cga ggt ggc caa ctt ctt
 1230
 Leu Gly His Cys Asn Arg Glu Trp Leu Ala Arg Gly Gly Gln Leu Leu
 345 350 355 360

aaa cgc acc cgc aaa ggt gat ctt cat tgg aaa ata gtt tca gtt tac
 1278
 Lys Arg Thr Arg Lys Gly Asp Leu His Trp Lys Ile Val Ser Val Tyr
 365 370 375

ata aac agg cta aat caa gtt ata ttg aag atg aag agc agg cat gta
 1326
 Ile Asn Arg Leu Asn Gln Val Ile Leu Lys Met Lys Ser Arg His Val
 380 385 390

gga ggg acc ttc acg aag aag aac aaa aat gtt gtg att gat gtg atc
 1374
 Gly Gly Thr Phe Thr Lys Lys Asn Lys Asn Val Val Ile Asp Val Ile
 395 400 405

aaa aac gtt caa gct tgg cca ggc cgc cat ttg ctg gaa gga gga gag
 1422
 Lys Asn Val Gln Ala Trp Pro Gly Arg His Leu Leu Glu Gly Gly Glu
 410 415 420
 gat ttg aga tac ttt ggg tta aag acg gtt ccg cga ggg att gta gaa
 1470
 Asp Leu Arg Tyr Phe Gly Leu Lys Thr Val Pro Arg Gly Ile Val Glu
 425 430 435 440
 ttt cag tgc aag agc cag aga gag tat gaa atg tgg aca caa ggt gtc
 1518
 Phe Gln Cys Lys Ser Gln Arg Glu Tyr Glu Met Trp Thr Gln Gly Val
 445 450 455
 tca agg ctt att gct gtt gct gcc gag agg aat aac aga tat agg ata
 1566
 Ser Arg Leu Ile Ala Val Ala Ala Glu Arg Asn Asn Arg Tyr Arg Ile
 460 465 470
 tga agggagtagt agttttaaga gttcagagct actttttgag gggtagatc
 1619
 taacttatgg ggccaaatta taacttgag aaagttaagg gtgttttctt tagagtaatg
 1679
 tctttttgta aggtatatag gattaaatgt ggcctctata agggtagcta gtgaaacaaa
 1739
 tcttggtggtt tgtatatata ttttttttgg ggaaaaagtt taatatcaaa tttttaattt
 1799
 aaaa
 1803

 <210> 420 <211> 472 <212> PRT <213> Arabidopsis thaliana <400>
 420
 Met Glu Lys Pro Val Phe Ala Pro Trp Arg Ser Asp Gln Val Phe Arg
 1 5 10 15
 Pro Pro Glu Thr Pro Leu Glu Pro Met Glu Phe Leu Ser Arg Ser Trp
 20 25 30
 Ser Val Ser Ala His Glu Val Ser Lys Ala Leu Thr Pro Ser Gln Gln
 35 40 45
 Leu Leu Ser Lys Ala Ser Ile Glu Asn Thr Thr Val Ile Leu Glu Glu
 50 55 60
 Pro Ile Ala Ala Gly Glu Thr Glu Thr Glu Asp Asn Ser Phe Val Ser
 65 70 75 80
 Gly Asn Pro Phe Ser Phe Ala Cys Ser Glu Thr Ser Gln Met Val Met
 85 90 95

Asp Arg Ile Leu Ser Gln Ser Gln Glu Val Ser Pro Arg Thr Ser Gly
 100 105 110

Arg Leu Ser His Ser Ser Gly Pro Leu Asn Gly Ser Leu Thr Asp Ser
 115 120 125

Pro Pro Ile Ser Pro His Gln Val Asp Asp Ile Lys Gln Phe Cys Arg
 130 135 140

Ser Asn Asn Asn Phe Asn Ser Gln Tyr Arg Ser Thr Gly Thr Thr Pro
 145 150 155 160

Gly Pro Ile Thr Ala Thr Thr Thr Gln Ser Lys Thr Val Gly Arg Trp
 165 170 175

Leu Lys Asp Arg Arg Glu Lys Lys Lys Glu Glu Met Arg Ala His Asn
 180 185 190

Ala Gln Ile His Ala Ala Val Ser Val Ala Gly Val Ala Ala Val
 195 200 205

Ala Ala Ile Ala Ala Ala Thr Ala Ala Ser Ser Ser Ala Gly Lys Asp
 210 215 220

Glu Asn Met Ala Lys Thr Asp Met Ala Val Ala Ser Ala Ala Thr Leu
 225 230 235 240

Val Ala Ala Gln Cys Val Glu Ala Ala Glu Val Met Gly Ala Glu Arg
 245 250 255

Asp His Leu Ala Ser Val Val Ser Ser Ala Val Asn Val Arg Ser Ala
 260 265 270

Gly Asp Ile Met Thr Leu Thr Ala Gly Ala Ala Thr Ala Leu Arg Gly
 275 280 285

Val Ala Thr Leu Lys Ala Arg Ala Met Lys Glu Val Trp His Ile Ala
 290 295 300

Ser Val Ile Pro Met Asp Lys Gly Ile Asn Leu Gly Gly Cys Ser Asn
 305 310 315 320

Val Asn Gly Asn Gly Ser Tyr Val Ser Ser Ser Ser Ser His Ser Gly
 325 330 335

Glu Phe Leu Val Glu Asp Asn Phe Leu Gly His Cys Asn Arg Glu Trp
 340 345 350

Leu Ala Arg Gly Gly Gln Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu
 355 360 365

His Trp Lys Ile Val Ser Val Tyr Ile Asn Arg Leu Asn Gln Val Ile
 370 375 380

Leu Lys Met Lys Ser Arg His Val Gly Gly Thr Phe Thr Lys Lys Asn
 385 390 395 400

Lys Asn Val Val Ile Asp Val Ile Lys Asn Val Gln Ala Trp Pro Gly
 405 410 415

Arg His Leu Leu Glu Gly Gly Glu Asp Leu Arg Tyr Phe Gly Leu Lys
 420 425 430

Thr Val Pro Arg Gly Ile Val Glu Phe Gln Cys Lys Ser Gln Arg Glu
 435 440 445

Tyr Glu Met Trp Thr Gln Gly Val Ser Arg Leu Ile Ala Val Ala Ala
 450 455 460

Glu Arg Asn Asn Arg Tyr Arg Ile
 465 470

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 <221> CDS <222> (1)..(1128) <223> G2331

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 48
 Met Asp Leu Ser Asn Arg Arg Asn Pro Leu Arg Asp Leu Ser Phe Pro
 1 5 10 15

cct cct ccg ccg cca cct att ttc cac cgt gcg agc tct acg ggg acg
 96
 Pro Pro Pro Pro Pro Pro Ile Phe His Arg Ala Ser Ser Thr Gly Thr
 20 25 30

agt ttt ccg atc tta gcc gtc gcg gtg atc gga atc tta gcc aca gca
 144
 Ser Phe Pro Ile Leu Ala Val Ala Val Ile Gly Ile Leu Ala Thr Ala
 35 40 45

ttt tta ctt gta agc tat tat gtt ttt gtt atc aaa tgt tgt ctc aac
 192
 Phe Leu Leu Val Ser Tyr Tyr Val Phe Val Ile Lys Cys Cys Leu Asn
 50 55 60

tgg cac cga atc gac att ctt ggt cga ttc tog tta tct cga agg cga
 240
 Trp His Arg Ile Asp Ile Leu Gly Arg Phe Ser Leu Ser Arg Arg Arg
 65 70 75 80

cgc aac gac caa gat cct tta atg gtt tac tct cca gag ctt aga agc
 288
 Arg Asn Asp Gln Asp Pro Leu Met Val Tyr Ser Pro Glu Leu Arg Ser
 85 90 95

cgc ggt ctt gat gaa tcc gtc att aga gca atc cca atc ttt aag ttc
 336
 Arg Gly Leu Asp Glu Ser Val Ile Arg Ala Ile Pro Ile Phe Lys Phe
 100 105 110

aag aag aga tac gac caa aac gac ggc gtt ttt aca gga gaa gga gaa
 384
 Lys Lys Arg Tyr Asp Gln Asn Asp Gly Val Phe Thr Gly Glu Gly Glu
 115 120 125

gaa gaa gaa gag aag aga tct caa gaa tgc tct gtt tgt ttg agt gag
 432
 Glu Glu Glu Glu Lys Arg Ser Gln Glu Cys Ser Val Cys Leu Ser Glu
 130 135 140

ttt caa gat gag gag aag ctg agg att atc cca aat tgt tct cat ttg
 480
 Phe Gln Asp Glu Glu Lys Leu Arg Ile Ile Pro Asn Cys Ser His Leu
 145 150 155 160

ttt cat atc gac tgt atc gat gtg tgg ctt cag aac aac gcc aat tgt
 528
 Phe His Ile Asp Cys Ile Asp Val Trp Leu Gln Asn Asn Ala Asn Cys
 165 170 175

cct ttg tgt aga act agg gtt tct tgt gac aca agt ttt cct ccg gat
 576
 Pro Leu Cys Arg Thr Arg Val Ser Cys Asp Thr Ser Phe Pro Pro Asp
 180 185 190

cgg gtt tct gcg ccg agc act tct ccc gag aat ctg gtc atg tta aga
 624
 Arg Val Ser Ala Pro Ser Thr Ser Pro Glu Asn Leu Val Met Leu Arg
 195 200 205

ggt gag aac gag tat gtg gtc att gag ctg ggc agt agc atc ggt agt
 672
 Gly Glu Asn Glu Tyr Val Val Ile Glu Leu Gly Ser Ser Ile Gly Ser
 210 215 220

gac aga gat agt cca aga cac gga agg tta ctt acg gga caa gaa agg
 720
 Asp Arg Asp Ser Pro Arg His Gly Arg Leu Leu Thr Gly Gln Glu Arg
 225 230 235 240

tca aat tca ggt tat cta ctg aac gaa aac acc caa aat tcg atc agt
 768
 Ser Asn Ser Gly Tyr Leu Leu Asn Glu Asn Thr Gln Asn Ser Ile Ser
 245 250 255

cca tct ccg aag aag ctt gac cgc gga ggg ctt cca aga aaa ttc cga
 816
 Pro Ser Pro Lys Lys Leu Asp Arg Gly Gly Leu Pro Arg Lys Phe Arg
 260 265 270

aag ctt cac aag atg acg agt atg gga gac gaa tgc atc gac ata aga
 864
 Lys Leu His Lys Met Thr Ser Met Gly Asp Glu Cys Ile Asp Ile Arg
 275 280 285

aga ggt aaa gac gaa cag ttc ggt agt att cag ccc att aga aga tca
 912
 Arg Gly Lys Asp Glu Gln Phe Gly Ser Ile Gln Pro Ile Arg Arg Ser
 290 295 300

atc tca atg gat tca tcg gcg gat aga cag ctt tac ttg gcg gtt caa
 960
 Ile Ser Met Asp Ser Ser Ala Asp Arg Gln Leu Tyr Leu Ala Val Gln
 305 310 315 320

gag gcg att ccg aaa aac cgc gaa gtt ctg gtg gtt gga gac gga gga
 1008
 Glu Ala Ile Arg Lys Asn Arg Glu Val Leu Val Val Gly Asp Gly Gly
 325 330 335

gga tgt agc agt agt agt ggc aat gtt agt aat tcc aaa gtg aag aga
 1056
 Gly Cys Ser Ser Ser Ser Gly Asn Val Ser Asn Ser Lys Val Lys Arg
 340 345 350

tct ttc ttc tct ttt ggg agc agt aga cgt tct aga agt tcc tct aaa
 1104
 Ser Phe Phe Ser Phe Gly Ser Ser Arg Arg Ser Arg Ser Ser Ser Lys
 355 360 365

ttg cca ctt tat ttt gaa ccc taa
 1128
 Leu Pro Leu Tyr Phe Glu Pro
 370 375

<210> 422 <211> 375 <212> PRT <213> Arabidopsis thaliana <400>
 422

Met Asp Leu Ser Asn Arg Arg Asn Pro Leu Arg Asp Leu Ser Phe Pro
 1 5 10 15

Pro Pro Pro Pro Pro Pro Ile Phe His Arg Ala Ser Ser Thr Gly Thr
 20 25 30

Ser Phe Pro Ile Leu Ala Val Ala Val Ile Gly Ile Leu Ala Thr Ala
 35 40 45

Phe Leu Leu Val Ser Tyr Tyr Val Phe Val Ile Lys Cys Cys Leu Asn
 50 55 60

Trp His Arg Ile Asp Ile Leu Gly Arg Phe Ser Leu Ser Arg Arg Arg

65	70	75	80
Arg Asn Asp Gln Asp Pro Leu Met Val Tyr Ser Pro Glu Leu Arg Ser	85	90	95
Arg Gly Leu Asp Glu Ser Val Ile Arg Ala Ile Pro Ile Phe Lys Phe	100	105	110
Lys Lys Arg Tyr Asp Gln Asn Asp Gly Val Phe Thr Gly Glu Gly Glu	115	120	125
Glu Glu Glu Glu Lys Arg Ser Gln Glu Cys Ser Val Cys Leu Ser Glu	130	135	140
Phe Gln Asp Glu Glu Lys Leu Arg Ile Ile Pro Asn Cys Ser His Leu	145	150	155
Phe His Ile Asp Cys Ile Asp Val Trp Leu Gln Asn Asn Ala Asn Cys	165	170	175
Pro Leu Cys Arg Thr Arg Val Ser Cys Asp Thr Ser Phe Pro Pro Asp	180	185	190
Arg Val Ser Ala Pro Ser Thr Ser Pro Glu Asn Leu Val Met Leu Arg	195	200	205
Gly Glu Asn Glu Tyr Val Val Ile Glu Leu Gly Ser Ser Ile Gly Ser	210	215	220
Asp Arg Asp Ser Pro Arg His Gly Arg Leu Leu Thr Gly Gln Glu Arg	225	230	235
Ser Asn Ser Gly Tyr Leu Leu Asn Glu Asn Thr Gln Asn Ser Ile Ser	245	250	255
Pro Ser Pro Lys Lys Leu Asp Arg Gly Gly Leu Pro Arg Lys Phe Arg	260	265	270
Lys Leu His Lys Met Thr Ser Met Gly Asp Glu Cys Ile Asp Ile Arg	275	280	285
Arg Gly Lys Asp Glu Gln Phe Gly Ser Ile Gln Pro Ile Arg Arg Ser	290	295	300
Ile Ser Met Asp Ser Ser Ala Asp Arg Gln Leu Tyr Leu Ala Val Gln	305	310	315
			320

Glu Ala Ile Arg Lys Asn Arg Glu Val Leu Val Val Gly Asp Gly Gly
 325 330 335

Gly Cys Ser Ser Ser Ser Gly Asn Val Ser Asn Ser Lys Val Lys Arg
 340 345 350

Ser Phe Phe Ser Phe Gly Ser Ser Arg Arg Ser Arg Ser Ser Ser Lys
 355 360 365

Leu Pro Leu Tyr Phe Glu Pro
 370 375

<210> 423 <211> 1398 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(1398) <223> G2242

<400> 423
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 48
 Met Lys Trp Val Phe Pro Glu Ile Lys Thr Thr Gln Asn Phe Leu Ser
 1 5 10 15

cct tca tca ctt cca caa gaa cca ccg tta tct ctc cgc tcc agc gca
 96
 Pro Ser Ser Leu Pro Gln Glu Pro Pro Leu Ser Leu Arg Ser Ser Ala
 20 25 30

aac ttc gat cta aac agc aaa atc agt cca agt att ctc ctc ata atc
 144
 Asn Phe Asp Leu Asn Ser Lys Ile Ser Pro Ser Ile Leu Leu Ile Ile
 35 40 45

ata atc ctc tca atc atc ttc ttc atc tcc ggt ctc ctt cat ctc tta
 192
 Ile Ile Leu Ser Ile Ile Phe Phe Ile Ser Gly Leu Leu His Leu Leu
 50 55 60

gtc aga ttc ctc ctc aca cca tcg agc aga gac aga gaa gat tac ttc
 240
 Val Arg Phe Leu Leu Thr Pro Ser Ser Arg Asp Arg Glu Asp Tyr Phe
 65 70 75 80

gac aac gtc act gct ctt caa ggc cag ctt caa cag ctt ttt cat ctc
 288
 Asp Asn Val Thr Ala Leu Gln Gly Gln Leu Gln Gln Leu Phe His Leu
 85 90 95

cat gat tct gga gtt gac caa tcc ttc atc gac acg tta cct gtt ttc
 336
 His Asp Ser Gly Val Asp Gln Ser Phe Ile Asp Thr Leu Pro Val Phe
 100 105 110

cat tac aaa tcc ata atc ggt ctc aag aac tat cct ttt gat tgt gca
 384
 His Tyr Lys Ser Ile Ile Gly Leu Lys Asn Tyr Pro Phe Asp Cys Ala
 115 120 125

gtt tgt ctt tgt gag ttc gaa aca gag gat aag ctc agg ctc tta cct
 432
 Val Cys Leu Cys Glu Phe Glu Thr Glu Asp Lys Leu Arg Leu Leu Pro
 130 135 140

aaa tgc agc cac gcc ttt cac atg gat tgt atc gat act tgg ctt cta
 480
 Lys Cys Ser His Ala Phe His Met Asp Cys Ile Asp Thr Trp Leu Leu
 145 150 155 160

tct cac tct act tgt cct ttg tgt aga tcc agt ctc ctc tct gat ctc
 528
 Ser His Ser Thr Cys Pro Leu Cys Arg Ser Ser Leu Leu Ser Asp Leu
 165 170 175

tct tcg cac caa gat cct cgt tct tct ttc ctc ctt gtg ctc gag tct
 576
 Ser Ser His Gln Asp Pro Arg Ser Ser Phe Leu Leu Val Leu Glu Ser
 180 185 190

gcg agt gat cat agc tcg aga gag att gga gga gat aga gac agt gca
 624
 Ala Ser Asp His Ser Ser Arg Glu Ile Gly Gly Asp Arg Asp Ser Ala
 195 200 205

gct tgt gtg gct gca aat gat gat att gat gtg tct agt gct cat ctt
 672
 Ala Cys Val Ala Ala Asn Asp Asp Ile Asp Val Ser Ser Ala His Leu
 210 215 220

ggt ttg gtc gga aac aat gat ctt gga tca acc agg ata gat tcg ggt
 720
 Gly Leu Val Gly Asn Asn Asp Leu Gly Ser Thr Arg Ile Asp Ser Gly
 225 230 235 240

cac gga gat cag tac ctg gat ggt gaa ttg ggt ggt tcg gtt gga aag
 768
 His Gly Asp Gln Tyr Leu Asp Gly Glu Leu Gly Gly Ser Val Gly Lys
 245 250 255

gtt gtt cct ttt tca gtt aag cta ggg aag ttt agg aat ata gat att
 816
 Val Val Pro Phe Ser Val Lys Leu Gly Lys Phe Arg Asn Ile Asp Ile
 260 265 270

ggt gaa gga act agt agc aac aac aac att ggt aat agt agt agt tta
 864
 Gly Glu Gly Thr Ser Ser Asn Asn Asn Ile Gly Asn Ser Ser Ser Leu
 275 280 285

gat gag agg agg tgt ttc tca atg gga tca tat gag tat ata atg gat
 912
 Asp Glu Arg Arg Cys Phe Ser Met Gly Ser Tyr Glu Tyr Ile Met Asp
 290 295 300

gaa gaa acg act ctt aag gtt cat gtt tca acc aag aaa caa tca agc
 960
 Glu Glu Thr Thr Leu Lys Val His Val Ser Thr Lys Lys Gln Ser Ser
 305 310 315 320

aag aac cgt ggc ttg ccc ggt cat agg aca gcg atg tcc gaa tgc ggg
1008

Lys Asn Arg Gly Leu Pro Gly His Arg Thr Ala Met Ser Glu Cys Gly
325 330 335

ttt gat cca aca ggg aga ttg aaa ttc agt ggg agt gga tcg atg agg
1056

Phe Asp Pro Thr Gly Arg Leu Lys Phe Ser Gly Ser Gly Ser Met Arg
340 345 350

ata gtg gaa gaa gcg gcc gag aag aat gta gtg gaa aga gag agc ttt
1104

Ile Val Glu Glu Ala Ala Glu Lys Asn Val Val Glu Arg Glu Ser Phe
355 360 365

tcg gta tcg aaa ata tgg cta agg ggg aag aag gag aag cat agt aaa
1152

Ser Val Ser Lys Ile Trp Leu Arg Gly Lys Lys Glu Lys His Ser Lys
370 375 380

gtt caa gga aaa gag gat agt tca ttg gtt tct tcg tct tcg gga aga
1200

Val Gln Gly Lys Glu Asp Ser Ser Leu Val Ser Ser Ser Ser Gly Arg
385 390 395 400

gca ttc tct ttc agg tta tcg aac cag cgg aac cat ccc gat gcg atg
1248

Ala Phe Ser Phe Arg Leu Ser Asn Gln Arg Asn His Pro Asp Ala Met
405 410 415

atc gaa agt ggt tgc gaa gaa gat aat caa aag tgc gaa aac tcg gag
1296

Ile Glu Ser Gly Cys Glu Glu Asp Asn Gln Lys Cys Glu Asn Ser Glu
420 425 430

tct ttg gag act aaa aca cca tct ttt gct agg agg act atg ctt tgg
1344

Ser Leu Glu Thr Lys Thr Pro Ser Phe Ala Arg Arg Thr Met Leu Trp
435 440 445

ctt gca ggg aga caa aac aag gtt gtt cat tct tct tct tca act aat
1392

Leu Ala Gly Arg Gln Asn Lys Val Val His Ser Ser Ser Ser Thr Asn
450 455 460

gtc tag

1398

Val

465

<210> 424 <211> 465 <212> PRT <213> Arabidopsis thaliana <400>
424

Met Lys Trp Val Phe Pro Glu Ile Lys Thr Thr Gln Asn Phe Leu Ser
1 5 10 15

Pro Ser Ser Leu Pro Gln Glu Pro Pro Leu Ser Leu Arg Ser Ser Ala
20 25 30

Asn Phe Asp Leu Asn Ser Lys Ile Ser Pro Ser Ile Leu Leu Ile Ile
 35 40 45
 Ile Ile Leu Ser Ile Ile Phe Phe Ile Ser Gly Leu Leu His Leu Leu
 50 55 60
 Val Arg Phe Leu Leu Thr Pro Ser Ser Arg Asp Arg Glu Asp Tyr Phe
 65 70 75 80
 Asp Asn Val Thr Ala Leu Gln Gly Gln Leu Gln Gln Leu Phe His Leu
 85 90 95
 His Asp Ser Gly Val Asp Gln Ser Phe Ile Asp Thr Leu Pro Val Phe
 100 105 110
 His Tyr Lys Ser Ile Ile Gly Leu Lys Asn Tyr Pro Phe Asp Cys Ala
 115 120 125
 Val Cys Leu Cys Glu Phe Glu Thr Glu Asp Lys Leu Arg Leu Leu Pro
 130 135 140
 Lys Cys Ser His Ala Phe His Met Asp Cys Ile Asp Thr Trp Leu Leu
 145 150 155 160
 Ser His Ser Thr Cys Pro Leu Cys Arg Ser Ser Leu Leu Ser Asp Leu
 165 170 175
 Ser Ser His Gln Asp Pro Arg Ser Ser Phe Leu Leu Val Leu Glu Ser
 180 185 190
 Ala Ser Asp His Ser Ser Arg Glu Ile Gly Gly Asp Arg Asp Ser Ala
 195 200 205
 Ala Cys Val Ala Ala Asn Asp Asp Ile Asp Val Ser Ser Ala His Leu
 210 215 220
 Gly Leu Val Gly Asn Asn Asp Leu Gly Ser Thr Arg Ile Asp Ser Gly
 225 230 235 240
 His Gly Asp Gln Tyr Leu Asp Gly Glu Leu Gly Gly Ser Val Gly Lys
 245 250 255
 Val Val Pro Phe Ser Val Lys Leu Gly Lys Phe Arg Asn Ile Asp Ile
 260 265 270

Gly'Glu Gly Thr Ser Ser Asn Asn Asn Ile Gly Asn Ser Ser Ser Leu
 275 280 285

Asp Glu Arg Arg Cys Phe Ser Met Gly Ser Tyr Glu Tyr Ile Met Asp
 290 295 300

Glu Glu Thr Thr Leu Lys Val His Val Ser Thr Lys Lys Gln Ser Ser
 305 310 315 320

Lys Asn Arg Gly Leu Pro Gly His Arg Thr Ala Met Ser Glu Cys Gly
 325 330 335

Phe Asp Pro Thr Gly Arg Leu Lys Phe Ser Gly Ser Gly Ser Met Arg
 340 345 350

Ile Val Glu Glu Ala Ala Glu Lys Asn Val Val Glu Arg Glu Ser Phe
 355 360 365

Ser Val Ser Lys Ile Trp Leu Arg Gly Lys Lys Glu Lys His Ser Lys
 370 375 380

Val Gln Gly Lys Glu Asp Ser Ser Leu Val Ser Ser Ser Ser Gly Arg
 385 390 395 400

Ala Phe Ser Phe Arg Leu Ser Asn Gln Arg Asn His Pro Asp Ala Met
 405 410 415

Ile Glu Ser Gly Cys Glu Glu Asp Asn Gln Lys Cys Glu Asn Ser Glu
 420 425 430

Ser Leu Glu Thr Lys Thr Pro Ser Phe Ala Arg Arg Thr Met Leu Trp
 435 440 445

Leu Ala Gly Arg Gln Asn Lys Val Val His Ser Ser Ser Ser Thr Asn
 450 455 460

Val
 465

<210> 425 <211> 850 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (81)..(626) <223> G2347

<400> 425
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 60

acttaaaagct ttaccagaaa atg gag ggt cag aga aca caa cgc cgg ggt tac
 113

Met Glu Gly Gln Arg Thr Gln Arg Arg Gly Tyr
 1 5 10
 ttg aaa gac aag gct aca gtc tcc aac ctt gtt gaa gaa gaa atg gag
 161
 Leu Lys Asp Lys Ala Thr Val Ser Asn Leu Val Glu Glu Glu Met Glu
 15 20 25
 aat ggc atg gat gga gaa gag gag gat gga gga gac gaa gac aaa agg
 209
 Asn Gly Met Asp Gly Glu Glu Glu Asp Gly Gly Asp Glu Asp Lys Arg
 30 35 40
 aag aag gtg atg gaa aga gtt aga ggt cct agc act gac cgt gtt cca
 257
 Lys Lys Val Met Glu Arg Val Arg Gly Pro Ser Thr Asp Arg Val Pro
 45 50 55
 tcg cga ctg tgc cag gtc gat agg tgc act gtt aat ttg act gag gcc
 305
 Ser Arg Leu Cys Gln Val Asp Arg Cys Thr Val Asn Leu Thr Glu Ala
 60 65 70 75
 aag cag tat tac cgc aga cac aga gta tgt gaa gta cat gca aag gca
 353
 Lys Gln Tyr Tyr Arg Arg His Arg Val Cys Glu Val His Ala Lys Ala
 80 85 90
 tct gct gcg act gtt gca ggg gtc agg caa cgc ttt tgt caa caa tgc
 401
 Ser Ala Ala Thr Val Ala Gly Val Arg Gln Arg Phe Cys Gln Gln Cys
 95 100 105
 agc agg ttt cat gag cta cca gag ttt gat gaa gct aaa aga agc tgc
 449
 Ser Arg Phe His Glu Leu Pro Glu Phe Asp Glu Ala Lys Arg Ser Cys
 110 115 120
 agg agg cgc tta gct gga cac aat gag agg agg agg aag atc tct ggt
 497
 Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ile Ser Gly
 125 130 135
 gac agt ttt gga gaa ggg tca ggc cgg aga ggg ttt agc ggt caa ctg
 545
 Asp Ser Phe Gly Glu Gly Ser Gly Arg Arg Gly Phe Ser Gly Gln Leu
 140 145 150 155
 atc cag act caa gaa aga aac agg gta gac agg aaa ctt cct atg acc
 593
 Ile Gln Thr Gln Glu Arg Asn Arg Val Asp Arg Lys Leu Pro Met Thr
 160 165 170
 aac tca tca ttc aag cga cca cag atc aga taa accctccgc tctctctctt
 646
 Asn Ser Ser Phe Lys Arg Pro Gln Ile Arg
 175 180
 ctgtcatcta catatgctct atctacactc ttattagaca aataatggca tctaacaatg
 706

tcaagaaaag ttggatcatgg tattaaatcc tacacggata tataactata aacctctagt
766

cccctctatg ctgtcctgta atgaatatct atccggaaat gtattcgcac agtcttgcgt
826

ctaataatgt ttattgattt tgta
850

<210> 426 <211> 181 <212> PRT <213> Arabidopsis thaliana <400>
426

Met Glu Gly Gln Arg Thr Gln Arg Arg Gly Tyr Leu Lys Asp Lys Ala
1 5 10 15

Thr Val Ser Asn Leu Val Glu Glu Glu Met Glu Asn Gly Met Asp Gly
20 25 30

Glu Glu Glu Asp Gly Gly Asp Glu Asp Lys Arg Lys Lys Val Met Glu
35 40 45

Arg Val Arg Gly Pro Ser Thr Asp Arg Val Pro Ser Arg Leu Cys Gln
50 55 60

Val Asp Arg Cys Thr Val Asn Leu Thr Glu Ala Lys Gln Tyr Tyr Arg
65 70 75 80

Arg His Arg Val Cys Glu Val His Ala Lys Ala Ser Ala Ala Thr Val
85 90 95

Ala Gly Val Arg Gln Arg Phe Cys Gln Gln Cys Ser Arg Phe His Glu
100 105 110

Leu Pro Glu Phe Asp Glu Ala Lys Arg Ser Cys Arg Arg Arg Leu Ala
115 120 125

Gly His Asn Glu Arg Arg Arg Lys Ile Ser Gly Asp Ser Phe Gly Glu
130 135 140

Gly Ser Gly Arg Arg Gly Phe Ser Gly Gln Leu Ile Gln Thr Gln Glu
145 150 155 160

Arg Asn Arg Val Asp Arg Lys Leu Pro Met Thr Asn Ser Ser Phe Lys
165 170 175

Arg Pro Gln Ile Arg
180

<210> 427 <211> 762 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(630) <223> G2421

<400> 427
 atg gag ggt tgc tcc aaa ggg ttg agg aaa ggt gca tgg act gct gaa
 48
 Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu
 1 5 10 15
 gaa gat agt ctc ttg agg cag tgt att ggt aag tat gga gaa ggc aaa
 96
 Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys
 20 25 30
 tgg cat caa gtt cct tta aga gct ggg cta aat cgg tgc agg aaa agt
 144
 Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
 35 40 45
 tgt aga cta aga tgg tta aac tat ttg aag cca agt atc aag aga gga
 192
 Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
 50 55 60
 aaa ttt agt tct gat gaa gtt gat ctt ctt ctt cgt ctt cat aag ctt
 240
 Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
 65 70 75 80
 cta gga aat agg tgg tcc ttg att gct ggt cga tta cct ggt cgg acc
 288
 Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
 85 90 95
 gct aat gat gtc aag aac tac tgg aac acc cat ctg agt aag aag cat
 336
 Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
 100 105 110
 gaa ccg tgt tgt aaa act aag ata aaa agg ata aat att ata acc cct
 384
 Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro
 115 120 125
 cct aat aca ccg gcc caa aaa gtt tgt gaa aat agt atc aca tgt aac
 432
 Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn
 130 135 140
 aaa gat gat gag aaa gat gat ttt gtg gat aat ttt atg gtt gga gat
 480
 Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp
 145 150 155 160
 aat ata tgg ttg gag cgt ttg cta gac gag ggc caa gag gta gat gtg
 528
 Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val
 165 170 175
 ctg gtt aca gaa gcg gcg gca aca gaa aag gag ggc act ttg gcg ttt
 576

Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe
180 185 190

gac gtt gag caa ctt tgg aat ttg ttc gat gga gag act gtg atc ttt
624

Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe
195 200 205

gat tag tgtttataaa cgtttgtgtt ctctgtttg tgagggttct ctatttaatt
680

Asp

tagtatctat tttctaaatt aactaatatc ttatagtatt ttaggcaaac cttatgtttc
740

cgtttctgtg cgccgctct ag
762

<210> 428 <211> 209 <212> PRT <213> Arabidopsis thaliana <400>
428

Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu
1 5 10 15

Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys
20 25 30

Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50 55 60

Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro
115 120 125

Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn
130 135 140

Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp
145 150 155 160

Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val
 165 170 175

Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe
 180 185 190

Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe
 195 200 205

Asp

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<400> 429
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 48
 Met Gly Glu Ser Pro Lys Gly Leu Arg Lys Gly Thr Trp Thr Thr Glu
 1 5 10 15

gaa gat att ctc ttg agg caa tgc att gat aag tat gga gaa ggc aaa
 96
 Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys
 20 25 30

tgg cat cga gtt cct tta aga act ggt ctc aat cgg tgc cga aag agt
 144
 Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser
 35 40 45

tgt aga ctt aga tgg ttg aat tat ttg aag cca agt att aag aga gga
 192
 Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
 50 55 60

aaa ctc tgc tcc gat gaa gtt gat ctt gtt ctt cgc ctt cat aaa ctt
 240
 Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu
 65 70 75 80

cta gga aat agg tgg tcc ttg atc gct ggt aga ttg cct ggt cgg act
 288
 Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
 85 90 95

gct aat gat gtc aag aat tac tgg aac act cat ttg agt aag aag cac
 336
 Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
 100 105 110

gat gaa cga tgc tgt aag acg aag atg ata aac aaa aac att act tct
 384
 Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser
 115 120 125

cat cct act tca tcg gcc caa aaa atc gat gtt tta aag cct cgg cct
 432
 His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro
 130 135 140

 cga tcc ttc tcc gat aaa aat agt tgc aac gat gtc aat atc ttg cca
 480
 Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro
 145 150 155 160

 aaa gtt gac gtt gtt cct tta cat ctt gga ctc aac aac aat tat gtt
 528
 Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val
 165 170 175

 tgt gaa agt agt att aca tgt aac aaa gat gag caa aaa gat aag ctt
 576
 Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu
 180 185 190

 att aat att aat cta ttg gat gga gat aat atg tgg tgg gaa agt tta
 624
 Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu
 195 200 205

 ctg gag gca gat gtg ttg ggt cca gaa gct acg gaa aca gca aag ggt
 672
 Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly
 210 215 220

 gtg acc tta ccg ctt gac ttt gag caa att tgg gct cgg ttt gat gaa
 720
 Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu
 225 230 235 240

 gag act tta gaa ctg aat tag
 741
 Glu Thr Leu Glu Leu Asn
 245

<210> 430 <211> 246 <212> PRT <213> Arabidopsis thaliana <400>
 430

Met Gly Glu Ser Pro Lys Gly Leu Arg Lys Gly Thr Trp Thr Thr Glu
 1 5 10 15

Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys
 20 25 30

Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser
 35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
 50 55 60

Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser
115 120 125

His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro
130 135 140

Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro
145 150 155 160

Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val
165 170 175

Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu
180 185 190

Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu
195 200 205

Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly
210 215 220

Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu
225 230 235 240

Glu Thr Leu Glu Leu Asn
245

<210> 431 <211> 972 <212> DNA <213> Arabidopsis thaliana <220>
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<400> 431

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48

Met Asp Glu Lys Gly Arg Ser Leu Lys Asn Asn Asn Met Glu Asp Glu
1 5 10 15

atg gac cta aag aga ggt ccg tgg act gct gaa gaa gat ttt aag ctc
96

Met Asp Leu Lys Arg Gly Pro Trp Thr Ala Glu Glu Asp Phe Lys Leu
20 25 30

atg aat tac att gct act aat gga gaa ggt cgc tgg aac tct ctt tct
 144
 Met Asn Tyr Ile Ala Thr Asn Gly Glu Gly Arg Trp Asn Ser Leu Ser
 35 40 45
 cgt tgc gcc ggc ctc caa cgc acc ggt aaa agc tgt aga cta agg tgg
 192
 Arg Cys Ala Gly Leu Gln Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp
 50 55 60
 tta aac tat ctc cgc cct gac gtc cgc cgt gga aac att aca ctt gaa
 240
 Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu Glu
 65 70 75 80
 gaa caa ctc ttg atc ctc gaa ctt cat tcc cgt tgg gga aat aga tgg
 288
 Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg Trp
 85 90 95
 tca aaa atc gca caa tat tta ccg gga aga acg gac aac gag atc aag
 336
 Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
 100 105 110
 aac tac tgg agg acg cgg gtg caa aag cat gcg aaa cag ttg aaa tgt
 384
 Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys Cys
 115 120 125
 gat gtg aat agc caa caa ttc aaa gac aca atg aag tac ttg tgg atg
 432
 Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp Met
 130 135 140
 cct cga cta gtc gag agg att cag tca gcc tcg gcc tca tcc gca gca
 480
 Pro Arg Leu Val Glu Arg Ile Gln Ser Ala Ser Ala Ser Ser Ala Ala
 145 150 155 160
 gca gcc acc acc aca acc acc acc acc aca gga tca gcc ggc acg tca
 528
 Ala Ala Thr Thr Thr Thr Thr Thr Thr Gly Ser Ala Gly Thr Ser
 165 170 175
 tct tgc atc aca acc tct aac aat caa ttc atg aat tac gac tac aac
 576
 Ser Cys Ile Thr Thr Ser Asn Asn Gln Phe Met Asn Tyr Asp Tyr Asn
 180 185 190
 aac aac aac atg gga caa cag ttt ggt gta atg agc aac aat gat tat
 624
 Asn Asn Asn Met Gly Gln Gln Phe Gly Val Met Ser Asn Asn Asp Tyr
 195 200 205
 atc acg cct gaa aat tcc agc gtg gca gtg tct ccg gcg tca gac tta
 672
 Ile Thr Pro Glu Asn Ser Ser Val Ala Val Ser Pro Ala Ser Asp Leu
 210 215 220

acg gag tac tac agc gct cca aac cct aac ccg gaa tac tat tcg ggt
720

Thr Glu Tyr Tyr Ser Ala Pro Asn Pro Asn Pro Glu Tyr Tyr Ser Gly
225 230 235 240

caa atg ggg aat agt tat tat cca gat cag aat tta gtg agt tca caa
768

Gln Met Gly Asn Ser Tyr Tyr Pro Asp Gln Asn Leu Val Ser Ser Gln
245 250 255

tta tta ccg gat aat tat ttc gac tat agt gga tta tta gac gaa gat
816

Leu Leu Pro Asp Asn Tyr Phe Asp Tyr Ser Gly Leu Leu Asp Glu Asp
260 265 270

cta acg gct atg caa gag cag agt aac ctc agc tgg ttt gaa aac att
864

Leu Thr Ala Met Gln Glu Gln Ser Asn Leu Ser Trp Phe Glu Asn Ile
275 280 285

aat ggt gct gct tct tct tca gac agt tta tgg aac att gga gaa act
912

Asn Gly Ala Ala Ser Ser Ser Asp Ser Leu Trp Asn Ile Gly Glu Thr
290 295 300

gat gaa gaa ttc tgg ttc tta cag cag caa caa cag ttc aac aat aat
960

Asp Glu Glu Phe Trp Phe Leu Gln Gln Gln Gln Gln Phe Asn Asn Asn
305 310 315 320

ggt agc ttc tga

972

Gly Ser Phe

<210> 432 <211> 323 <212> PRT <213> Arabidopsis thaliana <400>
432

Met Asp Glu Lys Gly Arg Ser Leu Lys Asn Asn Asn Met Glu Asp Glu
1 5 10 15

Met Asp Leu Lys Arg Gly Pro Trp Thr Ala Glu Glu Asp Phe Lys Leu
20 25 30

Met Asn Tyr Ile Ala Thr Asn Gly Glu Gly Arg Trp Asn Ser Leu Ser
35 40 45

Arg Cys Ala Gly Leu Gln Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp
50 55 60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Leu Glu
65 70 75 80

Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg Trp
85 90 95

Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
 100 105 110

Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Lys Cys
 115 120 125

Asp Val Asn Ser Gln Gln Phe Lys Asp Thr Met Lys Tyr Leu Trp Met
 130 135 140

Pro Arg Leu Val Glu Arg Ile Gln Ser Ala Ser Ala Ser Ser Ala Ala
 145 150 155 160

Ala Ala Thr Thr Thr Thr Thr Thr Thr Gly Ser Ala Gly Thr Ser
 165 170 175

Ser Cys Ile Thr Thr Ser Asn Asn Gln Phe Met Asn Tyr Asp Tyr Asn
 180 185 190

Asn Asn Asn Met Gly Gln Gln Phe Gly Val Met Ser Asn Asn Asp Tyr
 195 200 205

Ile Thr Pro Glu Asn Ser Ser Val Ala Val Ser Pro Ala Ser Asp Leu
 210 215 220

Thr Glu Tyr Tyr Ser Ala Pro Asn Pro Asn Pro Glu Tyr Tyr Ser Gly
 225 230 235 240

Gln Met Gly Asn Ser Tyr Tyr Pro Asp Gln Asn Leu Val Ser Ser Gln
 245 250 255

Leu Leu Pro Asp Asn Tyr Phe Asp Tyr Ser Gly Leu Leu Asp Glu Asp
 260 265 270

Leu Thr Ala Met Gln Glu Gln Ser Asn Leu Ser Trp Phe Glu Asn Ile
 275 280 285

Asn Gly Ala Ala Ser Ser Ser Asp Ser Leu Trp Asn Ile Gly Glu Thr
 290 295 300

Asp Glu Glu Phe Trp Phe Leu Gln Gln Gln Gln Phe Asn Asn Asn
 305 310 315 320

Gly Ser Phe

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 <221> CDS <222> (1)..(849) <223> G2467

<400> 433

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 48
 Met Asp Pro Ser Ser Ser Ser Arg Ala Arg Ser Met Pro Pro Val
 1 5 10 15

cct atg gag gga ttg cag gaa gca ggg cct tct cct ttt cta aca aag
 96
 Pro Met Glu Gly Leu Gln Glu Ala Gly Pro Ser Pro Phe Leu Thr Lys
 20 25 30

acg ttc gag atg gtt ggt gat cca aac aca aac cac att gtg tct tgg
 144
 Thr Phe Glu Met Val Gly Asp Pro Asn Thr Asn His Ile Val Ser Trp
 35 40 45

aac agg gga ggc atc agt ttt gtc gtg tgg gat cca cat tcc ttc tcg
 192
 Asn Arg Gly Gly Ile Ser Phe Val Val Trp Asp Pro His Ser Phe Ser
 50 55 60

gcc act att ctg cct cta tac ttc aag cac aac aac ttc tcc agc ttt
 240
 Ala Thr Ile Leu Pro Leu Tyr Phe Lys His Asn Asn Phe Ser Ser Phe
 65 70 75 80

gtc aga caa ctt aac act tat gga ttc aga aag atc gag gca gag aga
 288
 Val Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu Arg
 85 90 95

tgg gag ttt atg aat gaa ggt ttc ttg atg ggt cag agg gac ctt ctc
 336
 Trp Glu Phe Met Asn Glu Gly Phe Leu Met Gly Gln Arg Asp Leu Leu
 100 105 110

aaa agc atc aag cga cga acc tcc tct tct tcc cct cct tcg ctt aac
 384
 Lys Ser Ile Lys Arg Arg Thr Ser Ser Ser Ser Pro Pro Ser Leu Asn
 115 120 125

tac tct cag tct cag ccc gag gct cat gac cca ggc gtc gag ctt ccg
 432
 Tyr Ser Gln Ser Gln Pro Glu Ala His Asp Pro Gly Val Glu Leu Pro
 130 135 140

cag ctc cga gaa gag agg cat gtc cta atg atg gag atc tcg acg ctc
 480
 Gln Leu Arg Glu Glu Arg His Val Leu Met Met Glu Ile Ser Thr Leu
 145 150 155 160

aga cag gag gag caa aga gcg aga ggc tac gtc caa gcc atg gag cag
 528
 Arg Gln Glu Glu Gln Arg Ala Arg Gly Tyr Val Gln Ala Met Glu Gln
 165 170 175

agg att aat gga gca gag aag aaa cag agg cat atg atg tcc ttc ttg
576

Arg Ile Asn Gly Ala Glu Lys Lys Gln Arg His Met Met Ser Phe Leu
180 185 190

agg cgt gcg gtg gag aat cct tcc ctt ctg cag cag att ttc gag cag
624

Arg Arg Ala Val Glu Asn Pro Ser Leu Leu Gln Gln Ile Phe Glu Gln
195 200 205

aag aga gac cga gag gag gcc gcg atg att gat cag gct ggc ttg atc
672

Lys Arg Asp Arg Glu Glu Ala Ala Met Ile Asp Gln Ala Gly Leu Ile
210 215 220

aaa atg gaa gag gtg gag cac ctg tcg gag ctg gag gct ctg gcg ctt
720

Lys Met Glu Glu Val Glu His Leu Ser Glu Leu Glu Ala Leu Ala Leu
225 230 235 240

gag atg caa gga tat gga cgg caa cgg act gat ggt gtg gag agg gag
768

Glu Met Gln Gly Tyr Gly Arg Gln Arg Thr Asp Gly Val Glu Arg Glu
245 250 255

ctt gac gac ggg ttt tgg gaa gag tta ctc atg aac aat gaa aac tcc
816

Leu Asp Asp Gly Phe Trp Glu Glu Leu Leu Met Asn Asn Glu Asn Ser
260 265 270

gac gaa gaa gag gcg aat gtg aag caa gat tag
849

Asp Glu Glu Glu Ala Asn Val Lys Gln Asp
275 280

<210> 434 <211> 282 <212> PRT <213> Arabidopsis thaliana <400>
434

Met Asp Pro Ser Ser Ser Ser Arg Ala Arg Ser Met Pro Pro Pro Val
1 5 10 15

Pro Met Glu Gly Leu Gln Glu Ala Gly Pro Ser Pro Phe Leu Thr Lys
20 25 30

Thr Phe Glu Met Val Gly Asp Pro Asn Thr Asn His Ile Val Ser Trp
35 40 45

Asn Arg Gly Gly Ile Ser Phe Val Val Trp Asp Pro His Ser Phe Ser
50 55 60

Ala Thr Ile Leu Pro Leu Tyr Phe Lys His Asn Asn Phe Ser Ser Phe
65 70 75 80

Val Arg Gln Leu Asn Thr Tyr Gly Phe Arg Lys Ile Glu Ala Glu Arg
85 90 95

Trp Glu Phe Met Asn Glu Gly Phe Leu Met Gly Gln Arg Asp Leu Leu
 100 105 110

Lys Ser Ile Lys Arg Arg Thr Ser Ser Ser Ser Pro Pro Ser Leu Asn
 115 120 125

Tyr Ser Gln Ser Gln Pro Glu Ala His Asp Pro Gly Val Glu Leu Pro
 130 135 140

Gln Leu Arg Glu Glu Arg His Val Leu Met Met Glu Ile Ser Thr Leu
 145 150 155 160

Arg Gln Glu Glu Gln Arg Ala Arg Gly Tyr Val Gln Ala Met Glu Gln
 165 170 175

Arg Ile Asn Gly Ala Glu Lys Lys Gln Arg His Met Met Ser Phe Leu
 180 185 190

Arg Arg Ala Val Glu Asn Pro Ser Leu Leu Gln Gln Ile Phe Glu Gln
 195 200 205

Lys Arg Asp Arg Glu Glu Ala Ala Met Ile Asp Gln Ala Gly Leu Ile
 210 215 220

Lys Met Glu Glu Val Glu His Leu Ser Glu Leu Glu Ala Leu Ala Leu
 225 230 235 240

Glu Met Gln Gly Tyr Gly Arg Gln Arg Thr Asp Gly Val Glu Arg Glu
 245 250 255

Leu Asp Asp Gly Phe Trp Glu Glu Leu Leu Met Asn Asn Glu Asn Ser
 260 265 270

Asp Glu Glu Glu Ala Asn Val Lys Gln Asp
 275 280

<210> 435 <211> 690 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (112)..(690) <223> G2514

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 60

gccacgtgtg aaaacccttc tccggcttgc tactaatata cgactaatag t atg aat
 117

Met Asn
 1

agt tca atg gct tct gcc ggc tta ggt agc cgg aga aag gat ccg gtg
 165
 Ser Ser Met Ala Ser Ala Gly Leu Gly Ser Arg Arg Lys Asp Pro Val
 5 10 15

tac aga gga atc cgg tgc cga agt ggg aaa tgg gtc tcc gag att cgt
 213
 Tyr Arg Gly Ile Arg Cys Arg Ser Gly Lys Trp Val Ser Glu Ile Arg
 20 25 30

gag ccg agg aaa acc acg aga atc tgg ctt gga act tac ccc atg gca
 261
 Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro Met Ala
 35 40 45 50

gag atg gca gca gcc gcc tat gat gtg gct gct atg gct ctt aaa gga
 309
 Glu Met Ala Ala Ala Tyr Asp Val Ala Ala Met Ala Leu Lys Gly
 55 60 65

aga gaa gct gtc ttg aac ttc cct gga tcc gtc ggg tca tac ccg gtt
 357
 Arg Glu Ala Val Leu Asn Phe Pro Gly Ser Val Gly Ser Tyr Pro Val
 70 75 80

cct gaa tca aca tcc gca gca gat ata cga gcc gct gcg gca gcc gca
 405
 Pro Glu Ser Thr Ser Ala Ala Asp Ile Arg Ala Ala Ala Ala Ala
 85 90 95

gca gca atg aag gga tgt gag gaa ggg gag gag gag aaa aag gca aag
 453
 Ala Ala Met Lys Gly Cys Glu Glu Gly Glu Glu Glu Lys Lys Ala Lys
 100 105 110

gag aag aag agt agt agt tcg aag tcg aga gcg cgt gag tgc cac gta
 501
 Glu Lys Lys Ser Ser Ser Ser Lys Ser Arg Ala Arg Glu Cys His Val
 115 120 125 130

gat aat gat gtt gga tct tcg tcg tgg tgt ggg aca gag ttc atg gac
 549
 Asp Asn Asp Val Gly Ser Ser Ser Trp Cys Gly Thr Glu Phe Met Asp
 135 140 145

gaa gaa gaa gtc ttg aat atg cct aat ctg ctg gct aat atg gca gaa
 597
 Glu Glu Glu Val Leu Asn Met Pro Asn Leu Leu Ala Asn Met Ala Glu
 150 155 160

ggg atg atg gtt gcg ccg ccg tcg tgg atg ggt tct ccg ccg tcg gat
 645
 Gly Met Met Val Ala Pro Pro Ser Trp Met Gly Ser Arg Pro Ser Asp
 165 170 175

gac tct ccg gag aat tca aat gat gag gac ttg tgg ggc tat tga
 690
 Asp Ser Pro Glu Asn Ser Asn Asp Glu Asp Leu Trp Gly Tyr
 180 185 190

<210> 436 <211> 192 <212> PRT <213> Arabidopsis thaliana <400>
436

Met Asn Ser Ser Met Ala Ser Ala Gly Leu Gly Ser Arg Arg Lys Asp
1 5 10 15

Pro Val Tyr Arg Gly Ile Arg Cys Arg Ser Gly Lys Trp Val Ser Glu
20 25 30

Ile Arg Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro
35 40 45

Met Ala Glu Met Ala Ala Ala Ala Tyr Asp Val Ala Ala Met Ala Leu
50 55 60

Lys Gly Arg Glu Ala Val Leu Asn Phe Pro Gly Ser Val Gly Ser Tyr
65 70 75 80

Pro Val Pro Glu Ser Thr Ser Ala Ala Asp Ile Arg Ala Ala Ala Ala
85 90 95

Ala Ala Ala Ala Met Lys Gly Cys Glu Glu Gly Glu Glu Glu Lys Lys
100 105 110

Ala Lys Glu Lys Lys Ser Ser Ser Ser Lys Ser Arg Ala Arg Glu Cys
115 120 125

His Val Asp Asn Asp Val Gly Ser Ser Ser Trp Cys Gly Thr Glu Phe
130 135 140

Met Asp Glu Glu Glu Val Leu Asn Met Pro Asn Leu Leu Ala Asn Met
145 150 155 160

Ala Glu Gly Met Met Val Ala Pro Pro Ser Trp Met Gly Ser Arg Pro
165 170 175

Ser Asp Asp Ser Pro Glu Asn Ser Asn Asp Glu Asp Leu Trp Gly Tyr
180 185 190

<210> 437 <211> 994 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (1)..(711) <223> G2547

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48
Met Asp Gln Glu Gln Thr Pro His Ser Pro Thr Arg His Ser Arg Ser
1 5 10 15


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ccc cca tcc tcc gcc tcc ggt tcc acc tca gca gaa ccg gtt cgg tcc
96
Pro Pro Ser Ser Ala Ser Gly Ser Thr Ser Ala Glu Pro Val Arg Ser
      20          25          30

cga tgg tca cct aaa ccg gaa caa ata ctc ata ctt gag tcg atc ttc
144
Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser Ile Phe
      35          40          45

cac agt ggt atg gtt aac cct ccc aaa gaa gag acg gta agg ata aga
192
His Ser Gly Met Val Asn Pro Pro Lys Glu Glu Thr Val Arg Ile Arg
      50          55          60

aag atg ctc gag aaa ttt ggc gcg gtg gga gat gca aat gtc ttc tat
240
Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala Asn Val Phe Tyr
      65          70          75          80

tgg ttt caa aac cgg cgg tca agg tcc cgt cgg aga cag cga cag cta
288
Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg Gln Leu
      85          90          95

cag gct gca gct gca gca gcg gac gca acc acc aac act tct agc tct
336
Gln Ala Ala Ala Ala Ala Ala Asp Ala Thr Thr Asn Thr Ser Ser Ser
      100          105          110

tct tct tct tat ggt ggt gga tgt gat aat caa agc aat agt ggc atg
384
Ser Ser Ser Tyr Gly Gly Gly Cys Asp Asn Gln Ser Asn Ser Gly Met
      115          120          125

gag aat ctc tta aca atg tct ggc caa atg agt tac cat gaa gct act
432
Glu Asn Leu Leu Thr Met Ser Gly Gln Met Ser Tyr His Glu Ala Thr
      130          135          140

cat cat cat tat caa aat cat agc tca aat gtc aca tcg att ttg tgc
480
His His His Tyr Gln Asn His Ser Ser Asn Val Thr Ser Ile Leu Cys
      145          150          155          160

cca tct gat caa aac tcc aat ttt caa tac caa caa ggg gct ata acg
528
Pro Ser Asp Gln Asn Ser Asn Phe Gln Tyr Gln Gln Gly Ala Ile Thr
      165          170          175

gtg ttt ata aac gga gtt ccg aca gaa gtg acg aga gga gga ata gac
576
Val Phe Ile Asn Gly Val Pro Thr Glu Val Thr Arg Gly Gly Ile Asp
      180          185          190

atg aaa gca acg ttt gga gaa gat ttg gtt ttg gtg cat tcc tca ggt
624
Met Lys Ala Thr Phe Gly Glu Asp Leu Val Leu Val His Ser Ser Gly
      195          200          205

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gtt cct ctt cct act gat gag ttt ggt ttt ttg atg cat agc tta caa
 672
 Val Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln
 210 215 220

cat ggt gaa gct tat ttc ctg gtt cca aga cag aca tga actggcttta
 721
 His Gly Glu Ala Tyr Phe Leu Val Pro Arg Gln Thr
 225 230 235

ctccgtatgtg tggatgatgca acagatgtct tgtttttcta ccttggactt tattgcaacg
 781

gtccttccat tttttctttt cttttcgagt ctatcgtata atcaaagttt cttctattgg
 841

ttttttttta aaaaatttta ttttgcaatt tattttataa agatgaagtc aaaagctctt
 901

gtacgacgaa gatattctagg ttgtatcaat ttagttattt agatgtaaaa tacgtatgta
 961

taattgattt gcaataaaat ctctgtctag gga
 994

<210> 438 <211> 236 <212> PRT <213> Arabidopsis thaliana <400>
 438

Met Asp Gln Glu Gln Thr Pro His Ser Pro Thr Arg His Ser Arg Ser
 1 5 10 15

Pro Pro Ser Ser Ala Ser Gly Ser Thr Ser Ala Glu Pro Val Arg Ser
 20 25 30

Arg Trp Ser Pro Lys Pro Glu Gln Ile Leu Ile Leu Glu Ser Ile Phe
 35 40 45

His Ser Gly Met Val Asn Pro Pro Lys Glu Glu Thr Val Arg Ile Arg
 50 55 60

Lys Met Leu Glu Lys Phe Gly Ala Val Gly Asp Ala Asn Val Phe Tyr
 65 70 75 80

Trp Phe Gln Asn Arg Arg Ser Arg Ser Arg Arg Arg Gln Arg Gln Leu
 85 90 95

Gln Ala Ala Ala Ala Ala Ala Asp Ala Thr Thr Asn Thr Ser Ser Ser
 100 105 110

Ser Ser Ser Tyr Gly Gly Gly Cys Asp Asn Gln Ser Asn Ser Gly Met
 115 120 125

Glu Asn Leu Leu Thr Met Ser Gly Gln Met Ser Tyr His Glu Ala Thr
 130 135 140

His His His Tyr Gln Asn His Ser Ser Asn Val Thr Ser Ile Leu Cys
 145 150 155 160

Pro Ser Asp Gln Asn Ser Asn Phe Gln Tyr Gln Gln Gly Ala Ile Thr
 165 170 175

Val Phe Ile Asn Gly Val Pro Thr Glu Val Thr Arg Gly Gly Ile Asp
 180 185 190

Met Lys Ala Thr Phe Gly Glu Asp Leu Val Leu Val His Ser Ser Gly
 195 200 205

Val Pro Leu Pro Thr Asp Glu Phe Gly Phe Leu Met His Ser Leu Gln
 210 215 220

His Gly Glu Ala Tyr Phe Leu Val Pro Arg Gln Thr
 225 230 235

<210> 439 <211> 1020 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(1020) <223> G2657

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 48
 Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro
 1 5 10 15
 ttc cat gct aga gat ttc caa tta cat ctt caa caa caa caa caa cat
 96
 Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Gln His
 20 25 30
 caa caa caa cat caa caa caa caa caa caa cag ttc ttt ctc cac cat
 144
 Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Phe Phe Leu His His
 35 40 45
 cat cag caa cca caa aga aac ctt gat caa gat cac gag cag caa gga
 192
 His Gln Gln Pro Gln Arg Asn Leu Asp Gln Asp His Glu Gln Gln Gly
 50 55 60
 ggg tca ata ttg aat aga tct atc aag atg gat cgc gaa gag aca agc
 240
 Gly Ser Ile Leu Asn Arg Ser Ile Lys Met Asp Arg Glu Glu Thr Ser
 65 70 75 80
 gat aac atg gac aac atc gct aat acc aac agc ggt agc gaa ggt aaa
 288
 Asp Asn Met Asp Asn Ile Ala Asn Thr Asn Ser Gly Ser Glu Gly Lys
 85 90 95

gag atg agt tta cac gga gga gaa gga gga agc ggt ggt gga gga agt
 336
 Glu Met Ser Leu His Gly Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser
 100 105 110

gga gaa cag atg aca aga agg cca aga gga aga cca gca gga tcc aag
 384
 Gly Glu Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
 115 120 125

aac aaa cct aaa gct cca ata atc ata aca aga gac agc gca aac gcg
 432
 Asn Lys Pro Lys Ala Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala
 130 135 140

ctt cga act cac gtc atg gag ata gga gac gga tgt gac ata gtt gac
 480
 Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Ile Val Asp
 145 150 155 160

tgt atg gct acg ttc gct aga cgc cgc caa aga ggc gtt tgc gtt atg
 528
 Cys Met Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met
 165 170 175

agc ggt aca gga agc gtt act aac gtc act ata cgt cag cct gga tcg
 576
 Ser Gly Thr Gly Ser Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser
 180 185 190

cca cct ggc tcg gtg gtt agc ctt cac ggc cgg ttt gaa atc ctc tct
 624
 Pro Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile Leu Ser
 195 200 205

ctt tcg gga tct ttc ttg cct ccg cct gcg ccg cct gca gcc acc gga
 672
 Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala Thr Gly
 210 215 220

cta agc gtt tac cta gcc gga gga caa ggg cag gtc gtt gga ggt agt
 720
 Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser
 225 230 235 240

gtg gtg gga cct ttg ttg tgt tcg ggt cct gtg gtg gtt atg gcg gct
 768
 Val Val Gly Pro Leu Leu Cys Ser Gly Pro Val Val Val Met Ala Ala
 245 250 255

tct ttt agc aat gcg gcg tac gaa agg ctg cct ttg gaa gaa gat gag
 816
 Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu
 260 265 270

atg cag acg cca gtt caa gga ggc ggt gga gga gga gga ggt ggt ggt
 864
 Met Gln Thr Pro Val Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 275 280 285

gga atg gga tct ccc ccg atg atg gga`cag caa caa gct atg gca gct
 912
 Gly Met Gly Ser Pro Pro Met Met Gly Gln Gln Gln Ala Met Ala Ala
 290 295 300
 atg gcg gcg gct caa gga cta cca ccg aat ctt ctt ggt tcg gtt cag
 960
 Met Ala Ala Ala Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln
 305 310 315 320
 ttg cca ccg cca caa cag aat gat cag cag tat tgg tct acg ggt cgg
 1008
 Leu Pro Pro Pro Gln Gln Asn Asp Gln Gln Tyr Trp Ser Thr Gly Arg
 325 330 335
 cca ccg tat tga
 1020
 Pro Pro Tyr

<210> 440 <211> 339 <212> PRT <213> Arabidopsis thaliana <400>
 440

Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro
 1 5 10 15

Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln His
 20 25 30

Gln Gln Gln His Gln Gln Gln Gln Gln Gln Phe Phe Leu His His
 35 40 45

His Gln Gln Pro Gln Arg Asn Leu Asp Gln Asp His Glu Gln Gln Gly
 50 55 60

Gly Ser Ile Leu Asn Arg Ser Ile Lys Met Asp Arg Glu Glu Thr Ser
 65 70 75 80

Asp Asn Met Asp Asn Ile Ala Asn Thr Asn Ser Gly Ser Glu Gly Lys
 85 90 95

Glu Met Ser Leu His Gly Gly Glu Gly Gly Ser Gly Gly Gly Ser
 100 105 110

Gly Glu Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
 115 120 125

Asn Lys Pro Lys Ala Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala
 130 135 140

Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Ile Val Asp

145 150 155 160

Cys Met Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met
165 170 175

Ser Gly Thr Gly Ser Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser
180 185 190

Pro Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile Leu Ser
195 200 205

Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala Thr Gly
210 215 220

Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser
225 230 235 240

Val Val Gly Pro Leu Leu Cys Ser Gly Pro Val Val Val Met Ala Ala
245 250 255

Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu
260 265 270

Met Gln Thr Pro Val Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly
275 280 285

Gly Met Gly Ser Pro Pro Met Met Gly Gln Gln Gln Ala Met Ala Ala
290 295 300

Met Ala Ala Ala Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln
305 310 315 320

Leu Pro Pro Pro Gln Gln Asn Asp Gln Gln Tyr Trp Ser Thr Gly Arg
325 330 335

Pro Pro Tyr

<210> 441 <211> 880 <212> DNA <213> Arabidopsis thaliana <220>
<221> CDS <222> (188)..(880) <223> G2659

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60

cactctaagc ttattttcgt ataaattata gtatagtcac attcttttag gacagaaccc
120

accgaaagaa agctccaaac ccaacaaaaa gggaggcggc ggagaagcaa acaacagcaa
180

caaaaaa atg cag cca gag gtt tca gat caa ata ttt tat gcc ttc ctc
229

Met Gln Pro Glu Val Ser Asp Gln Ile Phe Tyr Ala Phe Leu
1 5 10

acc gga gga tta tgt gcc tcg tct act tcc acc acc gtg acg tcg tcg
277

Thr Gly Gly Leu Cys Ala Ser Ser Thr Ser Thr Thr Val Thr Ser Ser
15 20 25 30

tct gac cct ttt gcc acg gtt tat gaa gac aaa gct ctt gct tct ctg
325

Ser Asp Pro Phe Ala Thr Val Tyr Glu Asp Lys Ala Leu Ala Ser Leu
35 40 45

agg aac cat aaa gag gct gag cga aag aga aga gca aga atc aat tcc
373

Arg Asn His Lys Glu Ala Glu Arg Lys Arg Arg Ala Arg Ile Asn Ser
50 55 60

cat ctc aac aag ctc cgc aag tta ctc tct tgt aac tcc aag aca gac
421

His Leu Asn Lys Leu Arg Lys Leu Leu Ser Cys Asn Ser Lys Thr Asp
65 70 75

aaa tcc aca cta cta gca aaa gtg gtt caa cga gtc aaa gaa cta aaa
469

Lys Ser Thr Leu Leu Ala Lys Val Val Gln Arg Val Lys Glu Leu Lys
80 85 90

caa caa acc cta gaa atc acc gac gaa aca ata ccg tcg gag act gac
517

Gln Gln Thr Leu Glu Ile Thr Asp Glu Thr Ile Pro Ser Glu Thr Asp
95 100 105 110

gaa atc agt gta ctc aac att gag gac tgt tcc aga ggc gac gat cga
565

Glu Ile Ser Val Leu Asn Ile Glu Asp Cys Ser Arg Gly Asp Asp Arg
115 120 125

cgg ata atc ttt aag gta tcg ttt tgc tgc gag gac cgg cca gag ctc
613

Arg Ile Ile Phe Lys Val Ser Phe Cys Cys Glu Asp Arg Pro Glu Leu
130 135 140

ttg aaa gat ctc atg gag aca ctc aaa tct ctt cag atg gaa act ctc
661

Leu Lys Asp Leu Met Glu Thr Leu Lys Ser Leu Gln Met Glu Thr Leu
145 150 155

ttt gcc gac atg aca aca gtc ggt ggt cga aca aga aac gtt ctc gtt
709

Phe Ala Asp Met Thr Thr Val Gly Gly Arg Thr Arg Asn Val Leu Val
160 165 170

gtg gcc gct gac aaa gag cat cac ggc gtc cag tcg gtg aat ttt cta
757

Val Ala Ala Asp Lys Glu His His Gly Val Gln Ser Val Asn Phe Leu

175 180 185 190
 cag aac gca ctc aag tct tta ctc gaa cgg tca agc aag tcg gtg atg
 805
 Gln Asn Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Val Met
 195 200 205
 gtg gga cat ggt ggt ggt ggt ggg gaa gaa agg tta aaa cga cgt cgt
 853
 Val Gly His Gly Gly Gly Gly Gly Glu Glu Arg Leu Lys Arg Arg Arg
 210 215 220
 gcg ctg gat cac atc ata atg gtc tga
 880
 Ala Leu Asp His Ile Ile Met Val
 225 230

 <210> 442 <211> 230 <212> PRT <213> Arabidopsis thaliana <400>
 442
 Met Gln Pro Glu Val Ser Asp Gln Ile Phe Tyr Ala Phe Leu Thr Gly
 1 5 10 15

 Gly Leu Cys Ala Ser Ser Thr Ser Thr Thr Val Thr Ser Ser Ser Asp
 20 25 30

 Pro Phe Ala Thr Val Tyr Glu Asp Lys Ala Leu Ala Ser Leu Arg Asn
 35 40 45

 His Lys Glu Ala Glu Arg Lys Arg Arg Ala Arg Ile Asn Ser His Leu
 50 55 60

 Asn Lys Leu Arg Lys Leu Leu Ser Cys Asn Ser Lys Thr Asp Lys Ser
 65 70 75 80

 Thr Leu Leu Ala Lys Val Val Gln Arg Val Lys Glu Leu Lys Gln Gln
 85 90 95

 Thr Leu Glu Ile Thr Asp Glu Thr Ile Pro Ser Glu Thr Asp Glu Ile
 100 105 110

 Ser Val Leu Asn Ile Glu Asp Cys Ser Arg Gly Asp Asp Arg Arg Ile
 115 120 125

 Ile Phe Lys Val Ser Phe Cys Cys Glu Asp Arg Pro Glu Leu Leu Lys
 130 135 140

 Asp Leu Met Glu Thr Leu Lys Ser Leu Gln Met Glu Thr Leu Phe Ala
 145 150 155 160

Asp Met Thr Thr Val Gly Gly Arg Thr Arg Asn Val Leu Val Val Ala
 165 170 175

Ala Asp Lys Glu His His Gly Val Gln Ser Val Asn Phe Leu Gln Asn
 180 185 190

Ala Leu Lys Ser Leu Leu Glu Arg Ser Ser Lys Ser Val Met Val Gly
 195 200 205

His Gly Gly Gly Gly Gly Glu Glu Arg Leu Lys Arg Arg Arg Ala Leu
 210 215 220

Asp His Ile Ile Met Val
 225 230

<210> 443 <211> 866 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (46)..(837) <223> G2701

<400> 443
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 57

Met Glu Thr Leu
 1

cat tca ttc tct cac cta cct atc tct gac cac cgg ttc gtt gtt caa
 105

His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg Phe Val Val Gln
 5 10 15 20

gag atg gtg agc tta cac agc tcg agt agc ggt agc tgg act aaa gaa
 153

Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser Trp Thr Lys Glu
 25 30 35

gag aac aag atg ttc gaa cga gct ctt gcg ata tac gct gaa gac tcg
 201

Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr Ala Glu Asp Ser
 40 45 50

cct gat cgc tgg ttt aaa gtt gct tcc atg atc cct gga aag act gtt
 249

Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro Gly Lys Thr Val
 55 60 65

ttt gat gtt atg aag caa tat agt aag ctt gaa gaa gac gtt ttc gat
 297

Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu Asp Val Phe Asp
 70 75 80

att gaa gca gga cgt gtt ccc att cct ggt tat cct gca gct tct tct
 345

Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro Ala Ala Ser Ser
 85 90 95 100

ccc ttg ggg ttt gac acg gac atg tgt cgt aaa cgg cct agt gga gct
 393

Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg Pro Ser Gly Ala
 105 110 115
 aga gga tct gat caa gat cga aag aaa gga gtc cct tgg aca gag gaa
 441
 Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro Trp Thr Glu Glu
 120 125 130
 gaa cac agg aga ttc ttg tta ggc ctt ctc aag tac ggt aaa gga gat
 489
 Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly Lys Gly Asp
 135 140 145
 tgg aga aac ata tcg aga aac ttc gtg gtg tca aag acg cca acg caa
 537
 Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys Thr Pro Thr Gln
 150 155 160
 gtg gcg agc cac gcc caa aag tat tac cag aga cag ctc tcc gga gcc
 585
 Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu Ser Gly Ala
 165 170 175 180
 aag gac aaa cgc agg cca agt atc cat gac atc aca acc ggc aat ctt
 633
 Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr Gly Asn Leu
 185 190 195
 ctc aat gcc aat ctc aac cgt tcc ttt tcc gat cat aga gat att ctc
 681
 Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His Arg Asp Ile Leu
 200 205 210
 cct gat tta ggg ttt atc gat aag gat gat acg gag gag gga gta ata
 729
 Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu Glu Gly Val Ile
 215 220 225
 ttt atg ggt cag aat ctc tct tca gaa aat ctg ttt tct cca tca cca
 777
 Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe Ser Pro Ser Pro
 230 235 240
 act tca ttc gaa gct gcc att aac ttc gcc gga gaa aat gtc ttc agt
 825
 Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu Asn Val Phe Ser
 245 250 255 260
 gcc gga gct taa ggcaacatag aatccccaaa ctgagcggc
 866
 Ala Gly Ala

<210> 444 <211> 263 <212> PRT <213> Arabidopsis thaliana <400>
 444

Met Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg
 1 5 10 15

Phe Val Val Gln Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser
 20 25 30

Trp Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr
 35 40 45

Ala Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro
 50 55 60

Gly Lys Thr Val Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu
 65 70 75 80

Asp Val Phe Asp Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro
 85 90 95

Ala Ala Ser Ser Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg
 100 105 110

Pro Ser Gly Ala Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro
 115 120 125

Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr
 130 135 140

Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys
 145 150 155 160

Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln
 165 170 175

Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr
 180 185 190

Thr Gly Asn Leu Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His
 195 200 205

Arg Asp Ile Leu Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu
 210 215 220

Glu Gly Val Ile Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe
 225 230 235 240

Ser Pro Ser Pro Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu
 245 250 255

Asn Val Phe Ser Ala Gly Ala

260

<210> 445 <211> 972 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(972) <223> G2741

<400> 445
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 48
 Met Gly Glu Glu Val Gln Met Ser Asp Tyr Asp Val Ser Gly Asp Gly
 1 5 10 15
 gat agg gtt tct gaa tgg gag atg gga tta cca agc gac gaa gat cta
 96
 Asp Arg Val Ser Glu Trp Glu Met Gly Leu Pro Ser Asp Glu Asp Leu
 20 25 30
 gca tct ctt tct tac tct ctg att cca ccg aat ttg gcg atg gcg ttt
 144
 Ala Ser Leu Ser Tyr Ser Leu Ile Pro Pro Asn Leu Ala Met Ala Phe
 35 40 45
 agt atc aca ccg gag aga agc cgt acg att cag gat gtg aat cgt gca
 192
 Ser Ile Thr Pro Glu Arg Ser Arg Thr Ile Gln Asp Val Asn Arg Ala
 50 55 60
 tcg gag acg acg ctc tcg tcg cta cgt ggt gga tct tca ggt cca aat
 240
 Ser Glu Thr Thr Leu Ser Ser Leu Arg Gly Gly Ser Ser Gly Pro Asn
 65 70 75 80
 acc tcg tcg tcg aat aat aac gtg gag gag gaa gat cga gtt gga tct
 288
 Thr Ser Ser Ser Asn Asn Asn Val Glu Glu Glu Asp Arg Val Gly Ser
 85 90 95
 agc agt cct gga tcg gat tcg aag aag caa aag aca tca aac ggt gat
 336
 Ser Ser Pro Gly Ser Asp Ser Lys Lys Gln Lys Thr Ser Asn Gly Asp
 100 105 110
 gga gat gac ggt ggc ggt gtg gat ccg gat tcg gcg atg gcg gcg gaa
 384
 Gly Asp Asp Gly Gly Gly Val Asp Pro Asp Ser Ala Met Ala Ala Glu
 115 120 125
 gaa gga gat tca gga act gaa gat cta tct ggg aaa aca ctt aaa cga
 432
 Glu Gly Asp Ser Gly Thr Glu Asp Leu Ser Gly Lys Thr Leu Lys Arg
 130 135 140
 ccg cgt tta gtg tgg aca ccg cag cta cac aag aga ttc gtt gac gtt
 480
 Pro Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val
 145 150 155 160
 gta gct cac tta ggg atc aaa aac gct gtt ccg aag acg att atg cag
 528
 Val Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln
 165 170 175

ctg atg aac gtt gaa gga tta act cgt gag aac gtt gcg tct cat ctt
 576
 Leu Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu
 180 185 190
 caa aag tat agg ctt tac ctc aaa agg atg cag gga ttg act aat gaa
 624
 Gln Lys Tyr Arg Leu Tyr Leu Lys Arg Met Gln Gly Leu Thr Asn Glu
 195 200 205
 ggt ccc tct gct tcg gat aag ctc ttc tct tca aca cct gtt cct cca
 672
 Gly Pro Ser Ala Ser Asp Lys Leu Phe Ser Ser Thr Pro Val Pro Pro
 210 215 220
 cag agc ttc caa gat atc ggt ggc ggt ggc ggt agc agc ggt aat gtt
 720
 Gln Ser Phe Gln Asp Ile Gly Gly Gly Gly Gly Ser Ser Gly Asn Val
 225 230 235 240
 gga gtg ccg att ccg ggg gcg tat gga acg caa cag atg atg cag atg
 768
 Gly Val Pro Ile Pro Gly Ala Tyr Gly Thr Gln Gln Met Met Gln Met
 245 250 255
 cca gtt tat gca cat cat atg ggt atg caa gga tat cat cat caa aat
 816
 Pro Val Tyr Ala His His Met Gly Met Gln Gly Tyr His His Gln Asn
 260 265 270
 cat aat cat gat cct tat cat cag aat cat cgt cat cat cat gga gct
 864
 His Asn His Asp Pro Tyr His Gln Asn His Arg His His His Gly Ala
 275 280 285
 ggt gga aat ggt gcg ttt gag tca aat cct tat atg atg cag cag aat
 912
 Gly Gly Asn Gly Ala Phe Glu Ser Asn Pro Tyr Met Met Gln Gln Asn
 290 295 300
 aag ttt gga tcc atg gct tct tat cct tct gtt gga ggt gga agc gca
 960
 Lys Phe Gly Ser Met Ala Ser Tyr Pro Ser Val Gly Gly Gly Ser Ala
 305 310 315 320
 aat gag aat taa
 972
 Asn Glu Asn

<210> 446 <211> 323 <212> PRT <213> Arabidopsis thaliana <400>
 446

Met Gly Glu Glu Val Gln Met Ser Asp Tyr Asp Val Ser Gly Asp Gly
 1 5 10 15

Asp Arg Val Ser Glu Trp Glu Met Gly Leu Pro Ser Asp Glu Asp Leu
 20 25 30

Ala Ser Leu Ser Tyr Ser Leu Ile Pro Pro Asn Leu Ala Met Ala Phe
 35 40 45
 Ser Ile Thr Pro Glu Arg Ser Arg Thr Ile Gln Asp Val Asn Arg Ala
 50 55 60
 Ser Glu Thr Thr Leu Ser Ser Leu Arg Gly Gly Ser Ser Gly Pro Asn
 65 70 75 80
 Thr Ser Ser Ser Asn Asn Asn Val Glu Glu Glu Asp Arg Val Gly Ser
 85 90 95
 Ser Ser Pro Gly Ser Asp Ser Lys Lys Gln Lys Thr Ser Asn Gly Asp
 100 105 110
 Gly Asp Asp Gly Gly Gly Val Asp Pro Asp Ser Ala Met Ala Ala Glu
 115 120 125
 Glu Gly Asp Ser Gly Thr Glu Asp Leu Ser Gly Lys Thr Leu Lys Arg
 130 135 140
 Pro Arg Leu Val Trp Thr Pro Gln Leu His Lys Arg Phe Val Asp Val
 145 150 155 160
 Val Ala His Leu Gly Ile Lys Asn Ala Val Pro Lys Thr Ile Met Gln
 165 170 175
 Leu Met Asn Val Glu Gly Leu Thr Arg Glu Asn Val Ala Ser His Leu
 180 185 190
 Gln Lys Tyr Arg Leu Tyr Leu Lys Arg Met Gln Gly Leu Thr Asn Glu
 195 200 205
 Gly Pro Ser Ala Ser Asp Lys Leu Phe Ser Ser Thr Pro Val Pro Pro
 210 215 220
 Gln Ser Phe Gln Asp Ile Gly Gly Gly Gly Gly Ser Ser Gly Asn Val
 225 230 235 240
 Gly Val Pro Ile Pro Gly Ala Tyr Gly Thr Gln Gln Met Met Gln Met
 245 250 255
 Pro Val Tyr Ala His His Met Gly Met Gln Gly Tyr His His Gln Asn
 260 265 270

His Asn His Asp Pro Tyr His Gln Asn His Arg His His His Gly Ala
 275 280 285

Gly Gly Asn Gly Ala Phe Glu Ser Asn Pro Tyr Met Met Gln Gln Asn
 290 295 300

Lys Phe Gly Ser Met Ala Ser Tyr Pro Ser Val Gly Gly Gly Ser Ala
 305 310 315 320

Asn Glu Asn

<210> 447 <211> 1362 <212> DNA <213> Arabidopsis thaliana <220>
 <221> CDS <222> (1)..(1362) <223> G2781

<400> 447
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 48
 Met Asp Gln Lys Ser Lys Thr Ile Gly Glu Gln Trp Trp Arg Ser Asn
 1 5 10 15

cca acg ttt aaa ccg cct gaa acg cca tta gat tct atg gag ttt ttg
 96
 Pro Thr Phe Lys Pro Pro Glu Thr Pro Leu Asp Ser Met Glu Phe Leu
 20 25 30

tca cgt act tgg agt gct tcc gct act gaa gtt tca aga gct gtc gtc
 144
 Ser Arg Thr Trp Ser Ala Ser Ala Thr Glu Val Ser Arg Ala Val Val
 35 40 45

gcg tct cca ccg act tct caa ccg ccg caa atg cgt ttc tcg gag atc
 192
 Ala Ser Pro Pro Thr Ser Gln Pro Pro Gln Met Arg Phe Ser Glu Ile
 50 55 60

caa aac ggt tct tct gac gtc act ttg gtg ccg gaa gat gaa gaa aac
 240
 Gln Asn Gly Ser Ser Asp Val Thr Leu Val Pro Glu Asp Glu Glu Asn
 65 70 75 80

ggc atc gtt ctt gga aat act ttt tct ttt gct tct tca gaa act tct
 288
 Gly Ile Val Leu Gly Asn Thr Phe Ser Phe Ala Ser Ser Glu Thr Ser
 85 90 95

tta atg gtc atg gaa cgt atc atg gct cag tca ccg gag att tca tcg
 336
 Leu Met Val Met Glu Arg Ile Met Ala Gln Ser Pro Glu Ile Ser Ser
 100 105 110

cca cga aca tca ggg aga ctt tct cat agc tca ttc acc gac agt cct
 384
 Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Phe Thr Asp Ser Pro
 115 120 125

ccg atc tct ccc tcc gac atc gac gac ttt aag caa ttc tac cgt 'gtg
 432
 Pro Ile Ser Pro Ser Asp Ile Asp Asp Phe Lys Gln Phe Tyr Arg Val
 130 135 140

agc cct tcc ttt aac ggc cac ata cgt ggt tca tca gcc att ccc ggc
 480
 Ser Pro Ser Phe Asn Gly His Ile Arg Gly Ser Ser Ala Ile Pro Gly
 145 150 155 160

acc gcc gga ggg tct aaa act gtt ggt cgt tgg cta aag gac cgg cga
 528
 Thr Ala Gly Gly Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg
 165 170 175

gag aag aag aga gaa gag acg cgt gca caa aat gca cag ctt cac gcg
 576
 Glu Lys Lys Arg Glu Glu Thr Arg Ala Gln Asn Ala Gln Leu His Ala
 180 185 190

gct gta tct gta gct gga gtg gct gcc gcg gtg gct gct atc gct gca
 624
 Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala
 195 200 205

gcc act gcc tct cag tcg agt tct gga act gac gag caa gtg gcc aaa
 672
 Ala Thr Ala Ser Gln Ser Ser Ser Gly Thr Asp Glu Gln Val Ala Lys
 210 215 220

aat gac tcc gcg gtg gct tct gcc gcg act ttg gtg gcg gcg aag tgt
 720
 Asn Asp Ser Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Lys Cys
 225 230 235 240

gtg gaa gct gca gag att atg gga gct gat cgt gag cac ttg gcc tcc
 768
 Val Glu Ala Ala Glu Ile Met Gly Ala Asp Arg Glu His Leu Ala Ser
 245 250 255

gtt gtt agt tct gcg gtt aac gtt cgt tct gcc gga gat atc atg act
 816
 Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr
 260 265 270

ttg acc gcc gct gct gcc aca gct ttg aga gga gct gca caa tta aag
 864
 Leu Thr Ala Ala Ala Ala Thr Ala Leu Arg Gly Ala Ala Gln Leu Lys
 275 280 285

gca aga gca ttg aag gag gta tgg aac att gcg gct gtg att cct gta
 912
 Ala Arg Ala Leu Lys Glu Val Trp Asn Ile Ala Ala Val Ile Pro Val
 290 295 300

gat aag ggt aca cca aaa ggc ggt ggt ggt ggt tat aga ggt ggc gag
 960
 Asp Lys Gly Thr Pro Lys Gly Gly Gly Gly Gly Tyr Arg Gly Gly Glu
 305 310 315 320

tta gcc cct gta gat aat ttt ctt ggg att tgc agt aaa gaa ttg cta
1008

Leu Ala Pro Val Asp Asn Phe Leu Gly Ile Cys Ser Lys Glu Leu Leu
325 330 335

gct aaa ggt tgc gaa ttg ctt aaa cgc acc cgc aaa ggt gat ctt cat
1056

Ala Lys Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His
340 345 350

tgg aaa gtt gtt tcg atc tac att aat aga aca aag cag gta ata ttg
1104

Trp Lys Val Val Ser Ile Tyr Ile Asn Arg Thr Lys Gln Val Ile Leu
355 360 365

aag act aag agc aaa cat gtt gct ggg acc atc aca aag aag aaa aag
1152

Lys Thr Lys Ser Lys His Val Ala Gly Thr Ile Thr Lys Lys Lys Lys
370 375 380

aat gtg gtg gtg gga ttg gtt aag gga tta ccg gcg tgg cct ggc cgg
1200

Asn Val Val Val Gly Leu Val Lys Gly Leu Pro Ala Trp Pro Gly Arg
385 390 395 400

gaa atg ctc gag ggt gga gag aat ttg agg tat ttc ggg ctg aag acg
1248

Glu Met Leu Glu Gly Gly Glu Asn Leu Arg Tyr Phe Gly Leu Lys Thr
405 410 415

gtg gag aaa aga gtg att gaa ttc gag tgc aaa agc caa agg gaa tat
1296

Val Glu Lys Arg Val Ile Glu Phe Glu Cys Lys Ser Gln Arg Glu Tyr
420 425 430

gat ctt tgg aca caa ggt gtt tcc atg ctt ctt tcc att gct tct gat
1344

Asp Leu Trp Thr Gln Gly Val Ser Met Leu Leu Ser Ile Ala Ser Asp
435 440 445

agg aaa cat aaa tgt tga
1362

Arg Lys His Lys Cys
450

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20 25 30

Ser Arg Thr Trp Ser Ala Ser Ala Thr Glu Val Ser Arg Ala Val Val
35 40 45

Ala Ser Pro Pro Thr Ser Gln Pro Pro Gln Met Arg Phe Ser Glu Ile
50 55 60

Gln Asn Gly Ser Ser Asp Val Thr Leu Val Pro Glu Asp Glu Glu Asn
65 70 75 80

Gly Ile Val Leu Gly Asn Thr Phe Ser Phe Ala Ser Ser Glu Thr Ser
85 90 95

Leu Met Val Met Glu Arg Ile Met Ala Gln Ser Pro Glu Ile Ser Ser
100 105 110

Pro Arg Thr Ser Gly Arg Leu Ser His Ser Ser Phe Thr Asp Ser Pro
115 120 125

Pro Ile Ser Pro Ser Asp Ile Asp Asp Phe Lys Gln Phe Tyr Arg Val
130 135 140

Ser Pro Ser Phe Asn Gly His Ile Arg Gly Ser Ser Ala Ile Pro Gly
145 150 155 160

Thr Ala Gly Gly Ser Lys Thr Val Gly Arg Trp Leu Lys Asp Arg Arg
165 170 175

Glu Lys Lys Arg Glu Glu Thr Arg Ala Gln Asn Ala Gln Leu His Ala
180 185 190

Ala Val Ser Val Ala Gly Val Ala Ala Ala Val Ala Ala Ile Ala Ala
195 200 205

Ala Thr Ala Ser Gln Ser Ser Ser Gly Thr Asp Glu Gln Val Ala Lys
210 215 220

Asn Asp Ser Ala Val Ala Ser Ala Ala Thr Leu Val Ala Ala Lys Cys
225 230 235 240

Val Glu Ala Ala Glu Ile Met Gly Ala Asp Arg Glu His Leu Ala Ser
245 250 255

Val Val Ser Ser Ala Val Asn Val Arg Ser Ala Gly Asp Ile Met Thr
260 265 270

Leu Thr Ala Ala Ala Ala Thr Ala Leu Arg Gly Ala Ala Gln Leu Lys
275 280 285

Ala Arg Ala Leu Lys Glu Val Trp Asn Ile Ala Ala Val Ile Pro Val

290 295 300
 Asp Lys Gly Thr Pro Lys Gly Gly Gly Gly Gly Tyr Arg Gly Gly Glu
 305 310 315 320
 Leu Ala Pro Val Asp Asn Phe Leu Gly Ile Cys Ser Lys Glu Leu Leu
 325 330 335
 Ala Lys Gly Cys Glu Leu Leu Lys Arg Thr Arg Lys Gly Asp Leu His
 340 345 350
 Trp Lys Val Val Ser Ile Tyr Ile Asn Arg Thr Lys Gln Val Ile Leu
 355 360 365
 Lys Thr Lys Ser Lys His Val Ala Gly Thr Ile Thr Lys Lys Lys Lys
 370 375 380
 Asn Val Val Val Gly Leu Val Lys Gly Leu Pro Ala Trp Pro Gly Arg
 385 390 395 400
 Glu Met Leu Glu Gly Gly Glu Asn Leu Arg Tyr Phe Gly Leu Lys Thr
 405 410 415
 Val Glu Lys Arg Val Ile Glu Phe Glu Cys Lys Ser Gln Arg Glu Tyr
 420 425 430
 Asp Leu Trp Thr Gln Gly Val Ser Met Leu Leu Ser Ile Ala Ser Asp
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 Arg Lys His Lys Cys
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 96
 Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly Gly
 20 25 30
 gag aaa cga gtt ttc cga tgc aag act tgt ctt aaa gag ttt tcg tcg
 144
 Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser
 35 40 45

ttt caa gct ttg gga ggt cat cgt gca agc cac aag aaa ctc att aac
 192
 Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Leu Ile Asn
 50 55 60
 agt agc gat cca tca ctt ctt gga tcc ttg tct aac aag aaa act aaa
 240
 Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys
 65 70 75 80
 acg gcg acg tct cat cct tgt ccg ata tgt ggc gtg gag ttt ccg atg
 288
 Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met
 85 90 95
 ggg caa gct ctt ggt ggt cac atg agg aga cat agg agt gag aaa gcc
 336
 Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala
 100 105 110
 tca cca ggc acg ttg gtt aca cgt tct ttt tta ccg gag acg acg acg
 384
 Ser Pro Gly Thr Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
 115 120 125
 gtg acg act ttg aaa aaa tcg agt agt ggg aag aga gtg gct tgt ttg
 432
 Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu
 130 135 140
 gac tta gat tcg atg gag agt tta gtc aat tgg aag ttg gag ttg gga
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 Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu Leu Gly
 145 150 155 160
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 495
 Arg Thr Ile Ser

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 20 25 30

Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser
 35 40 45

Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Leu Ile Asn
 50 55 60

Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys
65 70 75 80

Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met
85 90 95

Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala
100 105 110

Ser Pro Gly Thr Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
115 120 125

Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu
130 135 140

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Arg Thr Ile Ser

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120

aagattcgac ctttattaga tattaacgac tctggatttt tgggtttttg gagttggatc
180

cac atg ggt tct tat ccg gat gga ttc cct gga tcc atg gac gag ttg
228

Met Gly Ser Tyr Pro Asp Gly Phe Pro Gly Ser Met Asp Glu Leu
1 5 10 15

gat ttc aat aag gac ttt gat ttg cct ccc tcc tca aac caa acc tta
276

Asp Phe Asn Lys Asp Phe Asp Leu Pro Pro Ser Ser Asn Gln Thr Leu
20 25 30

ggt tta gct aat ggg ttc tat tta gat gac tta gat ttc tca tcc ttg
324

Gly Leu Ala Asn Gly Phe Tyr Leu Asp Asp Leu Asp Phe Ser Ser Leu
35 40 45

gat cct cca gag gca tat ccc tcc cag aac aac aac aac aac atc
372

Asp Pro Pro Glu Ala Tyr Pro Ser Gln Asn Asn Asn Asn Asn Asn Ile
50 55 60

aac aac aaa gct gta gca gga gat ctg tta tca tct tca tct gat gac
 420
 Asn Asn Lys Ala Val Ala Gly Asp Leu Leu Ser Ser Ser Ser Asp Asp
 65 70 75
 gct gat ttc tct gat tct gtt ttg aag tat ata agc caa gtt ctt atg
 468
 Ala Asp Phe Ser Asp Ser Val Leu Lys Tyr Ile Ser Gln Val Leu Met
 80 85 90 95
 gaa gag gat atg gaa gag aag cct tgt atg ttt cat gac gct ttg gct
 516
 Glu Glu Asp Met Glu Glu Lys Pro Cys Met Phe His Asp Ala Leu Ala
 100 105 110
 ctt caa gct gct gag aaa tct ctc tat gag gct ctt ggt gag aaa tac
 564
 Leu Gln Ala Ala Glu Lys Ser Leu Tyr Glu Ala Leu Gly Glu Lys Tyr
 115 120 125
 cct tct tcg tct tct gct tct tct gtg gat cat cct gag aga ttg gct
 612
 Pro Ser Ser Ser Ser Ala Ser Ser Val Asp His Pro Glu Arg Leu Ala
 130 135 140
 agt gat agc cct gac ggt tct tgt tca ggt ggt gct ttt agt gat tac
 660
 Ser Asp Ser Pro Asp Gly Ser Cys Ser Gly Gly Ala Phe Ser Asp Tyr
 145 150 155
 gct agc acc act acc act act tcc tct gat tct cac tgg agt gtt gat
 708
 Ala Ser Thr Thr Thr Thr Thr Ser Ser Asp Ser His Trp Ser Val Asp
 160 165 170 175
 ggt ttg gag aat aga cct tct tgg tta cat aca cct atg ccg agt aat
 756
 Gly Leu Glu Asn Arg Pro Ser Trp Leu His Thr Pro Met Pro Ser Asn
 180 185 190
 ttt gtt ttc cag tct act tct agg tcc aac agt gtc acc ggt ggt ggt
 804
 Phe Val Phe Gln Ser Thr Ser Arg Ser Asn Ser Val Thr Gly Gly Gly
 195 200 205
 ggt ggt ggt aat agt gcg gtt tac ggt tca ggt ttt ggc gat gat ttg
 852
 Gly Gly Gly Asn Ser Ala Val Tyr Gly Ser Gly Phe Gly Asp Asp Leu
 210 215 220
 gtt tcg aat atg ttt aaa gat gat gaa ttg gct atg cag ttc aag aaa
 900
 Val Ser Asn Met Phe Lys Asp Asp Glu Leu Ala Met Gln Phe Lys Lys
 225 230 235
 ggg gtt gag gaa gct agt aag ttc ctt cct aag tct tct cag ctc ttt
 948
 Gly Val Glu Glu Ala Ser Lys Phe Leu Pro Lys Ser Ser Gln Leu Phe
 240 245 250 255

att gat gtg gat agt tac atc cct atg aat tct ggt tcc aag gaa aat
 996
 Ile Asp Val Asp Ser Tyr Ile Pro Met Asn Ser Gly Ser Lys Glu Asn
 260 265 270

ggt tct gag gtt ttt gtt aag acg gag aag aaa gat gag aca gag cat
 1044
 Gly Ser Glu Val Phe Val Lys Thr Glu Lys Lys Asp Glu Thr Glu His
 275 280 285

cat cat cat cat agc tat gct cct cct ccc aac aga tta act ggt aag
 1092
 His His His His Ser Tyr Ala Pro Pro Pro Asn Arg Leu Thr Gly Lys
 290 295 300

aaa agc cat tgg cgc gac gaa gat gaa gat ttc gtt gaa gaa aga agt
 1140
 Lys Ser His Trp Arg Asp Glu Asp Glu Asp Phe Val Glu Glu Arg Ser
 305 310 315

aac aag caa tca gct gtt tat gtt gag gaa agc gag ctt tct gaa atg
 1188
 Asn Lys Gln Ser Ala Val Tyr Val Glu Glu Ser Glu Leu Ser Glu Met
 320 325 330 335

ttt gat aag atc ttg gta tgt ggc cct ggg aaa cct gta tgc att ctt
 1236
 Phe Asp Lys Ile Leu Val Cys Gly Pro Gly Lys Pro Val Cys Ile Leu
 340 345 350

aac cag aac ttt cct aca gaa tcc gct aaa gtc gtg acc gca cag tca
 1284
 Asn Gln Asn Phe Pro Thr Glu Ser Ala Lys Val Val Thr Ala Gln Ser
 355 360 365

aat gga gca aag att cgt ggg aag aaa tca act tct act agt cat agt
 1332
 Asn Gly Ala Lys Ile Arg Gly Lys Lys Ser Thr Ser Thr Ser His Ser
 370 375 380

aac gat tct aag aaa gaa act gct gat ttg agg act ctt ttg gtg tta
 1380
 Asn Asp Ser Lys Lys Glu Thr Ala Asp Leu Arg Thr Leu Leu Val Leu
 385 390 395

tgt gca caa gct gta tca gtg gat gat cgt aga acc gcc aac gaa atg
 1428
 Cys Ala Gln Ala Val Ser Val Asp Asp Arg Arg Thr Ala Asn Glu Met
 400 405 410 415

cta agg cag ata cga gag cat tct tcg cct cta ggc aat ggt tca gag
 1476
 Leu Arg Gln Ile Arg Glu His Ser Ser Pro Leu Gly Asn Gly Ser Glu
 420 425 430

cgg ttg gct cat tat ttt gca aat agt ctt gaa gca cgc tta gct ggg
 1524
 Arg Leu Ala His Tyr Phe Ala Asn Ser Leu Glu Ala Arg Leu Ala Gly
 435 440 445

acc ggt aca cag atc tac acc gct tta tct tcg aag aaa acg tct gca
1572
Thr Gly Thr Gln Ile Tyr Thr Ala Leu Ser Ser Lys Lys Thr Ser Ala
450 455 460

gca gac atg ttg aag gct tac cag aca tac atg tcg gtc tgc cct ttc
1620
Ala Asp Met Leu Lys Ala Tyr Gln Thr Tyr Met Ser Val Cys Pro Phe
465 470 475

aag aaa gct gct atc ata ttt gct aac cac agc atg atg cgt ttc act
1668
Lys Lys Ala Ala Ile Ile Phe Ala Asn His Ser Met Met Arg Phe Thr
480 485 490 495

gca aac gcc aac acg atc cac ata ata gat ttc gga ata tct tac ggt
1716
Ala Asn Ala Asn Thr Ile His Ile Ile Asp Phe Gly Ile Ser Tyr Gly
500 505 510

ttt cag tgg cct gct ctg att cat cgc ctc tcg ctc agc aga cct ggt
1764
Phe Gln Trp Pro Ala Leu Ile His Arg Leu Ser Leu Ser Arg Pro Gly
515 520 525

ggt tcg cct aag ctt cga att acc ggt ata gag ctt cct cag cgc ggt
1812
Gly Ser Pro Lys Leu Arg Ile Thr Gly Ile Glu Leu Pro Gln Arg Gly
530 535 540

ttt aga cca gcg gaa gag ttc agg aga cag gtc atc gct tgg ctc gat
1860
Phe Arg Pro Ala Glu Glu Phe Arg Arg Gln Val Ile Ala Trp Leu Asp
545 550 555

act gtc agc gac aca atg ttc cgt ttg agt aca acg caa ttg ctc aga
1908
Thr Val Ser Asp Thr Met Phe Arg Leu Ser Thr Thr Gln Leu Leu Arg
560 565 570 575

aat ggg gaa acg atc caa gtc gaa gac tta aag ctt cga caa gga gag
1956
Asn Gly Glu Thr Ile Gln Val Glu Asp Leu Lys Leu Arg Gln Gly Glu
580 585 590

tat gtg gtt gtg aac tct ttg ttc cgt ttc agg aac ctt cta gat gag
2004
Tyr Val Val Val Asn Ser Leu Phe Arg Phe Arg Asn Leu Leu Asp Glu
595 600 605

acc gtt ctg gta aac agc ccg aga gat gca gtt ttg aag ctg ata aga
2052
Thr Val Leu Val Asn Ser Pro Arg Asp Ala Val Leu Lys Leu Ile Arg
610 615 620

aaa ata aac ccg aat gtc ttc att cca gcg atc tta agc ggg aat tac
2100
Lys Ile Asn Pro Asn Val Phe Ile Pro Ala Ile Leu Ser Gly Asn Tyr
625 630 635

aac gcg cca ttc ttt gtc acg agg ttc aga gaa gcg ttg ttt cat tac
2148

Asn Ala Pro Phe Phe Val Thr Arg Phe Arg Glu Ala Leu Phe His Tyr
640 645 650 655

tcg gct gtg ttt gat atg tgt gac tcg aag cta gct agg gaa gac gag
2196

Ser Ala Val Phe Asp Met Cys Asp Ser Lys Leu Ala Arg Glu Asp Glu
660 665 670

atg agg ctg atg tat gag aaa gag ttt tat ggg aga gag att gtg aat
2244

Met Arg Leu Met Tyr Glu Lys Glu Phe Tyr Gly Arg Glu Ile Val Asn
675 680 685

gtt gtg gct tgt gaa gga aca gag aga gtg gag aga cca gag aca tat
2292

Val Val Ala Cys Glu Gly Thr Glu Arg Val Glu Arg Pro Glu Thr Tyr
690 695 700

aag cag tgg cag gcg aga ctg atc cga gcc gga ttt aga cag ctt ccg
2340

Lys Gln Trp Gln Ala Arg Leu Ile Arg Ala Gly Phe Arg Gln Leu Pro
705 710 715

ctt gag aag gaa ctg atg cag aat ctg aag ttg aaa atc gaa aac ggg
2388

Leu Glu Lys Glu Leu Met Gln Asn Leu Lys Leu Lys Ile Glu Asn Gly
720 725 730 735

tac gat aaa aac ttc gat gtt gat caa aac ggt aac tgg tta ctt caa
2436

Tyr Asp Lys Asn Phe Asp Val Asp Gln Asn Gly Asn Trp Leu Leu Gln
740 745 750

ggg tgg aaa ggt aga atc gtg tat gct tca tct cta tgg gtt cct tcg
2484

Gly Trp Lys Gly Arg Ile Val Tyr Ala Ser Ser Leu Trp Val Pro Ser
755 760 765

tct tca tag atgttggttc ttacgttcta agcgactggg atttatgtag
2533

Ser Ser

ggcttttctg ttgatagtct ctgcgaaca cgagtggatt aagttcagag ttagggttct
2593

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2653

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2693

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 20 25 30

Leu Ala Asn Gly Phe Tyr Leu Asp Asp Leu Asp Phe Ser Ser Leu Asp
 35 40 45

Pro Pro Glu Ala Tyr Pro Ser Gln Asn Asn Asn Asn Asn Ile Asn
 50 55 60

Asn Lys Ala Val Ala Gly Asp Leu Leu Ser Ser Ser Ser Asp Asp Ala
 65 70 75 80

Asp Phe Ser Asp Ser Val Leu Lys Tyr Ile Ser Gln Val Leu Met Glu
 85 90 95

Glu Asp Met Glu Glu Lys Pro Cys Met Phe His Asp Ala Leu Ala Leu
 100 105 110

Gln Ala Ala Glu Lys Ser Leu Tyr Glu Ala Leu Gly Glu Lys Tyr Pro
 115 120 125

Ser Ser Ser Ser Ala Ser Ser Val Asp His Pro Glu Arg Leu Ala Ser
 130 135 140

Asp Ser Pro Asp Gly Ser Cys Ser Gly Gly Ala Phe Ser Asp Tyr Ala
 145 150 155 160

Ser Thr Thr Thr Thr Thr Ser Ser Asp Ser His Trp Ser Val Asp Gly
 165 170 175

Leu Glu Asn Arg Pro Ser Trp Leu His Thr Pro Met Pro Ser Asn Phe
 180 185 190

Val Phe Gln Ser Thr Ser Arg Ser Asn Ser Val Thr Gly Gly Gly Gly
 195 200 205

Gly Gly Asn Ser Ala Val Tyr Gly Ser Gly Phe Gly Asp Asp Leu Val
 210 215 220

Ser Asn Met Phe Lys Asp Asp Glu Leu Ala Met Gln Phe Lys Lys Gly
 225 230 235 240

Val Glu Glu Ala Ser Lys Phe Leu Pro Lys Ser Ser Gln Leu Phe Ile
 245 250 255

Asp Val Asp Ser Tyr Ile Pro Met Asn Ser Gly Ser Lys Glu Asn Gly
 260 265 270

Ser Glu Val Phe Val Lys Thr Glu Lys Lys Asp Glu Thr Glu His His
 275 280 285

His His His Ser Tyr Ala Pro Pro Pro Asn Arg Leu Thr Gly Lys Lys
 290 295 300

Ser His Trp Arg Asp Glu Asp Glu Asp Phe Val Glu Glu Arg Ser Asn
 305 310 315 320

Lys Gln Ser Ala Val Tyr Val Glu Glu Ser Glu Leu Ser Glu Met Phe
 325 330 335

Asp Lys Ile Leu Val Cys Gly Pro Gly Lys Pro Val Cys Ile Leu Asn
 340 345 350

Gln Asn Phe Pro Thr Glu Ser Ala Lys Val Val Thr Ala Gln Ser Asn
 355 360 365

Gly Ala Lys Ile Arg Gly Lys Lys Ser Thr Ser Thr Ser His Ser Asn
 370 375 380

Asp Ser Lys Lys Glu Thr Ala Asp Leu Arg Thr Leu Leu Val Leu Cys
 385 390 395 400

Ala Gln Ala Val Ser Val Asp Asp Arg Arg Thr Ala Asn Glu Met Leu
 405 410 415

Arg Gln Ile Arg Glu His Ser Ser Pro Leu Gly Asn Gly Ser Glu Arg
 420 425 430

Leu Ala His Tyr Phe Ala Asn Ser Leu Glu Ala Arg Leu Ala Gly Thr
 435 440 445

Gly Thr Gln Ile Tyr Thr Ala Leu Ser Ser Lys Lys Thr Ser Ala Ala
 450 455 460

Asp Met Leu Lys Ala Tyr Gln Thr Tyr Met Ser Val Cys Pro Phe Lys
 465 470 475 480

Lys Ala Ala Ile Ile Phe Ala Asn His Ser Met Met Arg Phe Thr Ala
 485 490 495

Asn Ala Asn Thr Ile His Ile Ile Asp Phe Gly Ile Ser Tyr Gly Phe

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Ser Pro Lys Leu Arg Ile Thr Gly Ile Glu Leu Pro Gln Arg Gly Phe		
530	535	540
Arg Pro Ala Glu Glu Phe Arg Arg Gln Val Ile Ala Trp Leu Asp Thr		
545	550	555 560
Val Ser Asp Thr Met Phe Arg Leu Ser Thr Thr Gln Leu Leu Arg Asn		
565	570	575
Gly Glu Thr Ile Gln Val Glu Asp Leu Lys Leu Arg Gln Gly Glu Tyr		
580	585	590
Val Val Val Asn Ser Leu Phe Arg Phe Arg Asn Leu Leu Asp Glu Thr		
595	600	605
Val Leu Val Asn Ser Pro Arg Asp Ala Val Leu Lys Leu Ile Arg Lys		
610	615	620
Ile Asn Pro Asn Val Phe Ile Pro Ala Ile Leu Ser Gly Asn Tyr Asn		
625	630	635 640
Ala Pro Phe Phe Val Thr Arg Phe Arg Glu Ala Leu Phe His Tyr Ser		
645	650	655
Ala Val Phe Asp Met Cys Asp Ser Lys Leu Ala Arg Glu Asp Glu Met		
660	665	670
Arg Leu Met Tyr Glu Lys Glu Phe Tyr Gly Arg Glu Ile Val Asn Val		
675	680	685
Val Ala Cys Glu Gly Thr Glu Arg Val Glu Arg Pro Glu Thr Tyr Lys		
690	695	700
Gln Trp Gln Ala Arg Leu Ile Arg Ala Gly Phe Arg Gln Leu Pro Leu		
705	710	715 720
Glu Lys Glu Leu Met Gln Asn Leu Lys Leu Lys Ile Glu Asn Gly Tyr		
725	730	735
Asp Lys Asn Phe Asp Val Asp Gln Asn Gly Asn Trp Leu Leu Gln Gly		
740	745	750

Trp Lys Gly Arg Ile Val Tyr Ala Ser Ser Leu Trp Val Pro Ser Ser
 755 760 765

Ser

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 tct tct gat cct ttc ctc tcc tct tca gaa aat ggg gtc acc acc aca
 96
 Ser Ser Asp Pro Phe Leu Ser Ser Ser Glu Asn Gly Val Thr Thr Thr
 20 25 30
 aac aca tcc act cag aag agg aaa aga aga cct gca ggt acc cca gat
 144
 Asn Thr Ser Thr Gln Lys Arg Lys Arg Arg Pro Ala Gly Thr Pro Asp
 35 40 45
 cca gat gca gaa gtt gtg tct tta tca cca aga act ctt ctt gaa tca
 192
 Pro Asp Ala Glu Val Val Ser Leu Ser Pro Arg Thr Leu Leu Glu Ser
 50 55 60
 gac aga tac ata tgt gag atc tgt aac caa ggg ttt caa aga gac cag
 240
 Asp Arg Tyr Ile Cys Glu Ile Cys Asn Gln Gly Phe Gln Arg Asp Gln
 65 70 75 80
 aat ctc cag atg cat aga aga cgt cac aaa gtt cca tgg aag ctt ctt
 288
 Asn Leu Gln Met His Arg Arg Arg His Lys Val Pro Trp Lys Leu Leu
 85 90 95
 aaa aga gac aac aac ata gag gtg aag aaa cga gtc tat gtt tgc cct
 336
 Lys Arg Asp Asn Asn Ile Glu Val Lys Lys Arg Val Tyr Val Cys Pro
 100 105 110
 gaa ccc act tgc ctt cac cat aat cct tgt cat gct ctg gga gat ctt
 384
 Glu Pro Thr Cys Leu His His Asn Pro Cys His Ala Leu Gly Asp Leu
 115 120 125
 gtc ggc atc aaa aaa cat ttc aga aga aaa cat agt aac cat aag caa
 432
 Val Gly Ile Lys Lys His Phe Arg Arg Lys His Ser Asn His Lys Gln
 130 135 140
 tgg gtt tgt gag aga tgc tct aaa ggt tat gct gtt caa tct gat tac
 480

Trp Val Cys Glu Arg Cys Ser Lys Gly Tyr Ala Val Gln Ser Asp Tyr
 145 150 155 160
 aaa gct cat ctc aaa act tgt ggt act aga gga cat tct tgt gac tgt
 528
 Lys Ala His Leu Lys Thr Cys Gly Thr Arg Gly His Ser Cys Asp Cys
 165 170 175
 ggt cgt gtc ttc tcc agg gtg gag agt ttt att gaa cat caa gat aat
 576
 Gly Arg Val Phe Ser Arg Val Glu Ser Phe Ile Glu His Gln Asp Asn
 180 185 190
 tgt tcc gca cgg aga gtt cac cgt gaa ccg cct cga cca cca caa acc
 624
 Cys Ser Ala Arg Arg Val His Arg Glu Pro Pro Arg Pro Pro Gln Thr
 195 200 205
 gcg gta aca gtc ccg gca tgc tct tct aga acc gcc tca acc gtc agc
 672
 Ala Val Thr Val Pro Ala Cys Ser Ser Arg Thr Ala Ser Thr Val Ser
 210 215 220
 act ccg tct agt gaa acc aat tac ggc ggt aca gtt gcg gtt acg act
 720
 Thr Pro Ser Ser Glu Thr Asn Tyr Gly Gly Thr Val Ala Val Thr Thr
 225 230 235 240
 cct caa cct cta gaa ggc cgt cca att cat cag aga atc tca tct tca
 768
 Pro Gln Pro Leu Glu Gly Arg Pro Ile His Gln Arg Ile Ser Ser Ser
 245 250 255
 att ctc acc aac tca tca aac aat ctc aac ctc gaa ctc caa ctt ctt
 816
 Ile Leu Thr Asn Ser Ser Asn Asn Leu Asn Leu Glu Leu Gln Leu Leu
 260 265 270
 cca tta tcg tcg aat caa aac cct aat caa gaa aac caa caa caa aaa
 864
 Pro Leu Ser Ser Asn Gln Asn Pro Asn Gln Glu Asn Gln Gln Gln Lys
 275 280 285
 gtt aaa gaa cca tct cat cat cat aat cat aat cat gat acc aca aac
 912
 Val Lys Glu Pro Ser His His His Asn His Asn His Asp Thr Thr Asn
 290 295 300
 tta aac ctc tcc att gca cca tca tca tca tat caa cat tac aac aac
 960
 Leu Asn Leu Ser Ile Ala Pro Ser Ser Ser Tyr Gln His Tyr Asn Asn
 305 310 315 320
 ttt gat cgt ata aaa gag att atg gcg agc gag caa att atg aag ata
 1008
 Phe Asp Arg Ile Lys Glu Ile Met Ala Ser Glu Gln Ile Met Lys Ile
 325 330 335
 gcg atg aag gag aaa gct tac gct gag gaa gct aaa aga gaa gcc aag
 1056
 Ala Met Lys Glu Lys Ala Tyr Ala Glu Glu Ala Lys Arg Glu Ala Lys

340 345 350
 agg caa cga gag ata gcg gaa aac gag ttt gca aat gcc aaa aag att
 1104
 Arg Gln Arg Glu Ile Ala Glu Asn Glu Phe Ala Asn Ala Lys Lys Ile
 355 360 365
 agg caa aaa gca caa gct gaa ctc gag aga gct aag ttt tta aag gaa
 1152
 Arg Gln Lys Ala Gln Ala Glu Leu Glu Arg Ala Lys Phe Leu Lys Glu
 370 375 380
 caa tct atg aag aag ata agt tca acg atc atg cag gtc act tgt caa
 1200
 Gln Ser Met Lys Lys Ile Ser Ser Thr Ile Met Gln Val Thr Cys Gln
 385 390 395 400
 aca tgt aaa gga cag ttt caa gca gtt gcg gtt ccg gcg gct acg gct
 1248
 Thr Cys Lys Gly Gln Phe Gln Ala Val Ala Val Pro Ala Ala Thr Ala
 405 410 415
 gat gag acg tct ctt gtc gtg agt tac atg tcg tca gcg aat act gac
 1296
 Asp Glu Thr Ser Leu Val Val Ser Tyr Met Ser Ser Ala Asn Thr Asp
 420 425 430
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 Gly Glu Leu Glu Asn Gly Phe
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 35 40 45
 Pro Asp Ala Glu Val Val Ser Leu Ser Pro Arg Thr Leu Leu Glu Ser
 50 55 60
 Asp Arg Tyr Ile Cys Glu Ile Cys Asn Gln Gly Phe Gln Arg Asp Gln
 65 70 75 80
 Asn Leu Gln Met His Arg Arg Arg His Lys Val Pro Trp Lys Leu Leu
 85 90 95
 Lys Arg Asp Asn Asn Ile Glu Val Lys Lys Arg Val Tyr Val Cys Pro
 845

100 105 110
 Glu Pro Thr Cys Leu His His Asn Pro Cys His Ala Leu Gly Asp Leu
 115 120 125
 Val Gly Ile Lys Lys His Phe Arg Arg Lys His Ser Asn His Lys Gln
 130 135 140
 Trp Val Cys Glu Arg Cys Ser Lys Gly Tyr Ala Val Gln Ser Asp Tyr
 145 150 155 160
 Lys Ala His Leu Lys Thr Cys Gly Thr Arg Gly His Ser Cys Asp Cys
 165 170 175
 Gly Arg Val Phe Ser Arg Val Glu Ser Phe Ile Glu His Gln Asp Asn
 180 185 190
 Cys Ser Ala Arg Arg Val His Arg Glu Pro Pro Arg Pro Pro Gln Thr
 195 200 205
 Ala Val Thr Val Pro Ala Cys Ser Ser Arg Thr Ala Ser Thr Val Ser
 210 215 220
 Thr Pro Ser Ser Glu Thr Asn Tyr Gly Gly Thr Val Ala Val Thr Thr
 225 230 235 240
 Pro Gln Pro Leu Glu Gly Arg Pro Ile His Gln Arg Ile Ser Ser Ser
 245 250 255
 Ile Leu Thr Asn Ser Ser Asn Asn Leu Asn Leu Glu Leu Gln Leu Leu
 260 265 270
 Pro Leu Ser Ser Asn Gln Asn Pro Asn Gln Glu Asn Gln Gln Gln Lys
 275 280 285
 Val Lys Glu Pro Ser His His His Asn His Asn His Asp Thr Thr Asn
 290 295 300
 Leu Asn Leu Ser Ile Ala Pro Ser Ser Ser Tyr Gln His Tyr Asn Asn
 305 310 315 320
 Phe Asp Arg Ile Lys Glu Ile Met Ala Ser Glu Gln Ile Met Lys Ile
 325 330 335
 Ala Met Lys Glu Lys Ala Tyr Ala Glu Glu Ala Lys Arg Glu Ala Lys
 340 345 350

Arg Gln Arg Glu Ile Ala Glu Asn Glu Phe Ala Asn Ala Lys Lys Ile
 355 360 365

Arg Gln Lys Ala Gln Ala Glu Leu Glu Arg Ala Lys Phe Leu Lys Glu
 370 375 380

Gln Ser Met Lys Lys Ile Ser Ser Thr Ile Met Gln Val Thr Cys Gln
 385 390 395 400

Thr Cys Lys Gly Gln Phe Gln Ala Val Ala Val Pro Ala Ala Thr Ala
 405 410 415

Asp Glu Thr Ser Leu Val Val Ser Tyr Met Ser Ser Ala Asn Thr Asp
 420 425 430

Gly Glu Leu Glu Asn Gly Phe
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 120

tctacatttt tgaagacgac cctgtggttg ataggttcaa taggtttggc acggag atg
 179

Met
 1

tct gcc atg gtc tcg gcc ttg aca cag gtg gtt tct gct cgc tct cag
 227

Ser Ala Met Val Ser Ala Leu Thr Gln Val Val Ser Ala Arg Ser Gln
 5 10 15

act gag gct gaa ggt gct cac tct cag act gag gct gaa ggt gct cac
 275

Thr Glu Ala Glu Gly Ala His Ser Gln Thr Glu Ala Glu Gly Ala His
 20 25 30

tct tct tcc tct tcg gct gga cat aaa aga gga tgg ctt gga atc gat
 323

Ser Ser Ser Ser Ser Ala Gly His Lys Arg Gly Trp Leu Gly Ile Asp
 35 40 45

tct gct cct att ccc tca tca ttt gct cgt gta gac tct tca cat aat
 371

Ser Ala Pro Ile Pro Ser Ser Phe Ala Arg Val Asp Ser Ser His Asn
 50 55 60 65

ccg atc gaa gaa tcc atg agc aag gca ttt cca gag gaa gca agg gag
 419
 Pro Ile Glu Glu Ser Met Ser Lys Ala Phe Pro Glu Glu Ala Arg Glu
 70 75 80

aaa aaa agg agg tac aga gga gta agg cag aga cca tgg ggc aaa tgg
 467
 Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp
 85 90 95

gca gct gag ata cgt gat cca cat aga gcc gct agg gtt tgg ctc ggg
 515
 Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala Arg Val Trp Leu Gly
 100 105 110

acg ttt gat aca gcg gag gcc gcg gct aga gcc tac gac gag gct gca
 563
 Thr Phe Asp Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Glu Ala Ala
 115 120 125

ctc cgg ttc cgt gga aat aaa gca aag cta aat ttc cca gag gat gta
 611
 Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asp Val
 130 135 140 145

agg att ctt cct cct ccc cct cct ctt ctt cgt tca cca gct gac acg
 659
 Arg Ile Leu Pro Pro Pro Pro Pro Leu Leu Arg Ser Pro Ala Asp Thr
 150 155 160

gtg gcg aat aaa gca gaa gag gat ctg ata aat tat tgg agt tat aca
 707
 Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn Tyr Trp Ser Tyr Thr
 165 170 175

aag ttg ttg caa agt tca ggc caa cgg tca ttt ctc gag cga gga caa
 755
 Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe Leu Glu Arg Gly Gln
 180 185 190

gaa gag agt agt aac ata ttt gaa cat tca cca atg gaa caa cct ctg
 803
 Glu Glu Ser Ser Asn Ile Phe Glu His Ser Pro Met Glu Gln Pro Leu
 195 200 205

cct cct tca agt tct ggt cca agt tcc tct aat ttt cct gca cct tct
 851
 Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn Phe Pro Ala Pro Ser
 210 215 220 225

cta cct aat aca tag tttcactttt attaaagctc tacaaataca attaaataca
 906
 Leu Pro Asn Thr

tagctaaatg aaaatgattt tcttgtctgt ataccttctt aagtgtctaaa caatatattg
 966

tactctttgt tttccttaac taataaaaaa aaaaaaaa aaa
 1009

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456

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Gln Thr Glu Ala Glu Gly Ala His Ser Gln Thr Glu Ala Glu Gly Ala
20 25 30

His Ser Ser Ser Ser Ser Ala Gly His Lys Arg Gly Trp Leu Gly Ile
35 40 45

Asp Ser Ala Pro Ile Pro Ser Ser Phe Ala Arg Val Asp Ser Ser His
50 55 60

Asn Pro Ile Glu Glu Ser Met Ser Lys Ala Phe Pro Glu Glu Ala Arg
65 70 75 80

Glu Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys
85 90 95

Trp Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala Arg Val Trp Leu
100 105 110

Gly Thr Phe Asp Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Glu Ala
115 120 125

Ala Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn Phe Pro Glu Asp
130 135 140

Val Arg Ile Leu Pro Pro Pro Pro Leu Leu Arg Ser Pro Ala Asp
145 150 155 160

Thr Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn Tyr Trp Ser Tyr
165 170 175

Thr Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe Leu Glu Arg Gly
180 185 190

Gln Glu Glu Ser Ser Asn Ile Phe Glu His Ser Pro Met Glu Gln Pro
195 200 205

Leu Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn Phe Pro Ala Pro
210 215 220

Ser Leu Pro Asn Thr

225

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 Met Gly Arg Gln Pro Cys Cys Asp Lys Leu Met Val Lys Lys Gly Pro
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 tgg acg gcg gag gaa gac aag aaa ctg ata aac ttt atc ttg acc aac
 96
 Trp Thr Ala Glu Glu Asp Lys Lys Leu Ile Asn Phe Ile Leu Thr Asn
 20 25 30
 ggc cac tgt tgc tgg agg gct ttg ccg aag ctg gcc ggt ctc cgt cgc
 144
 Gly His Cys Cys Trp Arg Ala Leu Pro Lys Leu Ala Gly Leu Arg Arg
 35 40 45
 tgt ggg aag agc tgc cgt cta cgg tgg acc aat tat ctc cga cct gac
 192
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60
 ttg aag aga ggt ctt ctc tcc gac gcc gag gaa cag ctt gtc atc gac
 240
 Leu Lys Arg Gly Leu Leu Ser Asp Ala Glu Glu Gln Leu Val Ile Asp
 65 70 75 80
 ctt cat gct ctt ctc ggc aac aga tgg tcc aag atc gct gca aga tta
 288
 Leu His Ala Leu Leu Gly Asn Arg Trp Ser Lys Ile Ala Ala Arg Leu
 85 90 95
 cca gga aga aca gac aac gaa ata aaa aat cat tgg aat act cat atc
 336
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Thr His Ile
 100 105 110
 aag aag aag ctc ctt aag atg gaa atc gat cct tcg acc cat caa cct
 384
 Lys Lys Lys Leu Leu Lys Met Glu Ile Asp Pro Ser Thr His Gln Pro
 115 120 125
 tta aac aaa gta ttt acc gat aca aac tta gtc gat aaa tct gaa act
 432
 Leu Asn Lys Val Phe Thr Asp Thr Asn Leu Val Asp Lys Ser Glu Thr
 130 135 140
 tca tcg aaa gcc gac aat gta aat gat aat aaa atc gta gag atc gat
 480
 Ser Ser Lys Ala Asp Asn Val Asn Asp Asn Lys Ile Val Glu Ile Asp
 145 150 155 160
 ggg aca acg aca aat aca ata gat gat agc att atc act cat caa aat
 528
 Gly Thr Thr Thr Asn Thr Ile Asp Asp Ser Ile Ile Thr His Gln Asn
 165 170 175

agt tca aat gat gat tat gaa tta ctt ggt gat ata att cat aat tat
576

Ser Ser Asn Asp Asp Tyr Glu Leu Leu Gly Asp Ile Ile His Asn Tyr
180 185 190

gga gat tta ttt aat att cta tgg acc aac gat gaa cct cct cta gtc
624

Gly Asp Leu Phe Asn Ile Leu Trp Thr Asn Asp Glu Pro Pro Leu Val
195 200 205

gat gat gca tca tgg agc aat cat aac gtt ggt att gga gga aca gct
672

Asp Asp Ala Ser Trp Ser Asn His Asn Val Gly Ile Gly Gly Thr Ala
210 215 220

gca gtt gca gcc tca gac aag aac aac act gct gcc gag gaa gat ttc
720

Ala Val Ala Ala Ser Asp Lys Asn Asn Thr Ala Ala Glu Glu Asp Phe
225 230 235 240

ccg gaa aga tca ttt gaa aaa cag aac ggc gaa agt tgg atg ttc ttg
768

Pro Glu Arg Ser Phe Glu Lys Gln Asn Gly Glu Ser Trp Met Phe Leu
245 250 255

gat tat tgc caa gaa ttt ggt gtt gaa gat ttt ggg ttc gag tgt tac
816

Asp Tyr Cys Gln Glu Phe Gly Val Glu Asp Phe Gly Phe Glu Cys Tyr
260 265 270

cat ggt ttt ggt caa agc tcc atg aag acg ggt cac aag gac tag
861

His Gly Phe Gly Gln Ser Ser Met Lys Thr Gly His Lys Asp
275 280 285

<210> 458 <211> 286 <212> PRT <213> Arabidopsis thaliana <400>
458

Met Gly Arg Gln Pro Cys Cys Asp Lys Leu Met Val Lys Lys Gly Pro
1 5 10 15

Trp Thr Ala Glu Glu Asp Lys Lys Leu Ile Asn Phe Ile Leu Thr Asn
20 25 30

Gly His Cys Cys Trp Arg Ala Leu Pro Lys Leu Ala Gly Leu Arg Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Leu Leu Ser Asp Ala Glu Glu Gln Leu Val Ile Asp
65 70 75 80

Leu His Ala Leu Leu Gly Asn Arg Trp Ser Lys Ile Ala Ala Arg Leu

85 90 95
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Thr His Ile
 100 105 110
 Lys Lys Lys Leu Leu Lys Met Glu Ile Asp Pro Ser Thr His Gln Pro
 115 120 125
 Leu Asn Lys Val Phe Thr Asp Thr Asn Leu Val Asp Lys Ser Glu Thr
 130 135 140
 Ser Ser Lys Ala Asp Asn Val Asn Asp Asn Lys Ile Val Glu Ile Asp
 145 150 155 160
 Gly Thr Thr Thr Asn Thr Ile Asp Asp Ser Ile Ile Thr His Gln Asn
 165 170 175
 Ser Ser Asn Asp Asp Tyr Glu Leu Leu Gly Asp Ile Ile His Asn Tyr
 180 185 190
 Gly Asp Leu Phe Asn Ile Leu Trp Thr Asn Asp Glu Pro Pro Leu Val
 195 200 205
 Asp Asp Ala Ser Trp Ser Asn His Asn Val Gly Ile Gly Gly Thr Ala
 210 215 220
 Ala Val Ala Ala Ser Asp Lys Asn Asn Thr Ala Ala Glu Glu Asp Phe
 225 230 235 240
 Pro Glu Arg Ser Phe Glu Lys Gln Asn Gly Glu Ser Trp Met Phe Leu
 245 250 255
 Asp Tyr Cys Gln Glu Phe Gly Val Glu Asp Phe Gly Phe Glu Cys Tyr
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 275 280 285
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 120

tcgattctga ttttttttca aggtcaattt tttcttctct ttaaactctg caaaatcgtg
180

atcgattaaa ttcacctcag ggttttttga tttctgaaag aagttaatct ttttcgaagg
240

cgattgcaaa agagtgtctct gctgtgaatt tccactgag atg caa tca aaa ccg
294

Met Gln Ser Lys Pro
1 5

gga aga gaa aac gaa gag gaa gtc aat aat cac cat gct gtt cag cag
342

Gly Arg Glu Asn Glu Glu Val Asn Asn His His Ala Val Gln Gln
10 15 20

ccg atg atg tat gca gag ccc tgg tgg aaa aac aac tcc ttt ggt gtt
390

Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn Asn Ser Phe Gly Val
25 30 35

gta cct caa gcg aga cct tct gga att cca tca aat tcc tct tct ttg
438

Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser Asn Ser Ser Ser Leu
40 45 50

gat tgc ccc aat ggt tcc gag tca aac gat gtt cat tca gca tct gaa
486

Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val His Ser Ala Ser Glu
55 60 65

gac ggt gcg ttg aat ggt gaa aac gat ggc act tgg aag gat tca caa
534

Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr Trp Lys Asp Ser Gln
70 75 80 85

gct gca act tcc tct cgt tca gat aat cac gga atg gaa gga aat gac
582

Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly Met Glu Gly Asn Asp
90 95 100

cca gcg ctc tct atc cgt aac atg cat gat cag cca ctt gta caa cca
630

Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln Pro Leu Val Gln Pro
105 110 115

cca gag ctt gtt gga cac tat atc gct tgt gtc cca aac cca tat cag
678

Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val Pro Asn Pro Tyr Gln
120 125 130

gat cca tat tat ggg gga ttg atg gga gca tat ggt cat cag caa ttg
726

Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr Gly His Gln Gln Leu
135 140 145

ggt ttt cgt cca tat ctt gga atg cct cgt gaa aga aca gct ctg cca
774

Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu Arg Thr Ala Leu Pro
150 155 160 165

ctt gac atg gca caa gag ccc gtt tat gtg aat gca aag cag tac gag
 822
 Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn Ala Lys Gln Tyr Glu
 170 175 180

gga att cta agg cga aga aaa gca cgt gcc aag gca gag cta gag agg
 870
 Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys Ala Glu Leu Glu Arg
 185 190 195

aaa gtc atc cgg gac aga aag cca tat ctt cac gag tca aga cac aag
 918
 Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His Glu Ser Arg His Lys
 200 205 210

cat gca atg aga agg gca cga gcg agt gga ggc cgg ttt gcg aag aaa
 966
 His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly Arg Phe Ala Lys Lys
 215 220 225

agt gag gta gaa gcg gga gag gat gca gga ggg aga gac aga gaa agg
 1014
 Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly Arg Asp Arg Glu Arg
 230 235 240 245

ggt tca gca acc aac tca tca ggc tct gaa caa gtt gag aca gac tct
 1062
 Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln Val Glu Thr Asp Ser
 250 255 260

aat gag acc ctg aat tct tct ggt gca cca taa taaaaaaagc caaagctctg
 1115
 Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro
 265 270

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 1175

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ggtttaacag ttatgatgaa tgtacaaaga gcgagttatg ttaggtgtta gattttggag
 1295

acaagagaca aaggaatagc aagtaggtct tgtttttatt ctttgacctt ttttttctct
 1355

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 1388

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His Ala Val Gln Gln Pro Met Met Tyr Ala Glu Pro Trp Trp Lys Asn
 20 25 30

Asn Ser Phe Gly Val Val Pro Gln Ala Arg Pro Ser Gly Ile Pro Ser
35 40 45

Asn Ser Ser Ser Leu Asp Cys Pro Asn Gly Ser Glu Ser Asn Asp Val
50 55 60

His Ser Ala Ser Glu Asp Gly Ala Leu Asn Gly Glu Asn Asp Gly Thr
65 70 75 80

Trp Lys Asp Ser Gln Ala Ala Thr Ser Ser Arg Ser Asp Asn His Gly
85 90 95

Met Glu Gly Asn Asp Pro Ala Leu Ser Ile Arg Asn Met His Asp Gln
100 105 110

Pro Leu Val Gln Pro Pro Glu Leu Val Gly His Tyr Ile Ala Cys Val
115 120 125

Pro Asn Pro Tyr Gln Asp Pro Tyr Tyr Gly Gly Leu Met Gly Ala Tyr
130 135 140

Gly His Gln Gln Leu Gly Phe Arg Pro Tyr Leu Gly Met Pro Arg Glu
145 150 155 160

Arg Thr Ala Leu Pro Leu Asp Met Ala Gln Glu Pro Val Tyr Val Asn
165 170 175

Ala Lys Gln Tyr Glu Gly Ile Leu Arg Arg Arg Lys Ala Arg Ala Lys
180 185 190

Ala Glu Leu Glu Arg Lys Val Ile Arg Asp Arg Lys Pro Tyr Leu His
195 200 205

Glu Ser Arg His Lys His Ala Met Arg Arg Ala Arg Ala Ser Gly Gly
210 215 220

Arg Phe Ala Lys Lys Ser Glu Val Glu Ala Gly Glu Asp Ala Gly Gly
225 230 235 240

Arg Asp Arg Glu Arg Gly Ser Ala Thr Asn Ser Ser Gly Ser Glu Gln
245 250 255

Val Glu Thr Asp Ser Asn Glu Thr Leu Asn Ser Ser Gly Ala Pro
260 265 270

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cacacagatt ccttccttca tcacctcaca cactctctac gcttgac atg gcc ttc
 116

Met Ala Phe
 1

gat ctc cac cat ggc tca gct tca gat acg cat tca tca gaa ctt ccg
 164

Asp Leu His His Gly Ser Ala Ser Asp Thr His Ser Ser Glu Leu Pro
 5 10 15

tcg ttt tct ctc cca cct tat cct cag atg ata atg gaa gcg att gag
 212

Ser Phe Ser Leu Pro Pro Tyr Pro Gln Met Ile Met Glu Ala Ile Glu
 20 25 30 35

tcc ttg aac gat aag aac ggc tgc aac aaa acg acg att gct aag cac
 260

Ser Leu Asn Asp Lys Asn Gly Cys Asn Lys Thr Thr Ile Ala Lys His
 40 45 50

atc gag tcg act caa caa act cta ccg ccg tca cac atg acg ctg ctc
 308

Ile Glu Ser Thr Gln Gln Thr Leu Pro Pro Ser His Met Thr Leu Leu
 55 60 65

agc tac cat ctc aac cag atg aag aaa acc ggt cag cta atc atg gtg
 356

Ser Tyr His Leu Asn Gln Met Lys Lys Thr Gly Gln Leu Ile Met Val
 70 75 80

aag aac aat tat atg aaa cca gat cca gat gct cct cct aag cgt ggt
 404

Lys Asn Asn Tyr Met Lys Pro Asp Pro Asp Ala Pro Pro Lys Arg Gly
 85 90 95

cgt ggc cgt cct ccg aag cag aag act cag gcc gaa tct gac gcc gct
 452

Arg Gly Arg Pro Pro Lys Gln Lys Thr Gln Ala Glu Ser Asp Ala Ala
 100 105 110 115

gct gct gct gtt gtt gct gcc acc gtc gtc tct aca gat ccg cct aga
 500

Ala Ala Ala Val Val Ala Ala Thr Val Val Ser Thr Asp Pro Pro Arg
 120 125 130

tct cgt ggc cgt cca ccg aag ccg aaa gat cca tcg gag cct ccc cag
 548

Ser Arg Gly Arg Pro Pro Lys Pro Lys Asp Pro Ser Glu Pro Pro Gln
 135 140 145

gag aag gtc att acc gga tct gga agg cca cga gga cga cca ccg aag
 596

Glu Lys Val Ile Thr Gly Ser Gly Arg Pro Arg Gly Arg Pro Pro Lys
 150 155 160

aga ccg aga aca gat tcg gag acg gtt gct gcg ccg gaa ccg gca gct
644

Arg Pro Arg Thr Asp Ser Glu Thr Val Ala Ala Pro Glu Pro Ala Ala
165 170 175

cag gcg aca ggt gag cgt agg gga cgt ggg aga cct ccg aag gtg aag
692

Gln Ala Thr Gly Glu Arg Arg Gly Arg Gly Arg Pro Pro Lys Val Lys
180 185 190 195

ccg acg gtg gtt gct ccg gtt ggg tgc tga attaatacggg acttatgcaa
742

Pro Thr Val Val Ala Pro Val Gly Cys
200

tttcggaatc tttagttact gaaaaatgga atctcttaga gagtaagaga gtgctttaat
802

ttagcttaat tagatttatt tggatttctt tcagtatttg gattgtaaac tttagaattt
862

gtgtgtgtgt tgttgcttag tcctgagata agatataaca ttagcgactg tgtattatta
922

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982

a
983

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462

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20 25 30

Ala Ile Glu Ser Leu Asn Asp Lys Asn Gly Cys Asn Lys Thr Thr Ile
35 40 45

Ala Lys His Ile Glu Ser Thr Gln Gln Thr Leu Pro Pro Ser His Met
50 55 60

Thr Leu Leu Ser Tyr His Leu Asn Gln Met Lys Lys Thr Gly Gln Leu
65 70 75 80

Ile Met Val Lys Asn Asn Tyr Met Lys Pro Asp Pro Asp Ala Pro Pro
85 90 95

Lys Arg Gly Arg Gly Arg Pro Pro Lys Gln Lys Thr Gln Ala Glu Ser
100 105 110

Asp Ala Ala Ala Ala Val Val Ala Ala Thr Val Val Ser Thr Asp
115 120 125

Pro Pro Arg Ser Arg Gly Arg Pro Pro Lys Pro Lys Asp Pro Ser Glu
130 135 140

Pro Pro Gln Glu Lys Val Ile Thr Gly Ser Gly Arg Pro Arg Gly Arg
145 150 155 160

Pro Pro Lys Arg Pro Arg Thr Asp Ser Glu Thr Val Ala Ala Pro Glu
165 170 175

Pro Ala Ala Gln Ala Thr Gly Glu Arg Arg Gly Arg Gly Arg Pro Pro
180 185 190

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gct gtt tcc gcc gat ctt tcc ttt ggt gct ccc ctc tat gtg gtt gag
96

Ala Val Ser Ala Asp Leu Ser Phe Gly Ala Pro Leu Tyr Val Val Glu
20 25 30

agc atg tgc atg cgc tgc caa gaa aat gga aca acc aga ttt cta ttg
144

Ser Met Cys Met Arg Cys Gln Glu Asn Gly Thr Thr Arg Phe Leu Leu
35 40 45

acc tta att cct cac ttc aga aag gtc tta ata tct gca ttt gaa tgt
192

Thr Leu Ile Pro His Phe Arg Lys Val Leu Ile Ser Ala Phe Glu Cys
50 55 60

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240

Pro His Cys Gly Glu Arg Asn Asn Glu Val Gln Phe Ala Gly Glu Ile
65 70 75 80

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288

Gln Pro Arg Gly Cys Cys Tyr Asn Leu Glu Val Leu Ala Gly Asp Val
85 90 95

aag ata ttt gac cgg caa gtt gtg aaa tct gaa tca gcc act att aag
336
Lys Ile Phe Asp Arg Gln Val Val Lys Ser Glu Ser Ala Thr Ile Lys
100 105 110

att cct gaa ctg gat ttt gag att cca cca gag gcc caa cgt gga agt
384
Ile Pro Glu Leu Asp Phe Glu Ile Pro Pro Glu Ala Gln Arg Gly Ser
115 120 125

ttg tct act gtg gaa ggg ata tta gca cgg gct gct gat gaa ctg agt
432
Leu Ser Thr Val Glu Gly Ile Leu Ala Arg Ala Ala Asp Glu Leu Ser
130 135 140

gcc ctt caa gaa gaa cgc aag aaa gtt gat cct aaa act gct gaa gca
480
Ala Leu Gln Glu Glu Arg Lys Lys Val Asp Pro Lys Thr Ala Glu Ala
145 150 155 160

ata gac caa ttc ttg tcc aaa ctg aga gct tgt gct aaa gca gag aca
528
Ile Asp Gln Phe Leu Ser Lys Leu Arg Ala Cys Ala Lys Ala Glu Thr
165 170 175

tcc ttc acc ttc att ttg gat gat cct gct gga aac agt ttc att gag
576
Ser Phe Thr Phe Ile Leu Asp Asp Pro Ala Gly Asn Ser Phe Ile Glu
180 185 190

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624
Asn Pro His Ala Pro Ser Pro Asp Pro Ser Leu Thr Ile Lys Phe Tyr
195 200 205

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672
Glu Arg Thr Pro Glu Gln Gln Ala Thr Leu Gly Tyr Val Ala Asn Pro
210 215 220

tct cag gct gga caa tca gaa gga agc ctt ggc gca cct gtg atg act
720
Ser Gln Ala Gly Gln Ser Glu Gly Ser Leu Gly Ala Pro Val Met Thr
225 230 235 240

ttc cct tca act tgc gga gca tgt acg gag ccg tgt gag aca cgg atg
768
Phe Pro Ser Thr Cys Gly Ala Cys Thr Glu Pro Cys Glu Thr Arg Met
245 250 255

ttc aaa ata gaa atc ccg tac ttt cag gaa gtt att gtc atg gca tct
816
Phe Lys Ile Glu Ile Pro Tyr Phe Gln Glu Val Ile Val Met Ala Ser
260 265 270

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864
Thr Cys Asp Ser Cys Gly Tyr Arg Asn Ser Glu Leu Lys Pro Gly Gly
275 280 285

gca att cct gaa aag gga aag aag att act ctc tct gtg agg aac att
912

Ala Ile Pro Glu Lys Gly Lys Lys Ile Thr Leu Ser Val Arg Asn Ile
290 295 300

aca gac ctt agc cga gat gtt atc aag tcg gac act gca gga gtg ata
960

Thr Asp Leu Ser Arg Asp Val Ile Lys Ser Asp Thr Ala Gly Val Ile
305 310 315 320

atc cca gaa ctt gat ctg gag cta gct ggt ggt aca ctt ggt gga atg
1008

Ile Pro Glu Leu Asp Leu Glu Leu Ala Gly Gly Thr Leu Gly Gly Met
325 330 335

gta aca aca gtt gaa ggg ttg gtt aca cag atc aga gaa agc cta gcg
1056

Val Thr Thr Val Glu Gly Leu Val Thr Gln Ile Arg Glu Ser Leu Ala
340 345 350

aga gtt cac gga ttc act ttt ggt gat agt atg gaa gag agt aag ttg
1104

Arg Val His Gly Phe Thr Phe Gly Asp Ser Met Glu Glu Ser Lys Leu
355 360 365

aac aaa tgg aga gaa ttt gga gcc agg ctc act aag ctc cta agc ttt
1152

Asn Lys Trp Arg Glu Phe Gly Ala Arg Leu Thr Lys Leu Leu Ser Phe
370 375 380

gaa cag ccg tgg aca ttg att ctt gat gat gaa tta gca aat tcc ttt
1200

Glu Gln Pro Trp Thr Leu Ile Leu Asp Asp Glu Leu Ala Asn Ser Phe
385 390 395 400

att gca cca gta aca gat gat atc aaa gat gac cat cag ctc aca ttt
1248

Ile Ala Pro Val Thr Asp Asp Ile Lys Asp Asp His Gln Leu Thr Phe
405 410 415

gaa gag tac gag agg tca tgg gat caa aac gag gag ttg ggt ctc aac
1296

Glu Glu Tyr Glu Arg Ser Trp Asp Gln Asn Glu Glu Leu Gly Leu Asn
420 425 430

gac ata gat act tct tca gct gat gct gct tat gaa tcc aca gag acg
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act aaa tta cct taa

1359

Thr Lys Leu Pro
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<210> 464 <211> 452 <212> PRT <213> Arabidopsis thaliana <400>
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 20 25 30

Ser Met Cys Met Arg Cys Gln Glu Asn Gly Thr Thr Arg Phe Leu Leu
 35 40 45

Thr Leu Ile Pro His Phe Arg Lys Val Leu Ile Ser Ala Phe Glu Cys
 50 55 60

Pro His Cys Gly Glu Arg Asn Asn Glu Val Gln Phe Ala Gly Glu Ile
 65 70 75 80

Gln Pro Arg Gly Cys Cys Tyr Asn Leu Glu Val Leu Ala Gly Asp Val
 85 90 95

Lys Ile Phe Asp Arg Gln Val Val Lys Ser Glu Ser Ala Thr Ile Lys
 100 105 110

Ile Pro Glu Leu Asp Phe Glu Ile Pro Pro Glu Ala Gln Arg Gly Ser
 115 120 125

Leu Ser Thr Val Glu Gly Ile Leu Ala Arg Ala Ala Asp Glu Leu Ser
 130 135 140

Ala Leu Gln Glu Glu Arg Lys Lys Val Asp Pro Lys Thr Ala Glu Ala
 145 150 155 160

Ile Asp Gln Phe Leu Ser Lys Leu Arg Ala Cys Ala Lys Ala Glu Thr
 165 170 175

Ser Phe Thr Phe Ile Leu Asp Asp Pro Ala Gly Asn Ser Phe Ile Glu
 180 185 190

Asn Pro His Ala Pro Ser Pro Asp Pro Ser Leu Thr Ile Lys Phe Tyr
 195 200 205

Glu Arg Thr Pro Glu Gln Gln Ala Thr Leu Gly Tyr Val Ala Asn Pro
 210 215 220

Ser Gln Ala Gly Gln Ser Glu Gly Ser Leu Gly Ala Pro Val Met Thr
 225 230 235 240

Phe Pro Ser Thr Cys Gly Ala Cys Thr Glu Pro Cys Glu Thr Arg Met
 245 250 255

Phe Lys Ile Glu Ile Pro Tyr Phe Gln Glu Val Ile Val Met Ala Ser
 260 265 270

Thr Cys Asp Ser Cys Gly Tyr Arg Asn Ser Glu Leu Lys Pro Gly Gly
 275 280 285

Ala Ile Pro Glu Lys Gly Lys Lys Ile Thr Leu Ser Val Arg Asn Ile
 290 295 300

Thr Asp Leu Ser Arg Asp Val Ile Lys Ser Asp Thr Ala Gly Val Ile
 305 310 315 320

Ile Pro Glu Leu Asp Leu Glu Leu Ala Gly Gly Thr Leu Gly Gly Met
 325 330 335

Val Thr Thr Val Glu Gly Leu Val Thr Gln Ile Arg Glu Ser Leu Ala
 340 345 350

Arg Val His Gly Phe Thr Phe Gly Asp Ser Met Glu Glu Ser Lys Leu
 355 360 365

Asn Lys Trp Arg Glu Phe Gly Ala Arg Leu Thr Lys Leu Leu Ser Phe
 370 375 380

Glu Gln Pro Trp Thr Leu Ile Leu Asp Asp Glu Leu Ala Asn Ser Phe
 385 390 395 400

Ile Ala Pro Val Thr Asp Asp Ile Lys Asp Asp His Gln Leu Thr Phe
 405 410 415

Glu Glu Tyr Glu Arg Ser Trp Asp Gln Asn Glu Glu Leu Gly Leu Asn
 420 425 430

Asp Ile Asp Thr Ser Ser Ala Asp Ala Ala Tyr Glu Ser Thr Glu Thr
 435 440 445

Thr Lys Leu Pro
 450

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A01H 5/00; C12P 21/00; C12N 15/82
US CL : 435/69.1; 800/279, 281, 289, 290, 300, 301

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 435/69.1; 800/279, 281, 289, 290, 300, 301

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EAST, and SEQUENCE search of SEQ ID NOs: 1, 2, 3 and 4

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KRANZ, H.D. et al. Towards functional characterisation of the members of the R2R3-MYB gene family from Arabidopsis thaliana. The Plant Journal. 1998, Vol 16, No. 2, pages 263-276, see entire document.	1-5,7-22
X	ALLEN, M.D. et al. A novel mode of DNA recognition by a beta-sheet revealed by the solution structure of the GCC-box binding domain in complex with DNA. The EMBO Journal. 1998, Vol. 17, No. 18, pages 5484-5496, in particular page 5493, left column, section under Materials and Methods.	4,5
Y	SMALLE, J. et al. The trihelix DNA-binding motif in higher plants is not restricted to the transcription factors GT-1 and GT-2. Proc. Natl. Acad. Sci. USA. 1998, Vol. 95, pages 3318-3322, see entire document, in particular Fig. 1A on page 3319.	1-3,7-22
X		4,5
Y		1-3,7-22
X,P	Database NCBI on WEST, AN BE522812. WHITE, J.A. et al. 'A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil. Plant Physiol. 124,(4), 1582-1594. NCBI-Genbank (National Library of Medicine, Bethesda, MD), submitted 19 March 2001.	4
Y,P		1-3,5,7-22

☒ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

27 November 2001 (27.11.2001)

Date of mailing of the international search report

16 JAN 2002

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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Authorized officer
David H Kruse

Telephone No. 703-308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	OHME-TAKAGI, M. et al. Ethylene-inducible DNA binding proteins that interact with an ethylene-responsive element. The Plant Cell.	4,5
—		-----
Y	February 1995, Vol. 7, pages 173-182, see entire document.	1-3,7-22
A	BLOMAA, P. et al. Transformation of antisense constructs of the chalcone synthase gene superfamily into Gerbera hybrida: differential effect on the expression of family members. Molecular Breeding 1996, Vol. 2, pages 41-50, see entire document.	1-5,7-22
A	QUATTROCCHIO, F. et al. Analysis of bHLH and MYB domain proteins: species-specific regulatory differences are caused by divergent evolution of target anthocyanin genes. The Plant Journal. 1998, Vol. 13, No. 4, pages 475-488, see entire document.	1-5,7-22

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claim Nos.: 52-70
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Please See Continuation Sheet
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: Please See Continuation Sheet
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☒
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/26189

Continuation of Box I Reason 2:

Claims 52-60 constitute unsearchable subject matter under PCT Rule 39.1(iii) as a process of thought or a business method and claims 61-70 constitute unsearchable subject matter under PCT Rule 39.1(v) a mere presentation of information.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

Groups 1-232, claim(s) 1-5, 7-22 and 44-47 (Group 1 is claims 1-5, 7-22 and 44-47 and SEQ ID NOS: 1 & 2, Group 2 is claims 1-5, 7-22 and 44-47 and SEQ ID NOS: 3 & 4, etc), drawn to an isolated or recombinant polynucleotide, transgenic plants comprising said polynucleotide and a method of making said transgenic plant.

Groups 233-465, claim(s) 6 and 34-43 (Group 233 is claims 6 and 34-43 and SEQ ID NOS: 1 & 2, Group 234 is claims 6 and 34-43 and SEQ ID NOS: 3 & 4, etc), drawn to an isolated or recombinant polypeptide.

Groups 466-698, claim(s) 23-33 (Group 466 is claims 23-33 and SEQ ID NOS: 1 & 2, Group 467 is claims 23-33 and SEQ ID NOS: 3 & 4, etc), drawn to a method comprising expressing an antisense nucleic acid in a transformed plant and the plant produced by said method.

Groups 699-931, claim(s) 48-51 (Group 699 is claims 48-51 and SEQ ID NOS: 1 & 2, Group 700 is claims 48-51 and SEQ ID NOS: 3 & 4, etc), drawn to a computer readable medium.

The inventions listed as Groups 1-931 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The isolated polynucleotide is anticipated by the prior art because Applicant's SEQ ID NO: 66 is 99% identical to the MYB12 disclosed by Kranz *et al* (1998, The Plant Journal, 16(2):263-278). Because Applicant has claimed an isolated polynucleotide encoding a polypeptide having at least anywhere from 31-95% sequence identity outside of a conserved domain of the polypeptide of SEQ ID NO: 66 and an isolated polypeptide having at least 31-95% sequence identity over the entire length of the polypeptide of SEQ ID NO: 66, the claimed invention has been anticipated by the prior art and thus Unity of Invention is lacking as required under PCT Rule 13.1 and it lacks a special technical feature as required under PCT Rule 13.2.

2. Claims 52-60 constitute unsearchable subject matter under PCT Rule 39.1(iii) as a process of thought or a business method and Claims 61-70 constitute unsearchable subject matter under PCT Rule 39.1(v) as mere presentation of information.

Continuation of Box II Item 3:

1-5,7-22,44-45 and SEQ ID NOs. 1,2,3,4

Claims 46 and 47 were not searched because no additional fees were paid for the inventions to which the claims are directed.